

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840152	9555	31711	681	226

Description

6500730231 ampd:b0110 ampd protein (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b0110 b0110 Escherichia coli 562 -11534089 304546 ampd (de:ampd protein) (db:swissprot) AMPD_ECOLI P13016 ESCHERICHIA COLI 562 -11534089 162731 ampd signalling protein ampd (db:pir2.dat) (mp:2.6 min) S05569 S05569 Escherichia coli 562 -11534089 233652 (db:genpept-bct1) (de:e.coli genes for ampd and ampe for put. signalling proteins inbeta-lactamase regulation.) (nt:ampd protein (aa 1-183)) (le:435) (re:986) (di:direct) ECAMPDE X15237 g40908 Escherichia coli 562 -11534089 301590 ampd ampd signalling protein (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:7456) (re:8007) (di:direct) ECO82K D26562 g473779 Escherichia coli 562 -11534089 232351 ampd regulates ampC (fn:regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 10 of 400 of the completegenome.) (nt:ol83; 100 pct identical to ampd_ecoli sw: p13016) (le:1113) (re:1664) (di:direct) AE000120 AE000120 g1786300 Escherichia coli 562 -11534089 5000691314 (db:genpept) (de:e.coli genes for ampd and ampe for put. signalling proteins inbeta-lactamase regulation.) (nt:ampd protein (aa 1-183)) (le:435) (re:986) (di:direct) ECAMPDE X15237 g40908 Escherichia coli 562 -11534089 59361 ampd (de:ampd protein) (db:swissprot) AMPD_ECOLI P13016 ESCHERICHIA COLI 562 -11534089

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840154	9556	31712	192	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840157	9557	31713	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840160	9558	31714	699	232

Description

GTC ORF with score 167 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t19118 genomic sequence, complete sequence.) (nt:hypothetical protein) (le:13028:13438:13658) (re:13137:13642:13791) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840173	9559	31715	399	132

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840174	9560	31716	750	249

Description

6500730232 ampe:b0111 ampe protein (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b0111 b0111 Escherichia coli 562 -11534090 304547 ampe (de:ampe protein) (db:swissprot) AMPE_ECOLI P13017 ESCHERICHIA COLI 562 -11534090 164618 ampe signalling protein ampe (db:pir2.dat) (mp:2.6 min) S05570 S05570 Escherichia coli 562 -11534090 233653 (db:genpept-bct1) (de:e.coli genes for ampd and ampe for put. signalling proteins inbeta-lactamase regulation.) (nt:ampe protein (aa 1-284)) (le:983) (re:1837) (di:direct) ECAMPDE X15237 g40909 Escherichia coli 562 -11534090 301591 ampe ampe signalling protein (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara')) (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (le:8004) (re:8858) (di:direct) ECO82K D26562 g473780 Escherichia coli 562 -11534090 232352 ampe regulates ampc (fn:regulator; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 10 of 400 of the completegenome.) (nt:o284; 100 pct identical to ampe_ecoli sw: p13017) (le:1661) (re:2515) (di:direct) AE000120 AE000120 g1786301 Escherichia coli 562 -11534090 5000691315 (db:genpept) (de:e.coli genes for ampd and ampe for put. signalling proteins inbeta-lactamase regulation.) (nt:ampe protein (aa 1-284)) (le:983) (re:1837) (di:direct) ECAMPDE X15237 g40909 Escherichia coli 562 -11534090 59364 ampe (de:ampe protein) (db:swissprot) AMPE_ECOLI P13017 ESCHERICHIA COLI 562 -11534090

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840178	9561	31717	555	184

Description

6500730233 ampg:b0433 ampg protein (gtcfc:13.3) (keggfc:14.2)
(rileyfc:5.4.0) (db:gtc-escherichia coli) b0433 b0433 Escherichia coli 562
-11534091 59368 ampg (de:ampg protein) (db:swissprot) AMPG_ECOLI P36670
ESCHERICHIA COLI 562 -11534091 162732 ampg signal transducer ampg
(db:pir2.dat) (mp:9.6 min) S37391 S37391 Escherichia coli 562 -11534091
258635 ampg beta-lactamase induction signal transducer ampg
(db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.)
(le:31520) (re:32995) (di:complement) ECU82664 U82664 g1773117 Escherichia
coli 562 -11534091 7500876836 ampg ampg (sr:escherichia coli sno301)
(db:genpept-bct1) (de:ampg region: bola=carboxypeptidase regulator...cyoa=35
kdalipoprotein (escherichia coli, sno301, genomic, 4 genes, 3100 nt).)
(nt:beta-lactamase induction signal transducer; 53 kda.) (le:971)
(re:2446)... S67816 S67816 g459277 Escherichia coli 562 -11534091 240210
ampg regulates beta-lactamase synthesis (fn:regulator; drug/analog
sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 39
of 400 of the completegenome.) (nt:f491; 100 pct identical to ampg_ecoli sw:
p36670) (le:7510) (re:8985) (di:complement) AE000149 AE000149 g1786636
Escherichia coli 562 -11534091 5000691316 (de:(ecoli_417) (pn:regulates
beta-lactamase synthesis) (gn:ampg) (gtcfc:13.3) (ec:) (ampg_ecoli)
(keggfc:11.2) (rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_417 ECOLI_417
Escherichia coli 562 10002105

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840189	9562	31718	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840193	9563	31719	213	70

Description

6500730234 acrb:acre:b0462 acriflavin resistance protein b (gtcfc:11.1:13.3) (keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b0462 b0462
 Escherichia coli 562 -11534092 58292 acrb:acre (de:acriflavin resistance protein b) (db:swissprot) ACRB_ECOLI P31224 ESCHERICHIA COLI 562 -11534092 164404 acrb:acre acriflavin resistance protein acrb:probable transmembrane protein acre (cl:acriflavin resistance protein) (db:pir2.dat) B36938 B36938
 Escherichia coli 562 -11534092 238443 acrb acriflavine resistance protein (fn:resistance to acriflavine, hydrophobic) (sr:escherichia coli (strain k-12) (library: clarke-carbon) dna) (db:genpept-bct1) (de:e. coli acriflavine resistance proteins (acra and acrb) genes,complete cds.) (le:1545) (re:4694) (di:direct) ECOACRAB M94248 g290406 Escherichia coli 562 -11534092 240237 acrb 114 kda protein (fn:putative transporter protein) (db:genpept-bct1) (de:escherichia coli acra, acrb, and acrr genes, complete cds.) (nt:formally called acre; hydropathy plot suggests that) (le:2312) (re:5461) (di:direct) ECU00734 U00734 g532311 Escherichia coli 562 -11534092 7500876373 acre probable transmembrane protein acre (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:60702) (re:63851) (di:complement) ECU82664 U82664 g1773144 Escherichia coli 562 -11534092 233716 acrb acridine efflux pump (fn:transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 42 of 400 of the completegenome.) (nt:f1049; 100 pct identical to acrb_ecoli sw: p31224) (le:4668) (re:7817) (di:complement) AE000152 AE000152 g1786667 Escherichia coli 562 -11534092 5000691317 (de:(ecoli_445) (pn:acridine efflux pump) (gn:acrb) (gtcfc:13.3) (ec:) (acrb_ecoli) (keggfc:11.2) (rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_445 ECOLI_445 Escherichia coli 562 10001072

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840208	9564	31720	2217	738

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840210	9565	31721	549	182

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840216	9566	31722	672	223

Description

6500730235 teha:b1429 tellurite resistance protein teha (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b1429 b1429 Escherichia coli 562 -11534093 100990 teha (de:tellurite resistance protein teha) (db:swissprot) TEHA_ECOLI P25396 ESCHERICHIA COLI 562 -11534093 164998 teha tellurite resistance protein teha (db:pir2.dat) H64894 H64894 Escherichia coli 562 -11534093 223734 teha tellurite resistance protein teha. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.)) (nt:orf_id:o271#1; similar to (swissprot accession) (le:8983) (re:9975) (di:direct) D90782 D90782 g1742336 Escherichia coli 562 -11534093 300499 teha (fn:confers resistance to potassium tellurite) (db:genpept-bct1) (de:escherichia coli tellurite-resistance (teha) and teh genes,complete cds.) (le:133) (re:1125) (di:direct) ECOTEHAB M74072 g149017 Escherichia coli 562 -11534093 236074 teha tellurite resistance (fn:transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 130 of 400 of the completegenome.) (nt:o330; 100 pct identical to teha_ecoli sw: p25396;) (le:1932) (re:2924) (di:direct) AE000240 AE000240 g1787699 Escherichia coli 562 -11534093 7000686774 teha teha protein (db:pir) JQ1017 JQ1017 Klebsiella pneumoniae 573 -11534093 5000691319 (de:(ecoli_1389) (pn:tellurite resistance) (gn:teha) (gtcfc:13.3) (ec:) (teha_ecoli) (keggfc:11.2) (rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_1389 ECOLI_1389 Escherichia coli 562 10042834

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840217	9567	31723	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840233	9568	31724	882	293

Description

6500730236 teh:b1430 tellurite resistance protein teh (gtcfc:13.3)
(keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b1430 b1430
Escherichia coli 562 -11534094 100992 teh (de:tellurite resistance protein
teh) (db:swissprot) TEHB_ECOLI P25397 ESCHERICHIA COLI 562 -11534094
164999 teh tellurite resistance protein teh (db:pir2.dat) A64895 A64895
Escherichia coli 562 -11534094 223735 teh tellurite resistance protein
teh. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5
min.)) (nt:orf_id:o271#2; similar to (swissprot accession) (le:9972)
(re:10565) (di:direct) D90782 D90782 g1742337 Escherichia coli 562 -11534094
300500 teh (db:genpept-bct1) (de:escherichia coli tellurite-resistance
(teha) and teh genes,complete cds.) (le:1122) (re:1715) (di:direct)
ECOTEHAB M74072 g149018 Escherichia coli 562 -11534094 236075 teh
tellurite resistance (fn:putative transport; drug/analog sensitivity)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 130 of 400 of the
completegenome.) (nt:o197; 100 pct identical to teh_ecoli sw: p25397;)
(le:2921) (re:3514) (di:direct) AE000240 AE000240 g1787700 Escherichia coli
562 -11534094 7000686775 teh teh protein (db:pir) JQ1018 JQ1018
Klebsiella pneumoniae 573 -11534094 5000691320 (de:(ecoli_1390)
(pn:tellurite resistance) (gn:teh) (gtcfc:13.3) (ec:) (teh_ecoli)
(keggfc:11.2) (rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_1390
ECOLI_1390 Escherichia coli 562 10042836

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840239	9569	31725	666	221

Description

6500730237 marr:soxq:cfxb:inar:b1530 multiple antibiotic resistance protein:multiple antibiotic resistance protein marr (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b1530 b1530 Escherichia coli 562 -11534095 82996 marr:soxq:cfxb:inar (de:multiple antibiotic resistance protein marr) (db:swissprot) MARR_ECOLI P27245 ESCHERICHIA COLI 562 -11534095 7000685790 marr transcription regulator marr:probable mar operator repressor marr (db:pir2.dat) E64907 E64907 Escherichia coli 562 -11534095 7500885326 marr multiple antibiotic resistance protein (db:genpept-bct1) (de:escherichia coli multiple antibiotic resistance protein (marc),multiple antibiotic resistance protein (marr), and multipleantibiotic resistance protein (mara) genes, complete cds.) (le:1503) (re:1880) (di:direct) ECOMARAR M96235 g146731 Escherichia coli 562 -11534095 235061 marr multiple antibiotic resistance protein (fn:regulator; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:ol25; 100 pct identical to marr_ecoli sw: p27245;) (le:8414) (re:8791) (di:direct) AE000250 AE000250 g1787810 Escherichia coli 562 -11534095 5000691321 (de:(ecoli_1490) (pn:multiple antibiotic resistance protein; repressor of mar operon) (gn:marr) (gtcfc:13.3) (ec:) (marr_ecoli) (keggfc:11.2) (rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_1490 ECOLI_1490 Escherichia coli 562 10025216

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840240	9570	31726	315	104

Description

6500730238 mara:b1531 multiple antibiotic resistance protein:multiple antibiotic resistance protein mara (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b1531 b1531 Escherichia coli 562 -11534096 82993 mara (de:multiple antibiotic resistance protein mara) (db:swissprot) MARA_ECOLI P27246 ESCHERICHIA COLI 562 -11534096 164396 mara probable transcription activator mara:multiple antibiotic resistance protein mara (db:pir2.dat) (mp:34 min) B47072 B47072 Escherichia coli 562 -11534096 223897 mara multiple antibiotic resistance protein mara. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #305(34.7-35.1 min.).) (nt:orf_id:o306#2; similar to (swissprot accession) (le:8715) (re:9104) (di:direct) D90796 D90796 g1742513 Escherichia coli 562 -11534096 223910 mara multiple antibiotic resistance protein mara. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #306(34.8-35.1 min.).) (nt:orf_id:o306#2; similar to (swissprot accession) (le:2164) (re:2553) (di:direct) D90797 D90797 g1742527 Escherichia coli 562 -11534096 300629 mara multiple antibiotic resistance protein (db:genpept-bct1) (de:escherichia coli multiple antibiotic resistance protein (marc),multiple antibiotic resistance protein (marr), and multipleantibiotic resistance protein (mara) genes, complete cds.) (le:1894) (re:2283) (di:direct) ECOMARAR M96235 g146732 Escherichia coli 562 -11534096 235062 mara multiple antibiotic resistance:transcriptional (fn:regulator; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:o129; 100 pct identical to mara_ecoli sw: p27246;) (le:8805) (re:9194) (di:direct) AE000250 AE000250 g1787811 Escherichia coli 562 -11534096 5000691322 (de:(ecoli_1491) (pn:multiple antibiotic resistance; transcriptional activator of defense systems) (gn:marar) (gtcfc:13.3) (ec:) (mara_ecoli) (keggfc:11.2) (rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_1491 ECOLI_1491 Escherichia coli 562 10025213

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840248	9571	31727	897	298

Description

6500730239 marb:b1532 multiple antibiotic resistance protein marb (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b1532 b1532 Escherichia coli 562 -11534097 82994 marb (de:multiple antibiotic resistance protein marb) (db:swissprot) MARB_ECOLI P31121 ESCHERICHIA COLI 562 -11534097 164037 marb marb protein (db:pir2.dat) C47072 C47072 Escherichia coli 562 -11534097 223898 marb marb protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #305(34.7-35.1 min.)) (nt:orf_id:o306#3; similar to (pir accession number) (le:9136) (re:9354) (di:direct) D90796 D90796 g1742514 Escherichia coli 562 -11534097 223911 marb marb protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #306(34.8-35.1 min.)) (nt:orf_id:o306#3; similar to (pir accession number) (le:2585) (re:2803) (di:direct) D90797 D90797 g1742528 Escherichia coli 562 -11534097 300630 marb multiple antibiotic resistance protein (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:o72; 100 pct identical to marb_ecoli sw: p31121; cg) (le:9226) (re:9444) (di:direct) AE000250 AE000250 g1787812 Escherichia coli 562 -11534097 5000691323 (de:(ecoli_1492) (pn:multiple antibiotic resistance protein) (gn:marb) (gtcfc:13.3) (ec:) (marb_ecoli) (keggfc:11.2) (rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_1492 ECOLI_1492 Escherichia coli 562 10025214

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840253	9572	31728	429	142

Description

6500730240 bcr:bica:bicr:sur:suxa:b2182 bicyclomycin resistance protein:sulfonamide resistance protein (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b2182 b2182 Escherichia coli 562 -11534098 7000690859 bcr bicyclomycin resistance protein (cl:bicyclomycin resistance protein) (db:pir2.dat) E64987 E64987 Escherichia coli 562 -11534098 7500955800 bcr bicyclomycin resistance protein:transmembrane (fn:transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 198 of 400 of the completegenome.) (nt:f396; 99 pct identical to bcr_ecoli sw: p28246) (le:197) (re:1387) (di:complement) AE000308 AE000308 g1788509 Escherichia coli 562 -11534098 5000691324 (de:(ecoli_2131) (pn:bicyclomycin resistance protein; transmembrane protein) (gn:bcr) (gtcfc:13.3) (ec:) (bcr_ecoli) (keggfc:11.2) (rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_2131 ECOLI_2131 Escherichia coli 562 10123594

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840254	9573	31729	594	197

Description

6500730241 emra:b2685 multidrug resistance protein a (gtcfc:13.3)
(keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b2685 b2685
Escherichia coli 562 -11534099 70128 emra (de:multidrug resistance protein
a) (db:swissprot) EMRA_ECOLI P27303 ESCHERICHIA COLI 562 -11534099
7000685152 emra multidrug resistance protein a (cl:multidrug resistance
protein a:lipoyl/biotin-binding homology) (db:pir2.dat) (mp:57.5 min) F65048
F65048 Escherichia coli 562 -11534099 225237 emra multidrug resistant
protein emra (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#445(60.2-60.6 min.)) (nt:similar to (pir accession number jcl344))
(le:14900) (re:16072) (di:direct) D90891 D90891 g1800070 Escherichia coli
562 -11534099 225242 emra multidrug resistant protein emra (sr:escherichia
coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #446(60.5-60.9 min.)) (nt:similar to
(pir accession number jcl344)) (le:334) (re:1506) (di:direct) D90892 D90892
g1800076 Escherichia coli 562 -11534099 7500881002 emra multidrug
resistance secretion protein (fn:transport; drug/analog sensitivity)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 243 of 400 of the
completegenome.) (nt:o390; 99 pct identical to emra_ecoli sw: p27303)
(le:1902) (re:3074) (di:direct) AE000353 AE000353 g1789041 Escherichia coli
562 -11534099 5000691325 (de:(ecoli_2618) (pn:multidrug resistance
secretion protein) (gn:emra) (gtcfc:13.3) (ec:) (emra_ecoli) (keggfc:11.2)
(rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_2618 ECOLI_2618 Escherichia
coli 562 10120321

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840264	9574	31730	846	281

Description

6500730242 emrb:b2686 multidrug resistance protein b (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.4.0) (db:gtc-escherichia coli) b2686 b2686 Escherichia coli 562 -11534100 70130 emrb (de:multidrug resistance protein b) (db:swissprot) EMRB_ECOLI P27304 ESCHERICHIA COLI 562 -11534100 7000685153 emrb multidrug resistance protein b (db:pir2.dat) (mp:57.5 min) G65048 G65048 Escherichia coli 562 -11534100 225238 emrb multidrug resistant protein emrb (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6 min.)) (nt:similar to (pir accession number jcl345)) (le:16089) (re:17627) (di:direct) D90891 D90891 g1800071 Escherichia coli 562 -11534100 225243 emrb multidrug resistant protein emrb (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #446(60.5-60.9 min.)) (nt:similar to (pir accession number jcl345)) (le:1523) (re:3061) (di:direct) D90892 D90892 g1800077 Escherichia coli 562 -11534100 7500881004 emrb multidrug resistance:probably membrane (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 243 of 400 of the completegenome.) (nt:o512; 99 pct identical to emrb_ecoli sw: p27304) (le:3091) (re:4629) (di:direct) AE000353 AE000353 g1789042 Escherichia coli 562 -11534100 5000691326 (de:(ecoli_2619) (pn:multidrug resistance; probably membrane translocase) (gn:emrb) (gtcfc:13.3) (ec:) (emrb_ecoli) (keggfc:11.2) (rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_2619 ECOLI_2619 Escherichia coli 562 10120322

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840279	9575	31731	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840288	9576	31732	675	224

Description

GTC ORF with score 122 to: (db:genpept-pln2) (de:emerella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj), (stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840291	9577	31733	762	254

Description

6500730243 baca:b3057 bacitracin resistance protein:putative undecaprenol kinase (gtcfc:13.3) (ec:2.7.1.66) (keggfc:14.1) (rileyfc:5.4.0) (db:gtc-escherichia coli) b3057 b3057 Escherichia coli 562 -11534101 61358 baca (ec:2.7.1.66) (de:(ec 2.7.1.66)) (db:swissprot) BACA_ECOLI P31054 ESCHERICHIA COLI 562 -11534101 7000684684 baca bacitracin resistance protein baca:probable undecaprenol kinase (cl:escherichia coli bacitracin resistance protein baca) (db:pir2.dat) G65093 G65093 Escherichia coli 562 -11534101 7500877664 baca (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:cg site no. 29739) (le:8105) (re:8926) (di:complement) ECU28379 U28379 g882579 Escherichia coli 562 -11534101 239262 baca bacitracin resistance:possibly phosphorylates (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 277 of 400 of the completegenome.) (nt:f273; 95 pct identical to baca_ecoli sw: p31054; cg) (le:8230) (re:9051) (di:complement) AE000387 AE000387 g1789437 Escherichia coli 562 -11534101 5000691327 (de:(ecoli_2980) (pn:bacitracin resistance; possibly phosphorylates undecaprenol) (gn:baca) (gtcfc:13.3) (ec:2.7.1.66) (baca_ecoli) (keggfc:11.1) (rileyfc:5.4.0) (db:gtc-escherichia coli)) ECOLI_2980 ECOLI_2980 Escherichia coli 562 10004067

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840314	9578	31734	741	246

Description

6500730244 radc:b3638 dna repair protein radc (gtcfc:13.4) (keggfc:14.2) (rileyfc:5.5.0) (db:gtc-escherichia coli) b3638 b3638 Escherichia coli 562 -11534102 92960 radc (de:dna repair protein radc) (db:swissprot) RADC_ECOLI P25531 ESCHERICHIA COLI 562 -11534102 7000686267 radc dna repair protein radc (cl:dna repair protein radc) (db:pir2.dat) H65164 H65164 Escherichia coli 562 -11534102 7500889342 radc::cg site no. 1... (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:differs from radc sequence in x63366; similar to s.) (le:1283) (re:1957) (di:complement) ECOUW82 L10328 g290488 Escherichia coli 562 -11534102 236876 radc dna repair protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:f224; 100 pct identical amino acid sequence and) (le:3786) (re:4460) (di:complement) AE000441 AE000441 g1790069 Escherichia coli 562 -11534102 5000691328 (de:(ecoli_3558) (pn:sensitivity to radiation) (gn:radc) (gtcfc:13.4) (ec:) (radc_ecoli) (keggfc:11.2) (rileyfc:5.5.0) (db:gtc-escherichia coli)) ECOLI_3558 ECOLI_3558 Escherichia coli 562 10034977

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840319	9579	31735	717	238

Description

6500730245 tort:b0994 periplasmic protein tort precursor (gtcfc:11.1) (keggfc:14.2) (db:gtc-escherichia coli) b0994 b0994 Escherichia coli 562 -11534103 101832 tort (de:periplasmic protein tort precursor) (db:swissprot) TORT_ECOLI P38683 ESCHERICHIA COLI 562 -11534103 7000686818 tort tort protein precursor:periplasmic (db:pir2.dat) H64840 H64840 Escherichia coli 562 -11534103 7500893276 tort part of regulation of tor operon:periplasmic (fn:regulator; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 91 of 400 of the completegenome.) (nt:o342; 99 pct identical to ycch_ecoli sw: p38683) (le:5034) (re:6062) (di:direct) AE000201 AE000201 g1787228 Escherichia coli 562 -11534103 5000691928 tort periplasmic protein tort (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf_id:o227#1; similar to pir accession number) (le:1758) (re:2786) (di:direct) D90737 D90737 g4062554 Escherichia coli 562 -11534103 7502851990 tort periplasmic protein tort (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf_id:o227#1; similar to pir accession number) (le:10756) (re:11784) (di:direct) D90736 D90736 g4062711 Escherichia coli 562 -11534103

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840326	9580	31736	540	179

Description

5000691329 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0005 b0005 Escherichia coli 562 -11534104 7000690986 probable membrane protein b0005 (db:pir2.dat) E64720 E64720 Escherichia coli 562 -11534104 7500960426 b0005 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 1 of 400 of the completegenome.) (nt:o98; 54 pct identical (7 gaps) to 33 residues from) (le:5234) (re:5530) (di:direct) AE000111 AE000111 g1786186 Escherichia coli 562 -11534104 6500730246 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0005 b0005 Escherichia coli 562 -11534104

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840329	9581	31737	1581	526

Description

GTC ORF with score 548 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t16b24 genomic sequence,complete sequence.) (nt:unknown protein) (le:39566:39904:40152:40763) (re:39781:39999:40279:40936) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840330	9582	31738	381	126

Description

6500730247 yaaa:b0006 hypothetical 29.6 kd protein in thrc-talb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0006 b0006 Escherichia coli 562 -11534105 109484 yaaa (de:hypothetical 29.6 kd protein in thrc-talb intergenic region) (db:swissprot) YAAA_ECOLI P11288 ESCHERICHIA COLI 562 -11534105 163357 yaaa yaaa protein:protein f121 (db:pir2.dat) (mp:0 min) Q3ECTC S40534 Escherichia coli 562 -11534105 7500895958 orf (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (nt:hypothetical protein 126) (le:5344) (re:6120) (di:complement) ECO110K D10483 g216438 Escherichia coli 562 -11534105 233548 yaaa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 1 of 400 of the completegenome.) (nt:f258; 100 pct identical to yaaa_ecoli sw: p11288) (le:5683) (re:6459) (di:complement) AE000111 AE000111 g1786187 Escherichia coli 562 -11534105 5000691330 (de:(ecoli_6) (pn:hypothetical 29) (gn:yaaa) (gtcfc:13.7:14.1) (ec:) (yaaa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_6 ECOLI_6 Escherichia coli 562 10051216

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840337	9583	31739	252	83

Description

GTC ORF with score 216 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t16b24 genomic sequence,complete sequence.) (nt:unknown protein) (le:39566:39904:40152:40763) (re:39781:39999:40279:40936) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840338	9584	31740	402	133

Description

GTC ORF with score 159 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac t16b24 genomic sequence,complete sequence.) (nt:unknown protein) (le:39566:39904:40152:40763) (re:39781:39999:40279:40936) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840350	9585	31741	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840352	9586	31742	606	201

Description

6500730248 yaaj:b0007 hypothetical 51.7 kd protein in thrc-talb intergenic region:orf8 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0007 b0007 Escherichia coli 562 -11534106 109503 yaaj (de:hypothetical 51.7 kd protein in thrc-talb intergenic region (orf8)) (db:swissprot) YAAJ_ECOLI P30143 ESCHERICHIA COLI 562 -11534106 7000687112 yaaj probable amino acid transport protein yaaj:sodium-dependent (cl:sodium-dependent d-alanine/glycine transport protein) (db:pir2.dat) G64720 G64720 Escherichia coli 562 -11534106 7500895972 yaaj inner membrane transport protein (fn:putative transport; transport of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 1 of 400 of the completegenome.) (nt:f476; 100 pct identical to yaaj_ecoli sw: p30143) (le:6529) (re:7959) (di:complement) AE000111 AE000111 g1786188 Escherichia coli 562 -11534106 5000691331 (de:(ecoli_7) (pn:hypothetical 51) (gn:yaaj) (gtcfc:13.7:14.1) (ec:) (yaaj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_7 ECOLI_7 Escherichia coli 562 10051235

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840356	9587	31743	255	84

Description

6500730249 yaah:b0010 hypothetical 20.1 kd protein in mog-htga intergenic region:orf5 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0010 b0010 Escherichia coli 562 -11534107 7500895968 yaah (de:hypothetical 20.1 kd protein in mog-htga intergenic region (orf5)) (db:swissprot) YAAH_ECOLI P28695 ESCHERICHIA COLI 562 -11534107 163190 yaah protein yaah (db:pir2.dat) E56688 E56688 Escherichia coli 562 -11534107 5000691332 (db:genpept-bct1) (de:e.coli dnak and htga genes.) (nt:orf5) (le:1017) (re:1583) (di:complement) ECHTGA X67700 g41756 Escherichia coli 562 -11534107 233159 yaah orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 1 of 400 of the completegenome.) (nt:f188; 100 pct identical to yaah_ecoli sw: p28695) (le:9928) (re:10494) (di:complement) AE000111 AE000111 g1786191 Escherichia coli 562 -11534107 109499 yaah (de:hypothetical 20.1 kd protein in mog-htga intergenic region (orf5)) (db:swissprot) YAAH_ECOLI P28695 ESCHERICHIA COLI 562 -11534107

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840360	9588	31744	228	75

Description

5000691333 hypothetical protein 2 in dnaK 5-region (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0011 b0011
Escherichia coli 562 -11534108 7000690985 hypothetical protein b0011
(db:pir2.dat) C64721 C64721 Escherichia coli 562 -11534108 7500959854 b0011
putative oxidoreductase (fn:putative enzyme; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the
completegenome.) (nt:f237; 99 pct identical to pir: d56688; overlaps)
(le:105) (re:818) (di:complement) AE000112 AE000112 g1786193 Escherichia
coli 562 -11534108 6500730250 hypothetical protein 2 in dnaK 5-region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0011
b0011 Escherichia coli 562 -11534108

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840364	9589	31745	963	320

Description

6500730251 yaai:b0013 hypothetical 14.5 kd protein in htga-dnaK intergenic
region: hypothetical 14.5 kd protein in htga-dnaK intergenic region
precursor:orf3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0013 b0013 Escherichia coli 562 -11534109
7500895970 yaai (de:(orf3)) (db:swissprot) YAAI_ECOLI P28696 ESCHERICHIA
COLI 562 -11534109 162963 yaai probable membrane protein yaai (db:pir2.dat)
C56688 C56688 Escherichia coli 562 -11534109 5000691334 (db:genpept-bct1)
(de:e.coli dnaK and htga genes.) (nt:orf3) (le:2472) (re:2876)
(di:complement) ECHTGA X67700 g41758 Escherichia coli 562 -11534109 233162
yaai orf: hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 2 of 400 of the completegenome.)
(nt:f134; 100 pct identical to yaai_ecoli sw: p28696) (le:844) (re:1248)
(di:complement) AE000112 AE000112 g1786195 Escherichia coli 562 -11534109
109501 yaai (de:(orf3)) (db:swissprot) YAAI_ECOLI P28696 ESCHERICHIA COLI
562 -11534109

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840377	9590	31746	285	94

Description

5000691335 yi81_1:yi81_2:b0016 insertion element is186 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0016 b0016 Escherichia coli 562 -11534110 7500937262 b0016:b0582 (de:insertion element is186 40.9 kd hypothetical protein (orf1)) (db:swissprot) YI81_ECOLI P08409 ESCHERICHIA COLI 562 -11534110 7500937264 orf (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (nt:is186 47k hypothetical protein homolog(pir:a24221)) (le:15094) (re:16206) (di:direct) ECO110K D10483 g216442 Escherichia coli 562 -11534110 233552 yi81_1 is186 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the completegenome.) (nt:o370; n-terminal 353 aa are 100 pct identical to) (le:4907) (re:6019) (di:direct) AE000112 AE000112 g1786198 Escherichia coli 562 -11534110 7500937263 yi81_2 is186 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 53 of 400 of the completegenome.) (nt:o370; n-terminal 353 aa are 100 pct identical) (le:4720) (re:5832) (di:direct) AE000163 AE000163 g1786796 Escherichia coli 562 -11534110 7502851991 hypothetical protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf_id:o164#5; similar to pir accession number) (le:13403) (re:14515) (di:direct) D90700 D90700 g4062211 Escherichia coli 562 -11534110 6500730252 yi81_1:yi81_2 insertion element is186 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0016 b0016 Escherichia coli 562 -11534110 157311 (de:hypothetical protein - escherichia coli) S40538 S40538 Escherichia coli 562 -11534110

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840385	9591	31747	498	166

Description

6500730253 yi82_1:b0017 insertion elements is186 and is421 hypothetical 11 kd protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0017 b0017 Escherichia coli 562 -11534111 7500937265 b0017 (de:insertion elements is186 and is421 hypothetical 11 kd protein (orf2)) (db:swissprot) YI82_ECOLI P08410 ESCHERICHIA COLI 562 -11534111 163699 yi82_1 hypothetical protein yi82_1 (db:pir2.dat) S04881 S04881 Escherichia coli 562 -11534111 224952 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #416(54.1-54.5 min.)) (nt:similar to (pir accession number s04881)) (le:7599) (re:7907) (di:complement) D90869 D90869 g1799807 Escherichia coli 562 -11534111 233553 (db:genpept-bct1) (de:escherichia coli insertion sequence is421.) (nt:orfii (aa 1-103)) (le:542) (re:850) (di:complement) ECIS421 Y07501 g581118 Escherichia coli 562 -11534111 243735 orf (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (nt:hypothetical protein ii (insertion sequence) (le:15518) (re:15826) (di:complement) ECOL10K D10483 g285760 Escherichia coli 562 -11534111 5000691336 (db:genpept-bct1) (de:bacterial insertion sequence element is186.) (nt:orf2) (le:479) (re:787) (di:complement) IS186 X03123 g581270 Escherichia coli 562 -11534111 233251 yi82_1 is186 and is421 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the completegenome.) (nt:f102; 100 pct identical to yi82_ecoli sw: p08410) (le:5331) (re:5639) (di:complement) AE000112 AE000112 g1786199 Escherichia coli 562 -11534111 113104 b0017 (de:insertion elements is186 and is421 hypothetical 11 kd protein (orf2)) (db:swissprot) YI82_ECOLI P08410 ESCHERICHIA COLI 562 -11534111

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840401	9592	31748	678	225

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840402	9593	31749	1290	429

Description

5000691339 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0024 b0024 Escherichia coli 562 -11534112
7000690987 probable membrane protein b0024 (db:pir2.dat) H64722 H64722 Escherichia coli 562 -11534112 7500960427 b0024 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 3 of 400 of the completegenome.) (nt:o72; 43 pct identical (1 gap) to 32 residues from) (le:522) (re:740) (di:direct) AE000113 AE000113 g1786207 Escherichia coli 562 -11534112 6500730254 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0024 b0024 Escherichia coli 562 -11534112

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840408	9594	31750	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840410	9595	31751	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840421	9596	31752	1203	400

Description

6500730255 yaaf:b0030 hypothetical 32.6 kd protein in lytb-dapb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0030 b0030 Escherichia coli 562 -11534113 233567 yaaf (de:hypothetical 32.6 kd protein in lytb-dapb intergenic region) (db:swissprot) YAAF_ECOLI P22564 ESCHERICHIA COLI 562 -11534113 163268 yaaf probable glycosidase:yaaf (cl:yaaf protein) (ec:3.2.-.-) (db:pir2.dat) JE0404 JE0404 Escherichia coli 562 -11534113 5000691343 orf::3 (db:genpept-bct1) (de:e. coli lsp-dapb interval.) (nt:product appears to be membrane bound) (le:1613) (re:2527) (di:direct) ECLSPDAP X54945 g41934 Escherichia coli 562 -11534113 7500895965 orf (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (nt:hypothetical 32.6k protein(pir:je0404)) (le:26947) (re:27861) (di:direct) ECO110K D10483 g216457 Escherichia coli 562 -11534113 233331 yaaf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 3 of 400 of the completegenome.) (nt:o304; 100 pct identical to yaaf_ecoli sw: p22564) (le:6634) (re:7548) (di:direct) AE000113 AE000113 g1786213 Escherichia coli 562 -11534113 109496 yaaf (de:hypothetical 32.6 kd protein in lytb-dapb intergenic region) (db:swissprot) YAAF_ECOLI P22564 ESCHERICHIA COLI 562 -11534113

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840424	9597	31753	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840427	9598	31754	369	122

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840457	9599	31755	279	92

Description

6500730256 fixx:b0044 hypothetical 10.5 kd protein in fixc-kefc intergenic region:ferredoxin like protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0044 b0044 Escherichia coli 562 -11534114 71760 fixx (de:ferredoxin like protein) (db:swissprot) FIXX_ECOLI P31576 ESCHERICHIA COLI 562 -11534114 7000685256 fixx fixx protein (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) D64725 D64725 Escherichia coli 562 -11534114 7500881485 fixx putative ferredoxin (fn:putative carrier; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 4 of 400 of the completegenome.) (nt:o95; 98 pct identical to yaat_ecoli sw: p31576) (le:11377) (re:11664) (di:direct) AE000114 AE000114 g1786228 Escherichia coli 562 -11534114 5000691352 (de:(ecoli_44) (pn:ferredoxin like protein) (gn:fixx) (gtcfc:13.7:14.1) (ec:) (fixx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_44 ECOLI_44 Escherichia coli 562 10122629

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840460	9600	31756	900	299

Description

6500730257 yabf:b0046 hypothetical nadph oxidoreductase in fixc-kefc intergenic region:orf67 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0046 b0046 Escherichia coli 562 -11534115 109541 yabf (ec:1.6.99.-) (de:putative nad(p)h oxidoreductase yabf,) (db:swissprot) YABF_ECOLI P31577 ESCHERICHIA COLI 562 -11534115 7000687129 yabf probable nad p h oxidoreductase:yabf (cl:probable nad(p)h oxidoreductase yabf) (ec:1.6.-.-) (db:pir2.dat) F64725 F64725 Escherichia coli 562 -11534115 7500895999 yabf putative nad p h oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 5 of 400 of the completegenome.) (nt:o176; 98 pct identical to yabf_ecoli sw: p31577) (le:84) (re:614) (di:direct) AE000115 AE000115 g1786231 Escherichia coli 562 -11534115 5000691354 (de:(ecoli_46) (pn:hypothetical nad:ph oxidoreductase in fixc-kefc intergenic region:orf67) (gn:yabf) (gtcfc:13.7:14.1) (ec:) (yabf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_46 ECOLI_46 Escherichia coli 562 10122631

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840469	9601	31757	1317	438

Description

6500730258 yabh:b0055 hypothetical 30.6 kd protein in sura-hepa intergenic region:hypothetical 30.6 kd protein in imp-rlua intergenic region:orf81 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0055 b0055 Escherichia coli 562 -11534116 109545 djla (de:dnaj-like protein djla) (db:swissprot) DJLA_ECOLI P31680 ESCHERICHIA COLI 562 -11534116 7000687132 yabh yabh protein (cl:dnaj amino-terminal homology) (db:pir2.dat) G64726 G64726 Escherichia coli 562 -11534116 7500880346 yabh putative dna binding protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 6 of 400 of the completegenome.) (nt:o271; 100 pct identical to yabh_ecoli sw: p31680) (le:158) (re:973) (di:direct) AE000116 AE000116 g1786241 Escherichia coli 562 -11534116 5000691358 (de:(ecoli_55) (pn:hypothetical 30) (gn:yabh) (gtcfc:13.7:14.1) (ec:) (yabh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_55 ECOLI_55 Escherichia coli 562 10051277

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840470	9602	31758	384	127

Description

6500730259 yabp:b0056 hypothetical 5.9 kd protein in sura-hepa intergenic region:hypothetical 24.8 kd protein in imp-rlua intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0056 b0056 Escherichia coli 562 -11534117 109562 yabp (de:hypothetical 24.8 kd protein in djla-rlua intergenic region) (db:swissprot) YABP_ECOLI P39220 ESCHERICHIA COLI 562 -11534117 7000687143 yabp yabp protein (db:pir2.dat) H64726 H64726 Escherichia coli 562 -11534117 7500896015 yabp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 6 of 400 of the completegenome.) (nt:o216; 100 pct identical to yabp_ecoli sw: p39220) (le:1268) (re:1918) (di:direct) AE000116 AE000116 g1786242 Escherichia coli 562 -11534117 5000691359 (de:(ecoli_56) (pn:hypothetical 5) (gn:yabp) (gtcfc:13.7:14.1) (ec:) (yabp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_56 ECOLI_56 Escherichia coli 562 10122635

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840495	9603	31759	858	285

Description

6500730260 yabq:b0057 hypothetical 5.7 kd protein in sura-hepa intergenic region:hypothetical 5.7 kd protein in imp-rlua intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0057 b0057 Escherichia coli 562 -11534118 109564 yabq (de:hypothetical 5.7 kd protein in djla-rlua intergenic region) (db:swissprot) YABQ_ECOLI P39221 ESCHERICHIA COLI 562 -11534118 7000687145 yabq yabq protein (db:pir2.dat) A64727 A64727 Escherichia coli 562 -11534118 7500896017 yabq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 6 of 400 of the completegenome.) (nt:o52; 100 pct identical to yabq_ecoli sw: p39221) (le:1915) (re:2073) (di:direct) AE000116 AE000116 g1786243 Escherichia coli 562 -11534118 5000691360 (de:(ecoli_57) (pn:hypothetical 5) (gn:yabq) (gtcfc:13.7:14.1) (ec:) (yabq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_57 ECOLI_57 Escherichia coli 562 10051296

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840505	9604	31760	312	103

Description

6500730261 yabo:b0058 hypothetical 24.9 kd protein in sura-hepa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0058 b0058 Escherichia coli 562 -11534119 7000687141 yabo yabo protein (db:pir2.dat) B64727 B64727 Escherichia coli 562 -11534119 7500896012 yabo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 6 of 400 of the completegenome.) (nt:f219; 100 pct identical to yabo_ecoli sw: p39219) (le:2481) (re:3140) (di:complement) AE000116 AE000116 g1786244 Escherichia coli 562 -11534119 109559 yabo (de:hypothetical 24.9 kd protein in sura-hepa intergenic region) (db:swissprot) YABO_ECOLI P39219 ESCHERICHIA COLI 562 -11534119 5000691361 (de:(ecoli_58) (pn:hypothetical 24) (gn:yabo) (gtcfc:13.7:14.1) (ec:) (yabo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_58 ECOLI_58 Escherichia coli 562 10051291

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840506	9605	31761	345	115

Description

GTC ORF with score 102 to: (fn:pre-ribosomal rna processor) (sr:giardia lamblia (individual_isolate wb) (library: embl3) dna) (db:genpept-inv) (de:giardia lamblia fibrillarin gene, complete cds.) (nt:putative) (le:161) (re:1144) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840512	9606	31762	1455	484

Description

6500730262 yabi:b0065 hypothetical 26.3 kd protein in arac-tbpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0065 b0065 Escherichia coli 562 -11534120 7000690931 yabi probable membrane protein yabi (db:pir2.dat) A64728 A64728 Escherichia coli 562 -11534120 7500960430 yabi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 7 of 400 of the completegenome.) (nt:o254; 100 pct identical to yabi_ecoli sw:) (le:1164) (re:1928) (di:direct) AE000117 AE000117 g1786252 Escherichia coli 562 -11534120 5000691362 (de:(ecoli_65) (pn:hypothetical 26) (gn:yabi) (gtcfc:13.7:14.1) (ec:) (yabi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_65 ECOLI_65 Escherichia coli 562 10122639

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840513	9607	31763	555	184

Description

6500730263 yabn:b0069 hypothetical 63.9 kd protein in tbpa-leud intergenic region:orf103 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0069 b0069 Escherichia coli 562 -11534121 7000690967 yabn yabn protein (db:pir2.dat) E64728 E64728 Escherichia coli 562 -11534121 7500960481 yabn putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 7 of 400 of the completegenome.) (nt:f551; 99 pct identical to yabn_ecoli sw: p33595) (le:5457) (re:7112) (di:complement) AE000117 AE000117 g1786256 Escherichia coli 562 -11534121 5000691366 (de:(ecoli_69) (pn:hypothetical 63) (gn:yabn) (gtcfc:13.7:14.1) (ec:) (yabn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_69 ECOLI_69 Escherichia coli 562 10122643

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840517	9608	31764	816	271

Description

6500730264 yabm:b0070 hypothetical 42.7 kd protein in tbpa-leud intergenic region:orf104 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0070 b0070 Escherichia coli 562 -11534122 109555 yabm (de:hypothetical 42.7 kd protein in tbpa-leud intergenic region (orf104)) (db:swissprot) YABM_ECOLI P31675 ESCHERICHIA COLI 562 -11534122 7000687138 yabm hypothetical 42.7 kd protein in tbpa-leud intergenic region (db:pir2.dat) F64728 F64728 Escherichia coli 562 -11534122 7500896009 yabm putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 7 of 400 of the completegenome.) (nt:o392; 99 pct identical to yabm_ecoli sw: p31675) (le:7434) (re:8612) (di:direct) AE000117 AE000117 g1786257 Escherichia coli 562 -11534122 5000691367 (de:(ecoli_70) (pn:hypothetical 42) (gn:yabm) (gtcfc:13.7:14.1) (ec:) (yabm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_70 ECOLI_70 Escherichia coli 562 10122644

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840522	9609	31765	1428	475

Description

6500730265 yabb:b0081 hypothetical 17.4 kd protein in frur-fts1 intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0081 b0081 Escherichia coli 562 -11534123 304525 yabb (de:hypothetical 17.4 kd protein in frur-fts1 intergenic region (orf1)) (db:swissprot) YABB_ECOLI P22186 ESCHERICHIA COLI 562 -11534123 163537 yabb yabb protein (cl:hypothetical protein mg221) (db:pir2.dat) S14388 S14388 Escherichia coli 562 -11534123 227988 (db:genpept-bct1) (de:e. coli 2 minute region.) (nt:orf1 protein) (le:6164) (re:6622) (di:direct) EC2MIN X55034 g40849 Escherichia coli 562 -11534123 5000691368 (db:genpept-bct1) (de:e.coli pbpb gene regulatory region.) (nt:orf1) (le:77) (re:535) (di:direct) ECPBPBRR X52063 g42319 Escherichia coli 562 -11534123 237729 yabb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o152; 100 pct identical to yabb_ecoli sw: p22186) (le:6089) (re:6547) (di:direct) AE000118 AE000118 g1786269 Escherichia coli 562 -11534123 109530 yabb (de:hypothetical 17.4 kd protein in frur-fts1 intergenic region (orf1)) (db:swissprot) YABB_ECOLI P22186 ESCHERICHIA COLI 562 -11534123

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840546	9610	31766	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840594	9611	31767	1581	526

Description

6500730266 yabc:b0082 hypothetical 34.9 kd protein in frur-fts1 intergenic region:orfb (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0082 b0082 Escherichia coli 562 -11534124 304526 yabc (de:hypothetical 34.9 kd protein in frur-fts1 intergenic region (orfb)) (db:swissprot) YABC_ECOLI P18595 ESCHERICHIA COLI 562 -11534124 227989 (db:genpept-bct1) (de:e. coli 2 minute region.) (nt:orfb protein) (le:6624) (re:7565) (di:direct) EC2MIN X55034 g40850 Escherichia coli 562 -11534124 5000691369 (db:genpept-bct1) (de:e.coli pbpb gene regulatory region.) (nt:orfb) (le:537) (re:1478) (di:direct) ECPBPBRR X52063 g42318 Escherichia coli 562 -11534124 237730 yabc putative apolipoprotein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o313; 100 pct identical to yabc_ecoli sw: p18595) (le:6549) (re:7490) (di:direct) AE000118 AE000118 g1786270 Escherichia coli 562 -11534124 109533 yabc (de:hypothetical 34.9 kd protein in frur-fts1 intergenic region (orfb)) (db:swissprot) YABC_ECOLI P18595 ESCHERICHIA COLI 562 -11534124

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840609	9612	31768	402	133

Description

6500730267 yaca:b0097 hypothetical 16.0 kd protein in lpxc-seca intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0097 b0097 Escherichia coli 562 -11534125 7000689002 yaca yaca protein (db:pir1.dat) (mp:2 min) QQECAA A64732 Escherichia coli 562 -11534125 7500953709 yaca orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.) (nt:o195; 100 pct identical to yaca_ecoli sw:) (le:2386) (re:2973) (di:direct) AE000119 AE000119 g1786286 Escherichia coli 562 -11534125 5000691371 (de:(ecoli_97) (pn:hypothetical 16) (gn:yaca) (gtcfc:13.7:14.1) (ec:) (yaca_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_97 ECOLI_97 Escherichia coli 562 10122653

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840612	9613	31769	414	137

Description

5000691372 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0100 b0100 Escherichia coli 562 -11534126
7000690988 hypothetical protein b0100 (db:pir2.dat) D64732 D64732
Escherichia coli 562 -11534126 7500959855 b0100 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.) (nt:f44; 61 pct identical (1 gap) to 21 residues of an) (le:6320) (re:6454) (di:complement) AE000119 AE000119
g1786289 Escherichia coli 562 -11534126 6500730268 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0100 b0100 Escherichia coli 562 -11534126

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840614	9614	31770	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840632	9615	31771	633	210

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840653	9616	31772	498	165

Description

6500730269 yacf:b0102 hypothetical protein in mutt-guac intergenic region:hypothetical 28.3 kd protein in mutt-guac intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0102 b0102 Escherichia coli 562 -11534127 109599 yacf (de:hypothetical 28.3 kd protein in mutt-guac intergenic region) (db:swissprot) YACF_ECOLI P36680
ESCHERICHIA COLI 562 -11534127 7000687154 yacf hypothetical protein in mutt-guac intergenic region (db:pir2.dat) F64732 F64732 Escherichia coli 562 -11534127 7500896036 yacf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.) (nt:f247; 98 pct identical to yacf_ecoli sw: p36680) (le:6612) (re:7355) (di:complement) AE000119 AE000119 g1786291 Escherichia coli 562 -11534127 5000691374 (de:(ecoli_102) (pn:hypothetical 8) (gn:yacf) (gtcfc:13.7:14.1) (ec:) (yacf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_102 ECOLI_102 Escherichia coli 562 10122657

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840657	9617	31773	744	247

Description

5000691376 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0105 b0105 Escherichia coli 562 -11534128
7000690989 hypothetical protein b0105 (db:pir2.dat) A64733 A64733
Escherichia coli 562 -11534128 7500959856 b0105 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.) (nt:f35; 52 pct identical (1 gap) to 25 residues of an) (le:9163) (re:9270) (di:complement) AE000119 AE000119
g1786294 Escherichia coli 562 -11534128 6500730270 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0105 b0105 Escherichia coli 562 -11534128

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840669	9618	31774	1005	334

Description

6500730271 yach:b0117 hypothetical protein in lpda-sped intergenic region:hypothetical 69.4 kd protein in lpda-acnb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0117 b0117 Escherichia coli 562 -11534129 109604 yach (de:hypothetical 69.4 kd protein in lpda-acnb intergenic region) (db:swissprot) YACH_ECOLI P36682
ESCHERICHIA COLI 562 -11534129 7000687157 yach yach protein (db:pir2.dat) E64734 E64734 Escherichia coli 562 -11534129 7500896039 yach putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 11 of 400 of the completegenome.) (nt:f617; residues 111-402 are 100 pct identical to) (le:1688) (re:3541) (di:complement) AE000121 AE000121 g1786308 Escherichia coli 562 -11534129
5000691380 (de:(ecoli_117) (pn:hypothetical 36) (gn:yach) (gtcfc:13.7:14.1) (ec:) (yach_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_117 ECOLI_117 Escherichia coli 562 10122666

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840672	9619	31775	1266	422

Description

6500730272 yac1:b0119 hypothetical protein in lpda-sped intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0119 b0119 Escherichia coli 562 -11534130 7000691835 yac1 yac1 protein (cl:hypothetical protein hil724) (db:pir2.dat) G64734 G64734 Escherichia coli 562 -11534130 7500960484 yac1 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 11 of 400 of the completegenome.) (nt:o136; 100 pct identical to yac1_ecoli sw:) (le:6621) (re:7031) (di:direct) AE000121 AE000121 g1786310 Escherichia coli 562 -11534130 5000691382 (de:(ecoli_119) (pn:hypothetical 13) (gn:yac1) (gtcfc:13.7:14.1) (ec:) (yac1_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_119 ECOLI_119 Escherichia coli 562 10122668

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840673	9620	31776	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840677	9621	31777	1305	435

Description

GTC ORF with score 276 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 8543.) (nt:ylr319c; weak similarity to poly (adp-ribose)) (le:14332) (re:16698) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840706	9622	31778	234	77

Description

6500730273 yacc:b0122 hypothetical protein in spee-gcd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0122 b0122 Escherichia coli 562 -11534131 7000690850 yacc yacc protein (db:pir2.dat) B64735 B64735 Escherichia coli 562 -11534131 7500960482 yacc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 11 of 400 of the completegenome.) (nt:f156; 100 pct identical to yacc_ecoli sw:) (le:8851) (re:9321) (di:complement) AE000121 AE000121 g1786313 Escherichia coli 562 -11534131 5000691383 (de:(ecoli_122) (pn:hypothetical 12) (gn:yacc) (gtcfc:13.7:14.1) (ec:) (yacc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_122 ECOLI_122 Escherichia coli 562 10122669

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840710	9623	31779	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840713	9624	31780	1173	390

Description

6500730274 yack:b0123 hypothetical protein in spee-gcd intergenic region precursor:53.4 kd protein in spee-gcd intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0123 b0123 Escherichia coli 562 -11534132 109609 yack (de:probable 53.4 kd blue-copper protein yacq precursor) (db:swissprot) YACK_ECOLI P36649 ESCHERICHIA COLI 562 -11534132 7000687160 yack probable copper-binding protein yack (db:pir2.dat) C64735 C64735 Escherichia coli 562 -11534132 7500896042 yack orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 11 of 400 of the completegenome.) (nt:o516; 100 pct identical to 463 residues) (le:9364) (re:10914) (di:direct) AE000121 AE000121 g1786314 Escherichia coli 562 -11534132 5000691384 (de:(ecoli_123) (pn:48) (gn:yack) (gtcfc:13.7:14.1) (ec:) (yack_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_123 ECOLI_123 Escherichia coli 562 10122670

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840715	9625	31781	297	98

Description

6500730275 yadf:b0126 hypothetical protein in hpt-pand intergenic region:hypothetical 25.1 kd protein in hpt-pand intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0126 b0126 Escherichia coli 562 -11534133 109645 yadf (de:hypothetical 25.1 kd protein in hpt-pand intergenic region) (db:swissprot) YADF_ECOLI P36857 ESCHERICHIA COLI 562 -11534133 7000687169 yadf yadf protein (db:pir2.dat) F64735 F64735 Escherichia coli 562 -11534133 7500896067 yadf putative carbonic anhydrase ec 4.2.1.1 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 12 of 400 of the completegenome.) (nt:f220; residues 1-180 are 100 pct identical to) (le:3304) (re:3966) (di:complement) AE000122 AE000122 g1786318 Escherichia coli 562 -11534133 5000691385 (de:(ecoli_126) (pn:hypothetical 25) (gn:yadf) (gtcfc:13.7:14.1) (ec:) (yadf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_126 ECOLI_126 Escherichia coli 562 10122672

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840723	9626	31782	864	287

Description

6500730276 yadg:b0127 hypothetical abc transporter in hpt-pand intergenic region:hypothetical abc transporter atp-binding protein in hpt-pand intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0127 b0127 Escherichia coli 562 -11534134 109647 yadg (de:hypothetical abc transporter atp-binding protein yadg) (db:swissprot) YADG_ECOLI P36879 ESCHERICHIA COLI 562 -11534134 164168 yadg probable abc-type transport protein yagd (cl:atp-binding cassette homology) (db:pir2.dat) S45204 S45204 Escherichia coli 562 -11534134 301605 orf (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara')) (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (nt:'modulation protein nodi homology') (le:31387) (re:32313) (di:direct) ECO82K D26562 g473794 Escherichia coli 562 -11534134 233667 yadg putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 12 of 400 of the completegenome.) (nt:o308; 100 pct identical to yadg_ecoli sw: p36879) (le:4075) (re:5001) (di:direct) AE000122 AE000122 g1786319 Escherichia coli 562 -11534134 5000691386 (de:(ecoli_127) (pn:hypothetical abc transporter atp-binding protein in hpt-pand intergenic region) (gn:yadg) (gtcfc:13.7:14.1) (ec:) (yadg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_127 ECOLI_127 Escherichia coli 562 10051379

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840733	9627	31783	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840747	9628	31784	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840772	9629	31785	285	94

Description

6500730277 yadd:b0132 hypothetical 32.7 kd protein in panc-panc intergenic region:hypothetical 34.6 kd protein in pand-panc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0132 b0132 Escherichia coli 562 -11534135 109641 yadd (de:hypothetical 34.6 kd protein in pand-panc intergenic region) (db:swissprot) YADD_ECOLI P31665 ESCHERICHIA COLI 562 -11534135 7000687167 yadd yadd protein (db:pir2.dat) D64736 D64736 Escherichia coli 562 -11534135 7500896065 yadd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 12 of 400 of the completegenome.) (nt:o300; 100 pct identical to yadd_ecoli sw:) (le:8264) (re:9166) (di:direct) AE000122 AE000122 g1786324 Escherichia coli 562 -11534135 5000691390 (de:(ecoli_132) (pn:hypothetical 32) (gn:yadd) (gtcfc:13.7:14.1) (ec:) (yadd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_132 ECOLI_132 Escherichia coli 562 10122676

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840773	9630	31786	270	89

Description

6500730278 yadc:b0135 hypothetical fimbrial-like protein in panb-htre intergenic region:hypothetical fimbrial-like protein in panb-htre intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0135 b0135 Escherichia coli 562 -11534136 109639 yadc (de:precursor) (db:swissprot) YADC_ECOLI P31058 ESCHERICHIA COLI 562 -11534136 7000687166 yadc yadc protein (db:pir2.dat) G64736 G64736 Escherichia coli 562 -11534136 7500896064 yadc putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 13 of 400 of the completegenome.) (nt:f412; 100 pct identical to yadc_ecoli sw: p31058) (le:87) (re:1325) (di:complement) AE000123 AE000123 g1786328 Escherichia coli 562 -11534136 5000691391 (de:(ecoli_135) (pn:hypothetical fimbrial-like protein in panb-htre intergenic region precursor) (gn:yadc) (gtcfc:13.7:14.1) (ec:) (yadc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_135 ECOLI_135 Escherichia coli 562 10051371

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840778	9631	31787	1005	334

Description

6500730279 yadk:b0136 hypothetical 21.1 kd protein in panb-htre intergenic region:21.1 kd protein in panb-htre intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0136 b0136 Escherichia coli 562 -11534137 109652 yadk (de:21.1 kd protein in panb-htre intergenic region) (db:swissprot) YADK_ECOLI P37016 ESCHERICHIA COLI 562 -11534137 7000687172 yadk yadk protein (db:pir2.dat) H64736 H64736 Escherichia coli 562 -11534137 7500896071 yadk putative fimbrial protein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 13 of 400 of the completegenome.) (nt:f198; 100 pct identical to yadk_ecoli sw: p37016) (le:1375) (re:1971) (di:complement) AE000123 AE000123 g1786329 Escherichia coli 562 -11534137 5000691392 (de:(ecoli_136) (pn:hypothetical 21) (gn:yadk) (gtcfc:13.7:14.1) (ec:) (yadk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_136 ECOLI_136 Escherichia coli 562 10051384

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840781	9632	31788	519	172

Description

6500730280 yadl:b0137 hypothetical 21.0 kd protein in panb-htre intergenic region:hypothetical 21.0 kd protein in panb-htre intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0137 b0137 Escherichia coli 562 -11534138 109654 yadl (de:hypothetical 21.0 kd protein in panb-htre intergenic region precursor) (db:swissprot) YADL_ECOLI P37017 ESCHERICHIA COLI 562 -11534138 7000687173 yadl yadl protein (db:pir2.dat) A64737 A64737 Escherichia coli 562 -11534138 7500896072 yadl putative fimbrial protein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 13 of 400 of the completegenome.) (nt:f201; 100 pct identical to yadl_ecoli sw: p37017) (le:1998) (re:2603) (di:complement) AE000123 AE000123 g1786330 Escherichia coli 562 -11534138 5000691393 (de:(ecoli_137) (pn:hypothetical 21) (gn:yadl) (gtcfc:13.7:14.1) (ec:) (yadl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_137 ECOLI_137 Escherichia coli 562 10051386

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840782	9633	31789	456	151

Description

6500730281 yadm:b0138 hypothetical 20.3 kd protein in panb-htre intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0138 b0138 Escherichia coli 562 -11534139 7000690923 yadm yadm protein (db:pir2.dat) B64737 B64737 Escherichia coli 562 -11534139 7500960485 yadm putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 13 of 400 of the completegenome.) (nt:f203; 100 pct identical to yadm_ecoli sw:) (le:2615) (re:3226) (di:complement) AE000123 AE000123 g1786331 Escherichia coli 562 -11534139 5000691394 (de:(ecoli_138) (pn:hypothetical 20) (gn:yadm) (gtcfc:13.7:14.1) (ec:) (yadm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_138 ECOLI_138 Escherichia coli 562 10122677

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840783	9634	31790	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840788	9635	31791	642	213

Description

6500730282 yadn:b0141 hypothetical fimbrial-like protein in ecpd-folk intergenic region:hypothetical fimbrial-like protein in ecpd-folk intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0141 b0141 Escherichia coli 562 -11534140 109656 yadn (de:precursor) (db:swissprot) YADN_ECOLI P37050 ESCHERICHIA COLI 562 -11534140 7000687174 yadn yadn protein (db:pir2.dat) E64737 E64737 Escherichia coli 562 -11534140 7500896073 yadn putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 13 of 400 of the completegenome.) (nt:f194; 100 pct identical to yadn_ecoli sw: p37050) (le:6671) (re:7255) (di:complement) AE000123 AE000123 g1786334 Escherichia coli 562 -11534140 5000691395 (de:(ecoli_141) (pn:hypothetical fimbrial-like protein in ecpd-folk intergenic region precursor) (gn:yadn) (gtcfc:13.7:14.1) (ec:) (yadn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_141 ECOLI_141 Escherichia coli 562 10051388

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840809	9636	31792	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840822	9637	31793	438	145

Description

GTC ORF with score 186 to: (sr:aspergillus flavus (individual_isolate cra01-2b) (library: embl3) (db:genpept-pln1) (de:aspergillus flavus o-methyltransferase (omt-1) gene, complete cds.) (le:641:1071:1254:1416) (re:1010:1194:1363:1776) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840823	9638	31794	429	142

Description

GTC ORF with score 328 to: (sr:aspergillus flavus (individual_isolate cra01-2b) (library: embl3) (db:genpept-pln1) (de:aspergillus flavus o-methyltransferase (omt-1) gene, complete cds.) (le:641:1071:1254:1416) (re:1010:1194:1363:1776) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840827	9639	31795	333	110

Description

GTC ORF with score 221 to: (sr:aspergillus flavus (individual_isolate cra01-2b) (library: embl3) (db:genpept-pln1) (de:aspergillus flavus o-methyltransferase (omt-1) gene, complete cds.) (le:641:1071:1254:1416) (re:1010:1194:1363:1776) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501840838	9640	31796	492	163

Description

6500730283 yadb:b0144 hypothetical 29.3 kd protein in pcnb-dksa intergenic region:hypothetical 34.9 kd protein in pcnb-dksa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0144 b0144 Escherichia coli 562 -11534141 109637 yadb (de:hypothetical 34.9 kd protein in pcnb-dksa intergenic region) (db:swissprot) YADB_ECOLI P27305 ESCHERICHIA COLI 562 -11534141 7000687165 yadb glutamate--trna ligase homolog yadb:glutamyl-trna synthetase homolog (cl:glutamine--trna ligase homology) (db:pir2.dat) H64737 H64737 Escherichia coli 562 -11534141 7500896063 yadb putative trna synthetase (fn:putative enzyme; aminoacyl trna synthetases,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 13 of 400 of the completegenome.) (nt:f308; 100 pct identical to 250 aa of yadb_ecoli) (le:9558) (re:10484) (di:complement) AE000123 AE000123 g1786337 Escherichia coli 562 -11534141 5000691396 (de:(ecoli_144) (pn:hypothetical 29) (gn:yadb) (gtcfc:13.7:14.1) (ec:) (yadb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_144 ECOLI_144 Escherichia coli 562 10122680

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840842	9641	31797	525	174

Description

6500730284 yadp:b0147 hypothetical protein in sfsa-mrcb intergenic region:hypothetical 20.3 kd protein in sfsa-hrpb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0147 b0147 Escherichia coli 562 -11534142 7000687175 yadp yadp protein (db:pir2.dat) C64738 C64738 Escherichia coli 562 -11534142 7500960487 yadp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 14 of 400 of the completegenome.) (nt:f247; 100 pct identical to yadp_ecoli sw: p37025) (le:838) (re:1377) (di:complement) AE000124 AE000124 g1786341 Escherichia coli 562 -11534142 109657 yadp_ecoli (de:hypothetical 20.3 kd protein in sfsa-mrcb intergenic region.) P37025 P37025 Escherichia coli 562 -11534142 5000691397 (de:(ecoli_147) (pn:hypothetical 20) (gn:yadp) (gtcfc:13.7:14.1) (ec:) (yadp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_147 ECOLI_147 Escherichia coli 562 10051389

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840850	9642	31798	1113	370

Description

6500730285 yadq:b0155 hypothetical protein in heml-pfs intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0155 b0155 Escherichia coli 562 -11534143 7000690982 yadq yadq protein (cl:hypothetical protein sll0855) (db:pir2.dat) C64739 C64739 Escherichia coli 562 -11534143 7500960488 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to voltage-gated chloride channel protein) (le:6182) (re:7603) (di:direct) ECU70214 U70214 g1552733 Escherichia coli 562 -11534143 239784 yadq putative channel transporter (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 15 of 400 of the completegenome.) (nt:o473; 100 pct identical to yadq_ecoli sw:) (le:1614) (re:3035) (di:direct) AE000125 AE000125 g1786350 Escherichia coli 562 -11534143 5000691399 (de:(ecoli_155) (pn:hypothetical 46) (gn:yadq) (gtcfc:13.7:14.1) (ec:) (yadq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_155 ECOLI_155 Escherichia coli 562 10122688

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840860	9643	31799	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840863	9644	31800	432	143

Description

6500730286 yadr:b0156 hypothetical 12.1 kd protein in heml-pfs intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0156 b0156 Escherichia coli 562 -11534144 109659 yadr (de:hypothetical 12.1 kd protein in heml-pfs intergenic region) (db:swissprot) YADR_ECOLI P37026 ESCHERICHIA COLI 562 -11534144 163438 yadr yadr protein (cl:conserved hypothetical protein hi0376) (db:pir2.dat) S45225 S45225 Escherichia coli 562 -11534144 239785 orf (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (nt:'hypothetical protein 118 (nifs 5' region)) (le:65206) (re:65550) (di:direct) ECO82K D26562 g473815 Escherichia coli 562 -11534144 301626 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical protein) (le:7685) (re:8029) (di:direct) ECU70214 U70214 g1552734 Escherichia coli 562 -11534144 233688 yadr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 15 of 400 of the completegenome.) (nt:ol14; 100 pct identical to yadr_ecoli sw: p37026) (le:3117) (re:3461) (di:direct) AE000125 AE000125 g1786351 Escherichia coli 562 -11534144 5000691400 (de:(ecoli_156) (pn:hypothetical 12) (gn:yadr) (gtcfc:13.7:14.1) (ec:) (yadr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_156 ECOLI_156 Escherichia coli 562 10051391

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840876	9645	31801	306	101

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840885	9646	31802	1125	374

Description

6500730287 yads:b0157 hypothetical protein in heml-pfs intergenic region:hypothetical 22.1 kd protein in heml-pfs intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0157 b0157 Escherichia coli 562 -11534145 109661 yads (de:hypothetical 22.1 kd protein in heml-pfs intergenic region) (db:swissprot) YADS_ECOLI P37027 ESCHERICHIA COLI 562 -11534145 163399 yads yads protein (cl:hypothetical protein b1832) (db:pir2.dat) S45226 S45226 Escherichia coli 562 -11534145 239786 orf (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (nt:'vibrio cholerae reca protein homology') (le:65597) (re:66220) (di:complement) ECO82K D26562 g473816 Escherichia coli 562 -11534145 301627 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to vibrio cholerae reca protein) (le:8076) (re:8699) (di:complement) ECU70214 U70214 g1552735 Escherichia coli 562 -11534145 233689 yads orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 15 of 400 of the completegenome.) (nt:f207; 100 pct identical to yads_ecoli sw: p37027) (le:3508) (re:4131) (di:complement) AE000125 AE000125 g1786352 Escherichia coli 562 -11534145 5000691401 (de:(ecoli_157) (pn:hypothetical 22) (gn:yads) (gtcfc:13.7:14.1) (ec:) (yads_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_157 ECOLI_157 Escherichia coli 562 10051393

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840889	9647	31803	1161	386

Description

6500730288 yadt:b0158 hypothetical 29.4 kd protein in heml-pfs intergenic region:hypothetical 29.4 kd protein in heml-pfs intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0158 b0158 Escherichia coli 562 -11534146 109662 yadt (de:hypothetical 29.4 kd protein in heml-pfs intergenic region precursor) (db:swissprot) YADT_ECOLI P37028 ESCHERICHIA COLI 562 -11534146 7000687176 yadt yadt protein (db:pir2.dat) F64739 F64739 Escherichia coli 562 -11534146 7500896076 yadt (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:8737) (re:9537) (di:complement) ECU70214 U70214 g1552736 Escherichia coli 562 -11534146 239787 yadt orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 15 of 400 of the completegenome.) (nt:f266; 99 pct identical to yadt_ecoli sw: p37028) (le:4169) (re:4969) (di:complement) AE000125 AE000125 g1786353 Escherichia coli 562 -11534146 5000691402 (de:(ecoli_158) (pn:hypothetical 29) (gn:yadt) (gtcfc:13.7:14.1) (ec:) (yadt_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_158 ECOLI_158 Escherichia coli 562 10122689

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840897	9648	31804	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840910	9649	31805	525	174

Description

6500730289 yaeg:b0162 hypothetical 44.3 kd protein in htra-dapd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0162 b0162 Escherichia coli 562 -11534147 7000687182 yaeg yaeg protein (cl:hypothetical protein hi0093) (db:pir2.dat) B64740 B64740 Escherichia coli 562 -11534147 7500896091 yaeg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 15 of 400 of the completegenome.) (nt:o391; 100 pct identical to yaeg_ecoli sw: p37047) (le:8952) (re:10127) (di:direct) AE000125 AE000125 g1786357 Escherichia coli 562 -11534147 109689 yaeg (de:hypothetical 44.3 kd protein in htra-dapd intergenic region) (db:swissprot) YAEG_ECOLI P37047 ESCHERICHIA COLI 562 -11534147 5000691404 (de:(ecoli_162) (pn:hypothetical 44) (gn:yaeg) (gtcfc:13.7:14.1) (ec:) (yaeg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_162 ECOLI_162 Escherichia coli 562 10051421

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840935	9650	31806	618	205

Description

6500730290 yaeh:b0163 hypothetical 15.1 kd protein in htra-dapd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0163 b0163 Escherichia coli 562 -11534148 109691 yaeh (de:hypothetical 15.1 kd protein in htra-dapd intergenic region) (db:swissprot) YAEH_ECOLI P37048 ESCHERICHIA COLI 562 -11534148 163929 yaeh yaeh protein (db:pir2.dat) S45230 S45230 Escherichia coli 562 -11534148 239792 orf (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara')) (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (nt:'inter-alpha-trypsin inhibitor complex component ii) (le:72305) (re:72691) (d... ECO82K D26562 g473820 Escherichia coli 562 -11534148 301631 yaeh (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:14784) (re:15170) (di:complement) ECU70214 U70214 g1552741 Escherichia coli 562 -11534148 233693 yaeh putative structural protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 16 of 400 of the completegenome.) (nt:f128; 100 pct identical to yaeh_ecoli sw: p37048) (le:75) (re:461) (di:complement) AE000126 AE000126 g1786359 Escherichia coli 562 -11534148 5000691405 (de:(ecoli_163) (pn:hypothetical 15) (gn:yaeh) (gtcfc:13.7:14.1) (ec:) (yaeh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_163 ECOLI_163 Escherichia coli 562 10051423

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501840939	9651	31807	786	261

Description

6500730291 yaei:b0164 hypothetical protein in htra-dapd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0164 b0164 Escherichia coli 562 -11534149 7000691832 yaei probable phosphoesterase:yaei (cl:probable phosphoesterase yaei:phosphoesterase core homology) (ec:3.1.-.-) (db:pir2.dat) (mp:3.97) D64740 D64740 Escherichia coli 562 -11534149 7500954194 yaei orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 16 of 400 of the completegenome.) (nt:f247; 100 pct identical to yaei_ecoli sw:) (le:623) (re:1366) (di:complement) AE000126 AE000126 g1786360 Escherichia coli 562 -11534149 5000691406 (de:(ecoli_164) (pn:hypothetical 19) (gn:yaei) (gtcfc:13.7:14.1) (ec:) (yaei_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_164 ECOLI_164 Escherichia coli 562 10122690

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840941	9652	31808	1749	582

Description

5000691407 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0165 b0165 Escherichia coli 562 -11534150
7000690990 hypothetical protein b0165 (db:pir2.dat) E64740 E64740
Escherichia coli 562 -11534150 7500959857 b0165 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
16 of 400 of the completegenome.) (nt:f43; 37 pct identical to 32 residues
of an) (le:1353) (re:1484) (di:complement) AE000126 AE000126 g1786361
Escherichia coli 562 -11534150 6500730292 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0165 b0165
Escherichia coli 562 -11534150

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840958	9653	31809	1023	340

Description

GTC ORF with score 146 to: (fn:required for cytochrome oxidase activity)
(sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae cox18p
(cox18) gene, required for activityof mitochondrial cytochrome oxidase,
complete cds.) (le:349) (re:1299) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840963	9654	31810	1911	637

Description

6500730293 yaem:b0173 hypothetical protein in frr 3region:hypothetical 43.4 kd protein in frr-cdsa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0173 b0173 Escherichia coli 562 -11534151 109697 dxr (ec:1.1.1.-) (de:reductoisomerase)) (db:swissprot) DXR_ECOLI P45568 ESCHERICHIA COLI 562 -11534151 7000687185 yaem yaem protein (cl:conserved hypothetical protein hi0807) (db:pir2.dat) E64741 E64741 Escherichia coli 562 -11534151 7500896095 yaem (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:24596) (re:25792) (di:direct) ECU70214 U70214 g1552750 Escherichia coli 562 -11534151 7500896096 dxr 1-deoxy-d-xylulose 5-phosphate reductoisomerase (fn:involved in biosynthesis of isopentenyl) (sr:escherichia coli (strain:k-12, sub_strain:w3110) dna) (db:genpept-bct2) (de:escherichia coli dxr gene for 1-deoxy-d-xylulose 5-phosphatereductoisomerase, complete cds.) (nt:dxr was renamed from yaem) (le... AB013300 AB013300 g3434984 Escherichia coli 562 -11534151 239801 yaem putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 16 of 400 of the completegenome.) (nt:o398; 100 pct identical to fragment yaem_ecoli) (le:9887) (re:11083) (di:direct) AE000126 AE000126 g1786369 Escherichia coli 562 -11534151 5000691408 (de:(ecoli_173) (pn:hypothetical protein in frr:3"region:fragment) (gn:yaem) (gtcfc:13.7:14.1) (ec:) (yaem_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_173 ECOLI_173 Escherichia coli 562 10122693

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840964	9655	31811	270	89

Description

GTC ORF with score 310 to: (sr:n.crassa (strain 74-or23-1a) dna (library of r.geever and n.niles)) (db:genpept-pln1) (de:n.crassa plasma membrane atpase gene, complete cds.) (nt:plasma membrane atpase) (le:1247:1485:1816:2014) (re:1426:1691:1949:4208) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840986	9656	31812	912	303

Description

6500730294 yaes:b0174 hypothetical protein:hypothetical 18.8 kd protein in frr-cdsa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0174 b0174 Escherichia coli 562 -11534152 7000690991 conserved hypothetical protein b0174 (cl:conserved hypothetical protein ybr002c) (db:pir2.dat) F64741 F64741 Escherichia coli 562 -11534152 7500959711 yaes orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 17 of 400 of the completegenome.) (nt:o253; 61 pct identical to 229 residues of an) (le:123) (re:884) (di:direct) AE000127 AE000127 g1786371 Escherichia coli 562 -11534152 5000691409 (de:(ecoli_174) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_174 ECOLI_174 Escherichia coli 562 10122694

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840987	9657	31813	360	119

Description

GTC ORF with score 267 to: (sr:aspergillus niger n402) (db:genpept-pln1) (de:pkia=pyruvate kinase (aspergillus niger, n402, genomic, 3601 nt).) (nt:this sequence comes from fig. 2.) (le:1042:1267:1369:1468) (re:1165:1311:1412:1551) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501840992	9658	31814	252	83

Description

6500730295 yael:b0176 hypothetical protein in cdsa 3region:hypothetical 49.1 kd protein in cdsa-hlpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0176 b0176 Escherichia coli 562 -11534153 109695 yael (de:hypothetical 49.1 kd protein in cdsa-hlpa intergenic region) (db:swissprot) YAEL_ECOLI P37764 ESCHERICHIA COLI 562 -11534153 7000687184 yael yael protein (db:pir2.dat) H64741 H64741 Escherichia coli 562 -11534153 239804 unknown (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:alternate gene name yael) (le:6070) (re:7422) (di:direct) ECOTSF D83536 g1208948 Escherichia coli 562 -11534153 303243 yael (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:27621) (re:28973) (di:direct) ECU70214 U70214 g1552753 Escherichia coli 562 -11534153 236166 yael orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 17 of 400 of the completegenome.) (nt:o450; 100 pct identical to fragment yael_ecoli) (le:1766) (re:3118) (di:direct) AE000127 AE000127 g1786373 Escherichia coli 562 -11534153 5000691410 (de:(ecoli_176) (pn:hypothetical 49) (gn:yael) (gtcfc:13.7:14.1) (ec:) (yael_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_176 ECOLI_176 Escherichia coli 562 10051427

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841007	9659	31815	777	258

Description

6500730296 yaet:b0177 hypothetical protein:unknown protein from 2d-page precursor:spots m62/m63/o3/o9/t35 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0177 b0177 Escherichia coli 562 -11534154 103748 yaet (de:unknown protein from 2d-page precursor (spots m62/m63/o3/o9/t35)) (db:swissprot) UP05_ECOLI P39170 ESCHERICHIA COLI 562 -11534154 7000686893 hypothetical protein b0177 (cl:protective surface antigen d-15) (db:pir2.dat) A64742 A64742 Escherichia coli 562 -11534154 7500893820 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical protein) (le:29003) (re:31435) (di:direct) ECU70214 U70214 g1552754 Escherichia coli 562 -11534154 239805 yaet orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 17 of 400 of the completegenome.) (nt:o810; 45 pct identical (29 gaps) to 808 residues of) (le:3148) (re:5580) (di:direct) AE000127 AE000127 g1786374 Escherichia coli 562 -11534154 5000691411 (de:(ecoli_177) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_177 ECOLI_177 Escherichia coli 562 10122695

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841012	9660	31816	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841020	9661	31817	195	64

Description

GTC ORF with score 217 to: (sr:baker"s yeast strain=s288c (ab972))
(db:genpept-pln1) (de:saccharomyces cerevisiae chromosome viii cosmid 9186.)
(nt:highly similar to 6-phosphogluconate dehydrogenase,) (le:7281) (re:8750)
(di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841026	9662	31818	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841038	9663	31819	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841043	9664	31820	1128	375

Description

5000691412 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0187 b0187 Escherichia coli 562 -11534155
7000690992 conserved hypothetical protein b0187 (db:pir2.dat) C64743 C64743
Escherichia coli 562 -11534155 7500959712 yaer orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
18 of 400 of the completegenome.) (nt:o138; 65 pct identical to 126 residues
of an) (le:2251) (re:2667) (di:direct) AE000128 AE000128 g1786385
Escherichia coli 562 -11534155 6500730297 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0187 b0187
Escherichia coli 562 -11534155

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841044	9665	31821	513	170

Description

GTC ORF with score 319 to: (sr:serinus sp. hvc-associated telencephalon)
(db:genpept-vrt) (de:hat-2=bcr oncogene homolog {song control circuit}
(canaries,hvc-associated telencephalon, mrna, 1695 nt).) (nt:protein kinase
c homolog; human n-chimaerin) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841052	9666	31822	213	70

Description

6500730298 yaeo:b0189 hypothetical protein in acca-cutf intergenic
region:hypothetical 9.5 kd protein in mesj-cutf intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0189
b0189 Escherichia coli 562 -11534156 7000691824 yaeo yaeo protein
(db:pir2.dat) E64743_E64743 Escherichia coli 562 -11534156 7500960489 orf4
(db:genpept-bct1) (de:e.coli orfs and mesj gene.) (le:2338) (re:2598)
(di:complement) ECMESJORF Z50870 g971395 Escherichia coli 562 -11534156
233376 yaeo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 18 of 400 of the completegenome.)
(nt:f86; 100 pct identical to gb: ecmesjorf_4) (le:4079) (re:4339)
(di:complement) AE000128 AE000128 g1786387 Escherichia coli 562 -11534156
5000691414 (de:(ecoli_189) (pn:hypothetical 9) (gn:yaeo) (gtcfc:13.7:14.1)
(ec:) (yaeo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_189 ECOLI_189 Escherichia coli 562 10122700

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841068	9667	31823	1911	637

Description

6500730299 yaeq:b0190 hypothetical protein in acca-cutf intergenic region:hypothetical 20.9 kd protein in mesj-cutf intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0190 b0190 Escherichia coli 562 -11534157 109701 yaeq (de:hypothetical 20.9 kd protein in mesj-cutf intergenic region) (db:swissprot) YAEQ_ECOLI P52100 ESCHERICHIA COLI 562 -11534157 7000687186 yaeq yaeq protein (db:pir2.dat) F64743 F64743 Escherichia coli 562 -11534157 222549 yaeq:a hypothetica....:function yaeq (sr:escherichia coli (strain:k-12, isolate:w3110) dna) (db:genpept-bct1) (de:escherichia coli genes for dnae, acca, ldcc, yaer, yaen, yaeo,yaep, yaeq, yaej, nlpe, yaef complete cds and partial cds.) (le:5758) (re:6303) (di:direct) D49445 D49445 g1785844 Escherichia coli 562 -11534157 7500896098 yaeq (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:45366) (re:45911) (di:direct) ECU70214 U70214 g1552766 Escherichia coli 562 -11534157 239817 yaeq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 18 of 400 of the completegenome.) (nt:o181; 99 pct identical to gb: ecodnae_8) (le:4692) (re:5237) (di:direct) AE000128 AE000128 g1786388 Escherichia coli 562 -11534157 5000691415 (de:(ecoli_190) (pn:hypothetical 20) (gn:yaeq) (gtcfc:13.7:14.1) (ec:) (yaeq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_190 ECOLI_190 Escherichia coli 562 10118930

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841075	9668	31824	588	195

Description

6500730300 yaej:b0191 hypothetical protein in acca-cutf intergenic region:hypothetical 15.6 kd protein in mesj-cutf intergenic region:orf140 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0191 b0191 Escherichia coli 562 -11534158 109693 yaej (de:hypothetical 15.6 kd protein in mesj-cutf intergenic region (orf140)) (db:swissprot) YAEJ_ECOLI P40711 ESCHERICHIA COLI 562 -11534158 7000687183 yaej yaej protein (db:pir2.dat) G64743 G64743 Escherichia coli 562 -11534158 222550 yaej:a hypotheticala...:function yaej (sr:escherichia coli (strain:k-12, isolate:w3110) dna) (db:genpept-bct1) (de:escherichia coli genes for dnae, acca, ldcc, yaer, yaen, yaeo,yaep, yaeq, yaej, nlpe, yaef complete cds and partial cds.) (le:6300) (re:6722) (di:direct) D49445 D49445 g1785845 Escherichia coli 562 -11534158 239818 (sr:escherichia coli (strain mc4100) (clone: 1) dna) (db:genpept-bct1) (de:escherichia coli orf 140, lipoprotein (cutf), and lipoprotein(orf292) genes, complete cds.) (nt:orf 140; significant similarity to orf next to) (le:290) (re:712) (di:direct) ECOCUTF L38619 g845336 Escherichia coli 562 -11534158 7500896093 yaej (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:45908) (re:46330) (di:direct) ECU70214 U70214 g1552767 Escherichia coli 562 -11534158 234073 yaej orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 18 of 400 of the completengenome.) (nt:o140; 99 pct identical to gb: ecodnae_9) (le:5234) (re:5656) (di:direct) AE000128 AE000128 g1786389 Escherichia coli 562 -11534158 5000691416 (de:(ecoli_191) (pn:hypothetical 15) (gn:yaej) (gtcfc:13.7:14.1) (ec:) (yaej_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_191 ECOLI_191 Escherichia coli 562 10051425

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841076	9669	31825	477	158

Description

GTC ORF with score 557 to: (sr:baker"s yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome viii cosmid 9186.) (nt:highly similar to 6-phosphogluconate dehydrogenase,) (le:7281) (re:8750) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841077	9670	31826	312	103

Description

6500730301 yaef:b0193 hypothetical 32.1 kd lipoprotein in cutf-pros
intergenic region:hypothetical 32.1 kd lipoprotein in cutf-pros intergenic
region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0193 b0193 Escherichia coli 562 -11534159 109687
yaef (de:precursor) (db:swissprot) YAEF_ECOLI P37056 ESCHERICHIA COLI 562
-11534159 7000687181 yaef yaef protein (db:pir2.dat) A64744 A64744
Escherichia coli 562 -11534159 222552 yaef:a hypotheticala...:function yaef
(sr:escherichia coli (strain:k-12, isolate:w3110) dna) (db:genpept-bct1)
(de:escherichia coli genes for dnae, acca, ldcc, yaer, yaen, yaeo,yaep,
yaeq, yaej, nlpe, yaef complete cds and partial cds.) (le:7646) (re:8524)
(di:complement) D49445 D49445 g1122214 Escherichia coli 562 -11534159
236178 lipoprotein (fn:defect leads to temperature-sensitivity)
(sr:escherichia coli (strain mc4100) (clone: 1) dna) (db:genpept-bct1)
(de:escherichia coli orf 140, lipoprotein (cutf), and lipoprotein(orf292)
genes, complete cds.) (nt:orf 292; amino acid feature: lipobox... ECOCUTF
L38619 g845338 Escherichia coli 562 -11534159 239820 hypothetical 18.5 kd
protein (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1)
(de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:alternate gene name
yaef) (le:25735) (re:26613) (di:complement) ECOTSF D83536 g1208960
Escherichia coli 562 -11534159 303255 yaef (db:genpept-bct1)
(de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:47254)
(re:48132) (di:complement) ECU70214 U70214 g1552769 Escherichia coli 562
-11534159 234075 yaef orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 18 of 400 of the
completegenome.) (nt:f292; 100 pct identical to yaef_ecoli sw: p37056)
(le:6580) (re:7458) (di:complement) AE000128 AE000128 g1786391 Escherichia
coli 562 -11534159 5000691418 (de:(ecoli_193) (pn:hypothetical 32)
(gn:yaef) (gtcfc:13.7:14.1) (ec:) (yaef_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_193 ECOLI_193 Escherichia coli 562 10051419

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841087	9671	31827	456	151

Description

6500730302 yaeb:b0195 hypothetical 26.4 kd protein in pros-rscsf intergenic region:orf3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0195 b0195 Escherichia coli 562 -11534160 109676 yaeb (de:hypothetical 26.4 kd protein in pros-rscsf intergenic region (orf3)) (db:swissprot) YAEB_ECOLI P28634 ESCHERICHIA COLI 562 -11534160 7000687177 yaeb yaeb protein (db:pir2.dat) C64744 C64744 Escherichia coli 562 -11534160 239822 orf235 (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:e.coli genomic dna, 5'flanking region of rrnh gene.) (le:577) (re:1284) (di:complement) ECORRNHK12 D15061 g303558 Escherichia coli 562 -11534160 7500896088 yaeb (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:49962) (re:50669) (di:complement) ECU70214 U70214 g1552771 Escherichia coli 562 -11534160 235929 yaeb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 18 of 400 of the completegenome.) (nt:f235; 100 pct identical to yaeb_ecoli sw: p28634) (le:9288) (re:9995) (di:complement) AE000128 AE000128 g1786393 Escherichia coli 562 -11534160 5000691419 (de:(ecoli_195) (pn:hypothetical 26) (gn:yaeb) (gtcfc:13.7:14.1) (ec:) (yaeb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_195 ECOLI_195 Escherichia coli 562 10051408

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841088	9672	31828	579	192

Description

6500730303 yaec:b0197 hypothetical 29.4 kd lipoprotein in rcsf-rrnh intergenic region:hypothetical 29.4 kd lipoprotein in rcsf-abc intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0197 b0197 Escherichia coli 562 -11534161 109680 yaec (de:precursor) (db:swissprot) YAEK_ECOLI P28635 ESCHERICHIA COLI 562 -11534161 7000687178 yaec probable lipoprotein yaec (cl:lipoprotein-28) (db:pir2.dat) E64744 E64744 Escherichia coli 562 -11534161 236182 orf271 (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:e.coli genomic dna, 5'flanking region of rrnh gene.) (le:1803) (re:2618) (di:complement) ECORRNHK12 D15061 g303560 Escherichia coli 562 -11534161 239824 hypothetical 29.4 kd lipoprotein precursor (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:alternate gene name yaec) (le:29660) (re:30475) (di:complement) ECOTSF D83536 g1208964 Escherichia coli 562 -11534161 303259 yaec (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:51188) (re:52003) (di:complement) ECU70214 U70214 g1552773 Escherichia coli 562 -11534161 235931 yaec putative lipoprotein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 19 of 400 of the completegenome.) (nt:f271; 100 pct identical to yaec_ecoli sw: p28635) (le:89) (re:904) (di:complement) AE000129 AE000129 g1786396 Escherichia coli 562 -11534161 5000691420 (de:(ecoli_197) (pn:hypothetical 29) (gn:yaec) (gtcfc:13.7:14.1) (ec:) (yaec_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_197 ECOLI_197 Escherichia coli 562 10051412

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501841100	9673	31829	759	252

Description

6500730304 yaed:b0200 hypothetical 21.3 kd protein in abc-rrsh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0200 b0200 Escherichia coli 562 -11534162 109682 yaed (de:hypothetical 21.3 kd protein in abc-rrsh intergenic region) (db:swissprot) YAED_ECOLI P31546 ESCHERICHIA COLI 562 -11534162 7000687179 yaed yaed protein (cl:lmbk protein) (db:pir2.dat) H64744 H64744 Escherichia coli 562 -11534162 239827 hypothetical 21.3 kd protein (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:alternate gene name yaed) (le:32379) (re:32954) (di:direct) ECOTSF D83536 g1208967 Escherichia coli 562 -11534162 303262 yaed (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:53908) (re:54483) (di:direct) ECU70214 U70214 g1552776 Escherichia coli 562 -11534162 236185 yaed putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 19 of 400 of the completegenome.) (nt:o191; 100 pct identical to yaed_ecoli sw: p31546) (le:2809) (re:3384) (di:direct) AE000129 AE000129 g1786399 Escherichia coli 562 -11534162 5000691422 (de:(ecoli_200) (pn:hypothetical 21) (gn:yaed) (gtcfc:13.7:14.1) (ec:) (yaed_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_200 ECOLI_200 Escherichia coli 562 10051414

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501841105	9674	31830	327	108

Description

6500730305 yafb:b0207 hypothetical 29.4 kd protein in aspu-dnir intergenic region:hypothetical oxidoreductase in aspu-mltd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0207 b0207 Escherichia coli 562 -11534163 7000689026 yafb yafb protein (cl:aldehyde reductase) (db:pir2.dat) (mp:5.2 min) A64745 A64745 Escherichia coli 562 -11534163 7500953796 yafb (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:60242) (re:61045) (di:direct) ECU70214 U70214 g1552777 Escherichia coli 562 -11534163 239828 yafb putative aldose reductase ec 1.1.1.21 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 19 of 400 of the completegenome.) (nt:o267; 100 pct identical to yafb_ecoli sw: p30863) (le:9143) (re:9946) (di:direct) AE000129 AE000129 g1786400 Escherichia coli 562 -11534163 5000691423 (de:(ecoli_201) (pn:hypothetical 29) (gn:yafb) (gtcfc:13.7:14.1) (ec:) (yafb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_201 ECOLI_201 Escherichia coli 562 10122704

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841117	9675	31831	894	297

Description

6500730306 yafc:b0208 hypothetical transcriptional regulator in rrnh-dnir intergenic region:hypothetical transcriptional regulator in aspu-mltd intergenic region:orf304 (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0208 b0208 Escherichia coli 562 -11534164 109725 yafc (de:(orf304)) (db:swissprot) YAFC_ECOLI P30864 ESCHERICHIA COLI 562 -11534164 163271 yafc probable transcription regulator yafc (cl:conserved hypothetical protein hi1364) (db:pir2.dat) (mp:5.2 min) JS0716 JS0716 Escherichia coli 562 -11534164 236187 yafb orf304 (sr:escherichia coli (sub_strain w3110, strain k-12) (library) (db:genpept-bct1) (de:e.coli rrnh and yaf(a-d) genes for trna-asp and orfs.) (nt:stop codons of orf267 and orf304 overlap each) (le:1049) (re:1963) (di:complement) ECORRNHASP D12650 g216646 Escherichia coli 562 -11534164 239829 hypothetical 33.8 kd protein (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:alternate gene name yafc) (le:39508) (re:40422) (di:complement) ECOTSF D83536 g1208969 Escherichia coli 562 -11534164 303264 yafc (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:61042) (re:61956) (di:complement) ECU70214 U70214 g1552778 Escherichia coli 562 -11534164 235925 yafc putative transcriptional regulator lysr-type (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 19 of 400 of the completegenome.) (nt:f304; 99 pct identical to yafc_ecoli sw: p30864) (le:9943) (re:10857) (di:complement) AE000129 AE000129 g1786401 Escherichia coli 562 -11534164 5000691424 (de:(ecoli_202) (pn:hypothetical transcriptional regulator in aspu-dnir intergenic region:orf304) (gn:yafc) (gtcfc:13.7:14.1) (ec:) (yafc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_202 ECOLI_202 Escherichia coli 562 10051457

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841125	9676	31832	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841132	9677	31833	1401	467

Description

6500730307 yafd:b0209 hypothetical protein in aspu-dnir intergenic region
 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0209
 b0209 Escherichia coli 562 -11534165 7000690933 yafd yafd protein
 (db:pir2.dat) (mp:5.2 min) C64745 C64745 Escherichia coli 562 -11534165
 7500960490 yafd orf:hypothetical protein (fn:orf; unknown)
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 20 of 400 of the
 completegenome.) (nt:o266; 100 pct identical to 259 aa yafd_ecoli) (le:151)
 (re:951) (di:direct) AE000130 AE000130 g1786403 Escherichia coli 562
 -11534165 5000691425 (de:(ecoli_203) (pn:hypothetical 29) (gn:yafd)
 (gtcfc:13.7:14.1) (ec:) (yafd_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli)) ECOLI_203 ECOLI_203 Escherichia coli 562 10122705

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841158	9678	31834	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841159	9679	31835	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841171	9680	31836	1320	439

Description

6500730308 yafe:b0210 hypothetical 23.0 kd protein in aspu-dnir intergenic region:hypothetical 23.0 kd protein in aspu-mltd intergenic region:orf207 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0210 b0210 Escherichia coli 562 -11534166 109727 yafe (de:hypothetical 23.0 kd protein in aspu-mltd intergenic region (orf207)) (db:swissprot) YAFE_ECOLI P30866 ESCHERICHIA COLI 562 -11534166 163259 yafe yafe protein (cl:escherichia coli yafe protein:bioc homology) (db:pir2.dat) (mp:5.2 min) JS0718 JS0718 Escherichia coli 562 -11534166 236189 yafd orf207 (sr:escherichia coli (sub_strain w3110, strain k-12) (library) (db:genpept-bct1) (de:e.coli rrnh and yaf(a-d) genes for trna-asp and orfs.) (le:3008) (re:3631) (di:direct) ECORRNHASP D12650 g216648 Escherichia coli 562 -11534166 239831 hypothetical 23.0 kd protein (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:alternate gene name yafe) (le:41467) (re:42090) (di:direct) ECOTSF D83536 g1208971 Escherichia coli 562 -11534166 303266 yafe (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:63001) (re:63624) (di:direct) ECU70214 U70214 g1552780 Escherichia coli 562 -11534166 235927 yafe putative biotin synthesis protein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 20 of 400 of the completegenome.) (nt:o207; 100 pct identical to yafe_ecoli sw: p30866) (le:955) (re:1578) (di:direct) AE000130 AE000130 g1786404 Escherichia coli 562 -11534166 5000691426 (de:(ecoli_204) (pn:hypothetical 23) (gn:yafe) (gtcfc:13.7:14.1) (ec:) (yafe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_204 ECOLI_204 Escherichia coli 562 10051459

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841192	9681	31837	225	74

Description

6500730309 yafs:b0213 hypothetical protein:hypothetical 28.0 kd protein in glob-rnha intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0213 b0213 Escherichia coli 562 -11534167 4000709256 yafs (de:hypothetical 28.0 kd protein in glob-rnha intergenic region) (db:swissprot) YAFS_ECOLI P75672 ESCHERICHIA COLI 562 -11534167 7000687195 probable membrane protein yafs:conserved hypothetical protein b0213 (db:pir2.dat) G64745 G64745 Escherichia coli 562 -11534167 7500896137 yafs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 20 of 400 of the completegenome.) (nt:o246) (le:3827) (re:4567) (di:direct) AE000130 AE000130 g1786407 Escherichia coli 562 -11534167 5000691428 (de:(ecoli_207) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_207 ECOLI_207 Escherichia coli 562 10122707

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841200	9682	31838	624	207

Description

6500730310 yaft:b0217 hypothetical protein:hypothetical 29.6 kd lipoprotein in dnaq-gmha intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0217 b0217 Escherichia coli 562 -11534168 4000709257 yaft (de:precursor) (db:swissprot) YAFI_ECOLI P77339 ESCHERICHIA COLI 562 -11534168 7000687196 yaft yaft protein (db:pir2.dat) B64746 B64746 Escherichia coli 562 -11534168 7500896138 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical protein) (le:68410) (re:69195) (di:direct) ECU70214 U70214 g1552786 Escherichia coli 562 -11534168 239837 yaft putative aminopeptidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 20 of 400 of the completegenome.) (nt:o261) (le:6364) (re:7149) (di:direct) AE000130 AE000130 g1786410 Escherichia coli 562 -11534168 5000691429 (de:(ecoli_210) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_210 ECOLI_210 Escherichia coli 562 10122708

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841203	9683	31839	951	316

Description

6500730311 yafu:b0218 hypothetical protein:hypothetical 12.1 kd protein in dnaq-gmha intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0218 b0218 Escherichia coli 562 -11534169 4000709258 yafu (de:hypothetical 12.1 kd protein in dnaq-gmha intergenic region) (db:swissprot) YAFU_ECOLI P77354 ESCHERICHIA COLI 562 -11534169 7000687197 yafu yafu protein:hypothetical protein b0218 (db:pir2.dat) C64746 C64746 Escherichia coli 562 -11534169 7500896139 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical protein) (le:69821) (re:70159) (di:complement) ECU70214 U70214 g1552788 Escherichia coli 562 -11534169 239839 yafu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 20 of 400 of the completegenome.) (nt:f112) (le:7775) (re:8113) (di:complement) AE000130 AE000130 g1786411 Escherichia coli 562 -11534169 5000691430 (de:(ecoli_211) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_211 ECOLI_211 Escherichia coli 562 10122709

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841228	9684	31840	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841230	9685	31841	966	321

Description

6500730312 yafv:b0219 hypothetical protein:hypothetical 28.9 kd protein in dnaq-gmha intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0219 b0219 Escherichia coli 562 -11534170
 4000709937 yafv (de:hypothetical 28.9 kd protein in dnaq-gmha intergenic region) (db:swissprot) YAFV_ECOLI Q47679 ESCHERICHIA COLI 562 -11534170
 7000687198 yafv yafv protein:protein b0219 (db:pir2.dat) D64746 D64746 Escherichia coli 562 -11534170 239840 unknown (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:orf182; similar to staphylococcus aureus) (le:48960) (re:49730) (di:complement) ECOTSF D83536 g1208977 Escherichia coli 562 -11534170 303272 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical protein) (le:70494) (re:71264) (di:complement) ECU70214 U70214 g1552789 Escherichia coli 562 -11534170 236195 yafv putative ec 3.5. amidase-type enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 20 of 400 of the completegenome.) (nt:f256; 100 pct identical to hypothetical protein) (le:8448) (re:9218) (di:complement) AE000130 AE000130 g1786412 Escherichia coli 562 -11534170 5000691431 (de:(ecoli_212) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_212 ECOLI_212 Escherichia coli 562 10122710

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841238	9686	31842	861	286

Description

6500730313 ykfe:b0220 hypothetical protein:unknown protein 2d_0001sd from 2d-page precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0220 b0220 Escherichia coli 562 -11534171 103756 ykfe (de:unknown protein 2d_0001sd from 2d-page precursor) (db:swissprot) UP18_ECOLI P45502 ESCHERICHIA COLI 562 -11534171 7000686895 ykfe probable membrane protein ykfe:hypothetical protein b0220 (db:pir2.dat) E64746 E64746 Escherichia coli 562 -11534171 7500893822 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical protein) (le:71418) (re:71891) (di:direct) ECU70214 U70214 g1552790 Escherichia coli 562 -11534171 239841 ykfe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 20 of 400 of the completegenome.) (nt:o157) (le:9372) (re:9845) (di:direct) AE000130 AE000130 g1786413 Escherichia coli 562 -11534171 5000691432 (de:(ecoli_213) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_213 ECOLI_213 Escherichia coli 562 10122711

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841246	9687	31843	474	157

Description

5000691433 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0221 b0221 Escherichia coli 562 -11534172
7000690993 probable membrane protein b0221:hypothetical protein b0221
(db:pir2.dat) F64746 F64746 Escherichia coli 562 -11534172 7500960428 yafh
putative acyl-coa dehydrogenase ec 1.3.99.- (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 20 of
400 of the completegenome.) (nt:f826; 99 pct identical to 814 aa
hypothetical) (le:9888) (re:12368) (di:complement) AE000130 AE000130
g1786414 Escherichia coli 562 -11534172 6500730314 hypothetical protein
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0221
b0221 Escherichia coli 562 -11534172

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841249	9688	31844	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841250	9689	31845	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841255	9690	31846	285	94

Description

6500730315 yafj:b0223 hypothetical protein in gmha-fhia intergenic region:hypothetical 28.6 kd protein in gmha-dinj intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0223 b0223 Escherichia coli 562 -11534173 118666 yafj (de:hypothetical 28.6 kd protein in gmha-dinj intergenic region) (db:swissprot) YAFJ_ECOLI Q47147 ESCHERICHIA COLI 562 -11534173 7000687187 yafj yafj protein:protein b0223 (cl:hypothetical protein h1037) (db:pir2.dat) H64746 H64746 Escherichia coli 562 -11534173 239844 yafj (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yafl, yafm, fhia, mbha, dinp, yafn, yafp and yafp.') (nt:hypothetical) (le:1969) (re:2736) (di:d... ECODINJ D38582 g984579 Escherichia coli 562 -11534173 7500896126 yafj (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:75402) (re:76169) (di:direct) ECU70214 U70214 g1552793 Escherichia coli 562 -11534173 234157 yafj putative amidotransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the completegenome.) (nt:o255; 100 pct identical to gb: ecodinj_3) (le:916) (re:1683) (di:direct) AE000131 AE000131 g1786417 Escherichia coli 562 -11534173 5000691435 (de:(ecoli_216) (pn:hypothetical protein in gmha-fhia intergenic region) (gn:yafj) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_216 ECOLI_216 Escherichia coli 562 10060986

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841260	9691	31847	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841267	9692	31848	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841302	9693	31849	753	250

Description

GTC ORF with score 186 to: (fn:transfer of methyl group from sam to aklanonic) (sr:streptomyces sp. (strain c5) dna) (db:genpept-bct1) (de:streptomyces sp. acyltransferase (daua) gene, 3' end; aklanonicacid methyltransferase (dauc) gene, daud gene, and...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841303	9694	31850	438	145

Description

6500730316 yafk:b0224 hypothetical protein in gmha-fhia intergenic region:hypothetical 28.0 kd protein in gmha-dinj intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0224 b0224 Escherichia coli 562 -11534174 118667 yafk (de:hypothetical 28.0 kd protein in gmha-dinj intergenic region precursor) (db:swissprot) YAFK_ECOLI Q47148 ESCHERICHIA COLI 562 -11534174 7000687188 yafk probable membrane protein yafk (db:pir2.dat) A64747 A64747 Escherichia coli 562 -11534174 239845 yafk (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yaf1, yafm, fhia, mbha, dinp, yafn, yafo and yafp.) (nt:hypothetical) (le:2707) (re:3447) (di:c... ECODINJ D38582 g984580 Escherichia coli 562 -11534174 7500896128 yafk (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:76140) (re:76880) (di:complement) ECU70214 U70214 g1552794 Escherichia coli 562 -11534174 234158 yafk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the completegenome.) (nt:f246; 100 pct identical to gb: ecodinj_4) (le:1654) (re:2394) (di:complement) AE000131 AE000131 g1786418 Escherichia coli 562 -11534174 5000691436 (de:(ecoli_217) (pn:hypothetical protein in gmha-fhia intergenic region) (gn:yafk) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_217 ECOLI_217 Escherichia coli 562 10060987

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841308	9695	31851	309	102

Description

6500730317 yafq:b0225 hypothetical protein in gmha-fhia intergenic region:hypothetical 10.8 kd protein in gmha-dinj intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0225 b0225 Escherichia coli 562 -11534175 118672 yafq (de:hypothetical 10.8 kd protein in gmha-dinj intergenic region) (db:swissprot) YAFQ_ECOLI Q47149 ESCHERICHIA COLI 562 -11534175 7000687194 yafq yafq protein:conserved hypothetical protein b0225:10.8k (cl:conserved hypothetical protein hi0711) (db:pir2.dat) B64747 B64747 Escherichia coli 562 -11534175 7500896135 yafq yafq (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yafl, yafm, fhia, mbha, dinp, yafn, yafo and yafp.) (nt:hypothetical) (le:3603) (re:3881) (di:c... ECODINJ D38582 g984581 Escherichia coli 562 -11534175 234159 yafq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the completegenome.) (nt:f92; 100 pct identical to gb: ecodinj_5) (le:2550) (re:2828) (di:complement) AE000131 AE000131 g1786419 Escherichia coli 562 -11534175 5000691437 (de:(ecoli_218) (pn:hypothetical protein in gmha-fhia intergenic region) (gn:yafq) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_218 ECOLI_218 Escherichia coli 562 10060992

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841313	9696	31852	276	91

Description

6500730318 yaf1:b0227 hypothetical protein in gmha-fhia intergenic region:hypothetical 28.8 kd lipoprotein in dinj-fhia intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0227 b0227 Escherichia coli 562 -11534176 119931 yaf1 (de:precursor) (db:swissprot) YAF1_ECOLI Q47151 ESCHERICHIA COLI 562 -11534176 7000687189 yaf1 probable lipoprotein yaf1 (db:pir2.dat) D64747 D64747 Escherichia coli 562 -11534176 239846 yaf1 (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yaf1, yafm, fhia, mbha, dinp, yafn, yafp and yafp.) (nt:hypothetical; similarity to p60_lisiv (... ECODINJ D38582 g984583 Escherichia coli 562 -11534176 7500896129 yaf1 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:77787) (re:78536) (di:direct) ECU70214 U70214 g1552795 Escherichia coli 562 -11534176 234161 yaf1 putative lipoprotein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the completegenome.) (nt:o249; 100 pct identical to gb: ecodinj_7) (le:3301) (re:4050) (di:direct) AE000131 AE000131 g1786421 Escherichia coli 562 -11534176 5000691439 (de:(ecoli_220) (pn:hypothetical protein in gmha-fhia intergenic region) (gn:yaf1) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_220 ECOLI_220 Escherichia coli 562 10062684

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841324	9697	31853	468	155

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841327	9698	31854	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841332	9699	31855	408	135

Description

GTC ORF with score 148 to: (db:genpept-bct1) (de:pseudomonas aeruginosa pyoverdine chromophore biosynthesis genecluster including pvca (pvca), pvcb (pvcb), pvcc (pvcc), and pvcd(pvcd) genes, complete cds, and transcriptional activator ptxr(ptxr) gene, ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841334	9700	31856	1221	407

Description

GTC ORF with score 144 to: (db:genpept-bct1) (de:pseudomonas aeruginosa pyoverdine chromophore biosynthesis genecluster including pvca (pvca), pvcb (pvcb), pvcc (pvcc), and pvcd (pvcd) genes, complete cds, and transcriptional activator ptxr (ptxr) gene, ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841359	9701	31857	576	191

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841367	9702	31858	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841377	9703	31859	429	142

Description

6500730319 yafm:b0228 hypothetical protein in gmha-fhia intergenic region:hypothetical 20.0 kd protein in dinj-fhia intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0228 b0228 Escherichia coli 562 -11534177 118668 yafm (de:hypothetical 20.0 kd protein in dinj-fhia intergenic region) (db:swissprot) YAFM_ECOLI Q47152 ESCHERICHIA COLI 562 -11534177 7000687190 yafm yafm protein (cl:hypothetical protein hi0217) (db:pir2.dat) E64747 E64747 Escherichia coli 562 -11534177 239847 yafm (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yafl, yafm, fhia, mbha, dinp, yafn, yafo and yafp.) (nt:hypothetical) (le:5279) (re:5776) (di:d... ECODINJ D38582 g984584 Escherichia coli 562 -11534177 7500896130 yafm (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:78712) (re:79209) (di:direct) ECU70214 U70214 g1552796 Escherichia coli 562 -11534177 234162 yafm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the completegenome.) (nt:o165; 100 pct identical to gb: ecodinj_8) (le:4226) (re:4723) (di:direct) AE000131 AE000131 g1786422 Escherichia coli 562 -11534177 5000691440 (de:(ecoli_221) (pn:hypothetical protein in gmha-fhia intergenic region) (gn:yafm) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_221 ECOLI_221 Escherichia coli 562 10060988

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841380	9704	31860	519	173

Description

6500730320 fhia:b0229 hypothetical protein fhia:fhia protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0229 b0229 Escherichia coli 562 -11534178 118176 fhia (de:fhia protein) (db:swissprot) FHIA_ECOLI_Q47153 ESCHERICHIA COLI 562 -11534178 7000685232 fhia membrane protein fhia (db:pir2.dat) F64747 F64747 Escherichia coli 562 -11534178 239848 fhia (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yafl, yafm, fhia, mbha, dinp, yafn, yafo and yafp.) (nt:hypothetical; strong similarities to th... ECODINJ D38582 g984585 Escherichia coli 562 -11534178 7500881433 fhia fhia (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:79433) (re:81172) (di:complement) ECU70214 U70214 g1552797 Escherichia coli 562 -11534178 234163 fhia flagellar biosynthesis (fn:putative enzyme; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the completegenome.) (nt:f579; 100 pct identical to gb: ecodinj_9) (le:4947) (re:6686) (di:complement) AE000131 AE000131 g1786423 Escherichia coli 562 -11534178 5000691441 (de:(ecoli_222) (pn:hypothetical protein fhia) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_222 ECOLI_222 Escherichia coli 562 10060254

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841382	9705	31861	726	241

Description

6500730321 dinp:b0231 hypothetical protein dinp:dna-damage-inducible protein p (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0231 b0231 Escherichia coli 562 -11534179 121771 dinp (de:dna-damage-inducible protein p) (db:swissprot) DINP_ECOLI Q47155 ESCHERICHIA COLI 562 -11534179 7000685056 dinp dna-damage-inducible protein dinp (cl:umuc protein) (db:pir2.dat) H64747 H64747 Escherichia coli 562 -11534179 236199 dinp (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara')) (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj, yafI, yafm, fhia, mbha, dinp, yafn, yafo and yafp.) (nt:hypothetical; similarity to ylw6_caeel ... ECODINJ D38582 g984587 Escherichia coli 562 -11534179 239850 unknown (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:orf228) (le:60439) (re:61494) (di:direct) ECOTSF D83536 g1208981 Escherichia coli 562 -11534179 303276 dinp dinp (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:81973) (re:83028) (di:direct) ECU70214 U70214 g1552799 Escherichia coli 562 -11534179 234165 dinp damage-inducible protein p:putative trna (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the complete genome.) (nt:o351; 100 pct identical to gb: ecodinj_11) (le:7487) (re:8542) (di:direct) AE000131 AE000131 g1786425 Escherichia coli 562 -11534179 5000691443 (de:(ecoli_224) (pn:hypothetical protein dinp) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_224 ECOLI_224 Escherichia coli 562 10065246

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841399	9706	31862	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841400	9707	31863	531	176

Description

GTC ORF with score 97 to: (or:Glomerella cingulata) (db:genpept-pln1) (de:colletotrichum gloeosporioides nitrogen starvation-induced glutamine rich protein mrna, complete cds.) (nt:glutamine rich protein similar to glutenins;) (le:74) (re:721) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841403	9708	31864	561	186

Description

6500730322 yafn:b0232 hypothetical protein in mbha-prfh intergenic region:hypothetical 11.2 kd protein in dinp-prfh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0232 b0232 Escherichia coli 562 -11534180 118669 yafn (de:hypothetical 11.2 kd protein in dinp-prfh intergenic region) (db:swissprot) YAFN_ECOLI Q47156 ESCHERICHIA COLI 562 -11534180 7000687191 yafn yafn protein (db:pir2.dat) A64748 A64748 Escherichia coli 562 -11534180 239851 yafn (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yafl, yafm, fhia, mbha, dinp, yafn, yafo and yafp.) (nt:hypothetical) (le:9647) (re:9940) (di:d... ECODINJ D38582 g984588 Escherichia coli 562 -11534180 7500896132 yafn (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:83080) (re:83373) (di:direct) ECU70214 U70214 g1552800 Escherichia coli 562 -11534180 234166 yafn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the completegenome.) (nt:o97; 100 pct identical to gb: ecodinj_12) (le:8594) (re:8887) (di:direct) AE000131 AE000131 g1786426 Escherichia coli 562 -11534180 5000691444 (de:(ecoli_225) (pn:hypothetical protein in mbha-prfh intergenic region) (gn:yafn) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_225 ECOLI_225 Escherichia coli 562 10060989

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841409	9709	31865	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841411	9710	31866	609	203

Description

6500730323 yafo:b0233 hypothetical protein in mbha-prfh intergenic region:hypothetical 15.5 kd protein in dinp-prfh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0233 b0233 Escherichia coli 562 -11534181 118670 yafo (de:hypothetical 15.5 kd protein in dinp-prfh intergenic region) (db:swissprot) YAF0_ECOLI Q47157 ESCHERICHIA COLI 562 -11534181 7000687192 yafo yafo protein (db:pir2.dat) B64748 B64748 Escherichia coli 562 -11534181 239852 yafo (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yafl, yafm, fhia, mbha, dinp, yafn, yafo and yafp.) (nt:hypothetical) (le:9943) (re:10341) (di:... ECODINJ D38582 g984589 Escherichia coli 562 -11534181 7500896133 yafo (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:83376) (re:83774) (di:direct) ECU70214 U70214 g1552801 Escherichia coli 562 -11534181 234167 yafo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the completegenome.) (nt:o132; 100 pct identical to gb: ecodinj_13)' (le:8890) (re:9288) (di:direct) AE000131 AE000131 g1786427 Escherichia coli 562 -11534181 5000691445 (de:(ecoli_226) (pn:hypothetical protein in mbha-prfh intergenic region) (gn:yafo) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_226 ECOLI_226 Escherichia coli 562 10060990

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841419	9711	31867	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841420	9712	31868	684	227

Description

6500730324 yafp:b0234 hypothetical protein in mbha-prfh intergenic region:hypothetical 17.6 kd protein in dinp-prfh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0234 b0234 Escherichia coli 562 -11534182 118671 yafp (de:hypothetical 17.6 kd protein in dinp-prfh intergenic region) (db:swissprot) YAFP_ECOLI Q47158 ESCHERICHIA COLI 562 -11534182 7000687193 yafp protein yafp (cl:hypothetical protein sll1671) (db:pir2.dat) C64748 C64748 Escherichia coli 562 -11534182 239853 yafp (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yafl, yafm, fhia, mbha, dinp, yafn, yafp and yafp.') (nt:hypothetical) (le:10351) (re:10803) (di... ECODINJ D38582 g984590 Escherichia coli 562 -11534182 7500896134 yafp (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:83784) (re:84236) (di:direct) ECU70214 U70214 g1552802 Escherichia coli 562 -11534182 234168 yafp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the completengenome.) (nt:o150; 100 pct identical to gb: ecodinj_14) (le:9298) (re:9750) (di:direct) AE000131 AE000131 g1786428 Escherichia coli 562 -11534182 5000691446 (de:(ecoli_227) (pn:hypothetical protein in mbha-prfh intergenic region) (gn:yafp) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_227 ECOLI_227 Escherichia coli 562 10060991

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841425	9713	31869	522	173

Description

5000691447 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0235 b0235 Escherichia coli 562 -11534183 7000690994 conserved hypothetical protein b0235 (db:pir2.dat) D64748 D64748 Escherichia coli 562 -11534183 7500959713 b0235 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 22 of 400 of the completengenome.) (nt:o88) (le:183) (re:449) (di:direct) AE000132 AE000132 g1786430 Escherichia coli 562 -11534183 6500730325 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0235 b0235 Escherichia coli 562 -11534183

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841426	9714	31870	297	99

Description

6500730326 yafa:b0239 hypothetical protein in gpt-crl intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0239 b0239 Escherichia coli 562 -11534184 7000688990 yafa yafa protein:49k (cl:yafa protein) (db:pir1.dat) (mp:6 min) QQEC49 H64748 Escherichia coli 562 -11534184 7500953691 yafa (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:87602) (re:88846) (di:direct) ECU70214 U70214 g1552807 Escherichia coli 562 -11534184 239858 yafa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 22 of 400 of the completegenome.) (nt:o414; 99 pct identical to yafa_ecoli sw: p04335 but) (le:3243) (re:4487) (di:direct) AE000132 AE000132 g1786434 Escherichia coli 562 -11534184 5000691448 (de:(ecoli_232) (pn:hypothetical 49) (gn:yafa) (gtcfc:13.7:14.1) (ec:)(yafa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_232 ECOLI_232 Escherichia coli 562 10122716

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841431	9715	31871	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841432	9716	31872	399	132

Description

5000691449 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0245 b0245 Escherichia coli 562 -11534185 7500938469 ykfi (de:hypothetical 12.9 kd protein in proa-perr intergenic region) (db:swissprot) YKFI_ECOLI P77692 ESCHERICHIA COLI 562 -11534185 7000690995 hypothetical protein b0245 (db:pir2.dat) E64749 E64749 Escherichia coli 562 -11534185 239863 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to e. coli orf_o109) (le:93627) (re:93968) (di:complement) ECU70214 U70214 g1552812 Escherichia coli 562 -11534185 7500938471 b0245 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 22 of 400 of the completegenome.) (nt:f113; 31 pct identical (3 gaps) to 67 residues of) (le:9268) (re:9609) (di:complement) AE000132 AE000132 g1786439 Escherichia coli 562 -11534185 6500730327 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0245 b0245 Escherichia coli 562 -11534185

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841453	9717	31873	327	108

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841508	9718	31874	927	309

Description

6500730328 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0247 b0247 Escherichia coli 562 -11534186
7500938466 ykfg (de:hypothetical 18.1 kd protein in proa-perr intergenic region) (db:swissprot) YKFG_ECOLI Q47685 ESCHERICHIA COLI 562 -11534186
7000690996 hypothetical protein b0247 (db:pir2.dat) G64749 G64749 Escherichia coli 562 -11534186 236209 unknown (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:orf285; similar to radc, pir accession number) (le:72994) (re:73470) (di:complement) ECOTSF D83536 g1208991 Escherichia coli 562 -11534186 7500938468 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to e. coli orf_o160, also similar to radc) (le:94555) (re:95031) (di:complement) ECU70214 U70214 g1552815 Escherichia coli 562 -11534186 239866 ykfg putative dna repair protein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 23 of 400 of the completegenome.) (nt:f158; similar to radc_ecoli sw: p25531 (148 aa)) (le:50) (re:526) (di:complement) AE000133 AE000133 g2367100 Escherichia coli 562 -11534186 303286 unknown (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:orf285; similar to radc, pir accession number) (le:72994) (re:73470) (di:complement) ECOTSF D83536 g1208991 Escherichia coli 562 -11534186

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841509	9719	31875	921	306

Description

5000691452 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0249 b0249 Escherichia coli 562 -11534187
7500938463 ykff (de:hypothetical 9.0 kd protein in proa-perr intergenic region) (db:swissprot) YKFF_ECOLI P75677 ESCHERICHIA COLI 562 -11534187
7000690997 hypothetical protein b0249 (db:pir2.dat) A64750 A64750 Escherichia coli 562 -11534187 7500938465 ykff orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 23 of 400 of the completegenome.) (nt:f80; 30 pct identical (4 gaps) to 75 residues from) (le:1098) (re:1337) (di:complement) AE000133 AE000133 g1786443 Escherichia coli 562 -11534187 6500730329 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0249 b0249 Escherichia coli 562 -11534187

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841526	9720	31876	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841534	9721	31877	1179	393

Description

5000691458 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0255 b0255 Escherichia coli 562 -11534188
7000690998 hypothetical protein b0255 (db:pir2.dat) G64750 G64750 Escherichia coli 562 -11534188 7500959858 yi91a is911 hypothetical protein:variant is911a (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 23 of 400 of the completegenome.) (nt:o134; phage stats; 97 pct identical to 100 residues) (le:6036) (re:6440) (di:direct) AE000133 AE000133 g1786449 Escherichia coli 562 -11534188 6500730330 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0255 b0255 Escherichia coli 562 -11534188

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841541	9722	31878	198	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841548	9723	31879	672	223

Description

5000691460 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0257 b0257 Escherichia coli 562 -11534189
7000690999 hypothetical protein b0257 (db:pir2.dat) A64751 A64751 Escherichia coli 562 -11534189 7500959859 b0257 putative transposase (fn:is, phage, tn; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 23 of 400 of the completegenome.) (nt:o141; poor stats) (le:7624) (re:8049) (di:direct) AE000133 AE000133 g1786451 Escherichia coli 562 -11534189 6500730331 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0257 b0257 Escherichia coli 562 -11534189

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841554	9724	31880	453	150

Description

5000691462

yi52_1:yi52_2:yi52_3:yi52_4:yi52_7:yi52_8:yi52_9:yi52_10:yi52_11:b0259
insertion element is5 hypothetical 39.3 kd protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0259 b0259
Escherichia coli 562 -11534190 113090 b3218:b3505 (de:transposase for
insertion sequence element is5) (db:swissprot) TRS5_ECOLI P03837 ESCHERICHIA
COLI 562 -11534190 135239 yi52_11 hypothetical 39k protein insertion
sequence is5:hypothetical protein f338 (db:pir1.dat) IEEC5D A91483
Escherichia coli 562 -11534190 223597 is5 (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #260(29.8-30.2 min.)) (nt:orf_id:o261#1; similar to (pir
accession number) (le:14549) (re:15565) (di:direct) D90771 D90771 g1742188
Escherichia coli 562 -11534190 223607 is5 (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #261(30.0-30.3 min.)) (nt:orf_id:o261#1; similar to (pir
accession number) (le:4614) (re:5630) (di:direct) D90772 D90772 g1742199
Escherichia coli 562 -11534190 224397 is5 (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #339(42.4-42.8 min.)) (nt:orf_id:o339#6; similar to (pir
accession number) (le:9958) (re:10974) (di:complement) D90831 D90831
g1736552 Escherichia coli 562 -11534190 224554 is5 (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.))
(nt:orf_id:o351#4; similar to (pir accession number) (le:8195) (re:9211)
(di:complement) D90841 D90841 g1736719 Escherichia coli 562 -11534190
224646 is5 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#359(46.8-47.2 min.)) (nt:orf_id:o359#1; similar to (pir accession number)
(le:1605) (re:2621) (di:direct) D90848 D90848 g1736818 Escherichia coli 562
-11534190 301194 is5 transposase (db:genpept-bct1) (de:escherichia coli
transposon is5 within tdc operon.) (le:320) (re:1336) (di:complement)
ECI5STDC AJ001620 g2597886 Escherichia coli 562 -11534190 301286
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to
76.0 minutes.) (nt:orf_f338) (le:146447) (re:147463) (di:complement) ECOUW67
U18997 g606157 Escherichia coli 562 -11534190 5500684812 (sr:escherichia
coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1)
(de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:orf in is5)
(le:66441) (re:67457) (di:complement) ECOUW76 U00039 g466642 Escherichia
coli 562 -11534190 7500893509 (db:genpept-bct1) (de:escherichia coli k-12
genome; approximately 65 to 68 minutes.) (nt:orf_o338) (le:84569) (re:85585)
(di:direct) ECU28377 U28377 g882511 Escherichia coli 562 -11534190
7500893510 is5 39.3kda protein (db:genpept-bct1) (de:escherichia coli
chromosome minutes 4-6.) (le:104400) (re:105416) (di:complement) ECU70214
U70214 g1552827 Escherichia coli 562 -11534190 7500893511 (db:genpept-bct1)
(de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical
protein) (le:128627) (re:129643) (di:complement) ECU82598 U82598 g1778575

protein) (le:128627) (re:129643) (di:complement) ECU82598 U82598 g1778575
~~Escherichia coli 562 -11534190 7500893512 (db:genpept-bct1) (de:escherichia~~

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841556	9725	31881	288	95

Description

6500730333 yagc:b0262 hypothetical abc transporter in argf-proa intergenic region:hypothetical abc transporter atp-binding protein in perr-argf intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0262 b0262 Escherichia coli 562 -11534191 7000689373 yagc probable abc-type transport protein b0262 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) F64751 F64751 Escherichia coli 562 -11534191 7500955266 yagc (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:108055) (re:109113) (di:complement) ECU70214 U70214 g1552831 Escherichia coli 562 -11534191 239882 afuc putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 24 of 400 of the completegenome.) (nt:f352; formerly designated yagc) (le:2561) (re:3619) (di:complement) AE000134 AE000134 g1786457 Escherichia coli 562 -11534191 5000691465 (de:(ecoli_253) (pn:hypothetical abc transporter atp-binding protein in thrw-argf intergenic region) (gn:yagc) (gtcfc:13.7:14.1) (ec:) (yagc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_253 ECOLI_253 Escherichia coli 562 10122732

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841561	9726	31882	303	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841565	9727	31883	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841578	9728	31884	462	153

Description

5000691466 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0263 b0263 Escherichia coli 562 -11534192
7000691000 probable membrane protein b0263:hypothetical protein b0263 (db:pir2.dat) G64751 G64751 Escherichia coli 562 -11534192 7500959860 b0263 putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 24 of 400 of the completegenome.) (nt:f120; 76 pct identical to 42 residues of an) (le:3619) (re:3981) (di:complement) AE000134 AE000134 g1786458 Escherichia coli 562 -11534192 6500730334 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0263 b0263 Escherichia coli 562 -11534192

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841581	9729	31885	492	163

Description

6500730335 yaga:b0267 hypothetical protein in argf-proa intergenic region:hypothetical 43.8 kd protein in perr-argf intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0267 b0267 Escherichia coli 562 -11534193 109743 yaga (de:hypothetical 43.8 kd protein in perr-argf intergenic region) (db:swissprot) YAGA_ECOLI P37007 ESCHERICHIA COLI 562 -11534193 7000687203 yaga yaga protein (db:pir2.dat) C64752 C64752 Escherichia coli 562 -11534193 7500896148 yaga (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to e. coli orf_o105) (le:111128) (re:112282) (di:complement) ECU70214 U70214 g1552836 Escherichia coli 562 -11534193 239887 yaga orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 24 of 400 of the completegenome.) (nt:f384; 92 pct identical to fragment yaga_ecoli) (le:5634) (re:6788) (di:complement) AE000134 AE000134 g1786462 Escherichia coli 562 -11534193 5000691470 (de:(ecoli_258) (pn:hypothetical 42) (gn:yaga) (gtcfc:13.7:14.1) (ec:) (yaga_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_258 ECOLI_258 Escherichia coli 562 10122735

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841588	9730	31886	357	118

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841601	9731	31887	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841608	9732	31888	822	273

Description

6500730336 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0279 b0279 Escherichia coli 562 -11534194
 7500896158 yagm (de:hypothetical 32.7 kd protein in argf-intf intergenic region) (db:swissprot) YAGM_ECOLI P71296 ESCHERICHIA COLI 562 -11534194
 7000691001 yagm yagm protein (db:pir2.dat) G64753 G64753 Escherichia coli 562 -11534194 239901 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:1743) (re:2597) (di:complement) ECU73857 U73857 g1657480 Escherichia coli 562 -11534194 7500896160 yagm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 25 of 400 of the completegenome.) (nt:f284; 100 pct identical to gb: ecu73857 accession) (le:8694) (re:9548) (di:complement) AE000135 AE000135 g2367101 Escherichia coli 562 -11534194

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841609	9733	31889	1023	340

Description

6500730337 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0280 b0280 Escherichia coli 562 -11534195
 7500896162 yagn (de:hypothetical 15.8 kd protein in argf-intf intergenic region) (db:swissprot) YAGN_ECOLI P71297 ESCHERICHIA COLI 562 -11534195
 7000691002 yagn yagn protein (db:pir2.dat) H64753 H64753 Escherichia coli 562 -11534195 239902 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:2937) (re:3377) (di:complement) ECU73857 U73857 g1657481 Escherichia coli 562 -11534195 7500896164 yagn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 25 of 400 of the completegenome.) (nt:f146; 100 pct identical to gb: ecu73857 accession) (le:9888) (re:10328) (di:complement) AE000135 AE000135 g2367102 Escherichia coli 562 -11534195

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841621	9734	31890	234	77

Description

6500730338 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0281 b0281 Escherichia coli 562 -11534196
7500884185 intf (de:putative integrase intf) (db:swissprot) INTF_ECOLI P71298 ESCHERICHIA COLI 562 -11534196 7000691003 intf probable integrase intf (db:pir2.dat) A64754 A64754 Escherichia coli 562 -11534196 239903 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:3494) (re:4894) (di:complement) ECU73857 U73857 g1657482 Escherichia coli 562 -11534196 7500884187 intf putative phage integrase (fn:is, phage, tn; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completegenome.) (nt:f466; 100 pct identical to gb: ecu73857 accession) (le:77) (re:1477) (di:complement) AE000136 AE000136 g2367104 Escherichia coli 562 -11534196

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841632	9735	31891	1557	518

Description

6500730339 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0288 b0288 Escherichia coli 562 -11534197
7500938496 ykgj (de:hypothetical 11.8 kd protein in intf-eaeh intergenic region) (db:swissprot) YKGJ_ECOLI P71300 ESCHERICHIA COLI 562 -11534197 7000691004 ykgj ykgj protein:conserved hypothetical protein b0288 (db:pir2.dat) H64754 H64754 Escherichia coli 562 -11534197 239910 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to putative ferredoxin of a. calcoaceticus) (le:11651) (re:11980) (di:complement) ECU73857 U73857 g1657489 Escherichia coli 562 -11534197 7500938498 ykgj putative ferredoxin (fn:putative carrier; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completegenome.) (nt:f109; residues 9-103 are 47 pct identical (2 gaps)) (le:8234) (re:8563) (di:complement) AE000136 AE000136 g2367105 Escherichia coli 562 -11534197

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841636	9736	31892	588	195

Description

6500730340 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0294 b0294 Escherichia coli 562 -11534198
 7500938500 ykgk (de:hypothetical 23.3 kd protein in intf-eaeh intergenic region) (db:swissprot) YKGK_ECOLI P71301 ESCHERICHIA COLI 562 -11534198
 7000691005 ykgk ykgk protein (db:pir2.dat) F64755 F64755 Escherichia coli 562 -11534198 239916 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:18544) (re:19134) (di:complement) ECU73857 U73857 g1657495 Escherichia coli 562 -11534198
 7500938502 ykgk putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 26 of 400 of the completegenome.) (nt:f196; 100 pct identical to gb: ecu73857 accession) (le:15127) (re:15717) (di:complement) AE000136 AE000136 g2367106 Escherichia coli 562 -11534198

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841637	9737	31893	963	320

Description

6500730341 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0295 b0295 Escherichia coli 562 -11534199
 7500938504 ykgl (de:hypothetical 8.8 kd protein in intf-eaeh intergenic region) (db:swissprot) YKGL_ECOLI P56257 ESCHERICHIA COLI 562 -11534199
 7000691006 ykgl ykgl protein (db:pir2.dat) G64755 G64755 Escherichia coli 562 -11534199 7500938506 ykgl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 26 of 400 of the completegenome.) (nt:o75; residues 32-64 are 31 pct identical to aa) (le:16493) (re:16720) (di:direct) AE000136 AE000136 g2367107 Escherichia coli 562 -11534199

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841641	9738	31894	783	260

Description

GTC ORF with score 95 to: (sr:pyrococcus horikoshii (strain:ot3) dna) (db:genpept-bct1) (de:pyrococcus horikoshii ot3 genomic dna, 1-287000 nt. position (1/7).) (nt:similar to pir:s59860 percent identity: 54.268 in) (le:15743) (re:16264) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841644	9739	31895	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841645	9740	31896	414	137

Description

6500730342 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0296 b0296 Escherichia coli 562 -11534200
 7500938507 ykgm (de:hypothetical 9.9 kd protein in intf-eaeh intergenic region) (db:swissprot) YKGM_ECOLI P71302 ESCHERICHIA COLI 562 -11534200
 7000689321 ykgm probable ribosomal protein l31:ykgm protein (cl:escherichia coli ribosomal protein l31) (db:pir2.dat) H64755 H64755 Escherichia coli 562 -11534200 7500938509 ykgm putative ribosomal protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:f87; 100 pct identical to gb: ecu73857 accession) (le:130) (re:393) (di:complement) AE000137 AE000137 g2367109 Escherichia coli 562 -11534200

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841649	9741	31897	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841650	9742	31898	1155	384

Description

5000691494 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0302 b0302 Escherichia coli 562 -11534201
 7000691007 probable membrane protein b0302 (db:pir2.dat) F64756 F64756 Escherichia coli 562 -11534201 7500959861 b0302 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:o89; 32 pct identical to 55 residues of an approx.) (le:5918) (re:6187) (di:direct) AE000137 AE000137 g1786493 Escherichia coli 562 -11534201 6500730343 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0302 b0302 Escherichia coli 562 -11534201

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841652	9743	31899	438	145

Description

5000691495 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0303 b0303 Escherichia coli 562 -11534202
 7500938493 ykgi (de:hypothetical 9.1 kd protein in eaeh-beta intergenic region) (db:swissprot) YKGI_ECOLI P75687 ESCHERICHIA COLI 562 -11534202
 7000691008 ykgi ykgi protein precursor (db:pir2.dat) G64756 G64756 Escherichia coli 562 -11534202 7500938495 ykgi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:f83; 28 pct identical to 60 residues of an approx.) (le:5947) (re:6198) (di:complement) AE000137 AE000137 g1786494 Escherichia coli 562 -11534202 6500730344 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0303 b0303 Escherichia coli 562 -11534202

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841667	9744	31900	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841668	9745	31901	384	127

Description

5000691501 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0309 b0309 Escherichia coli 562 -11534203
 7000691009 probable membrane protein b0309 (db:pir2.dat) E64757 E64757 Escherichia coli 562 -11534203 7500959862 b0309 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:f70; 26 pct identical (3 gaps) to 60 residues of) (le:12024) (re:12236) (di:complement) AE000137 AE000137 g1786500 Escherichia coli 562 -11534203 6500730345 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0309 b0309 Escherichia coli 562 -11534203

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841670	9746	31902	240	79

Description

6500730346 yaha:b0315 hypothetical protein in bett 3 region:hypothetical 40.7 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0315 b0315 Escherichia coli 562 -11534204 109762 yaha (de:hypothetical 40.7 kd protein in bett-prpr intergenic region) (db:swissprot) YAHA_ECOLI P21514 ESCHERICHIA COLI 562 -11534204 7000687224 yaha yaha protein (db:pir2.dat) (mp:7.5 min) C64758 C64758 Escherichia coli 562 -11534204 7500896180 yaha orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 28 of 400 of the completegenome.) (nt:o362; 100 pct identical to fragment yaha_ecoli) (le:7743) (re:8831) (di:direct) AE000138 AE000138 g1786507 Escherichia coli 562 -11534204 5000691503 (de:(ecoli_299) (pn:hypothetical protein in bett:3"region:fragment) (gn:yaha) (gtcfc:13.7:14.1) (ec:) (yaha_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_299 ECOLI_299 Escherichia coli 562 10122768

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841671	9747	31903	1125	375

Description

6500730347 yahb:b0316 hypothetical protein:hypothetical transcriptional regulator in bett-prpr intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0316 b0316 Escherichia coli 562 -11534205 4000708147 yahb (de:hypothetical transcriptional regulator in bett-prpr intergenic region) (db:swissprot) YAHB_ECOLI P77700 ESCHERICHIA COLI 562 -11534205 7000687225 yahb probable transcription regulator yahb (cl:probable transcription regulator ybbs) (db:pir2.dat) D64758 D64758 Escherichia coli 562 -11534205 7500896181 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to e. coli ydhh) (le:41298) (re:42230) (di:complement) ECU73857 U73857 g1657514 Escherichia coli 562 -11534205 239935 yahb putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 28 of 400 of the completegenome.) (nt:f310; 29 pct identical (1 gap) to 285 residues of) (le:8873) (re:9805) (di:complement) AE000138 AE000138 g1786508 Escherichia coli 562 -11534205 5000691504 (de:(ecoli_300) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_300 ECOLI_300 Escherichia coli 562 10122769

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841681	9748	31904	1356	451

Description

6500730348 yahc:b0317 hypothetical protein:hypothetical 17.3 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0317 b0317 Escherichia coli 562 -11534206
 4000709281 yahc (de:hypothetical 17.3 kd protein in bett-prpr intergenic region) (db:swissprot) YAHC_ECOLI P77219 ESCHERICHIA COLI 562 -11534206
 7000687226 yahc membrane protein yahc (db:pir2.dat) E64758 E64758 Escherichia coli 562 -11534206 7500896182 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:42322) (re:42819) (di:complement) ECU73857 U73857 g1657515 Escherichia coli 562 -11534206 239936 yahc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 28 of 400 of the completegenome.) (nt:f165) (le:9897) (re:10394) (di:complement) AE000138 AE000138 g1786509 Escherichia coli 562 -11534206 5000691505 (de:(ecoli_301) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_301 ECOLI_301 Escherichia coli 562 10122770

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841686	9749	31905	588	195

Description

6500730349 yahd:b0318 hypothetical protein:hypothetical 21.7 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0318 b0318 Escherichia coli 562 -11534207
 4000709282 yahd (de:hypothetical 21.7 kd protein in bett-prpr intergenic region) (db:swissprot) YAHd_ECOLI P77736 ESCHERICHIA COLI 562 -11534207
 7000687227 yahd yahd protein (db:pir2.dat) F64758 F64758 Escherichia coli 562 -11534207 7500896183 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:43077) (re:43682) (di:direct) ECU73857 U73857 g1657516 Escherichia coli 562 -11534207 239937 yahd putative transcription factor (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 29 of 400 of the completegenome.) (nt:o201; 28 pct identical (6 gaps) to 195 residues of) (le:159) (re:764) (di:direct) AE000139 AE000139 g1786511 Escherichia coli 562 -11534207 5000691506 (de:(ecoli_302) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_302 ECOLI_302 Escherichia coli 562 10122771

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841689	9750	31906	717	238

Description

6500730350 yahe:b0319 hypothetical protein:hypothetical 32.3 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0319 b0319 Escherichia coli 562 -11534208
 4000709283 yahe (de:hypothetical 32.3 kd protein in bett-prpr intergenic region) (db:swissprot) YAHE_ECOLI P77297 ESCHERICHIA COLI 562 -11534208
 7000687228 yahe yahe protein (db:pir2.dat) G64758 G64758 Escherichia coli 562 -11534208 7500896184 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:43722) (re:44585) (di:direct) ECU73857 U73857 g1657517 Escherichia coli 562 -11534208 239938 yahe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 29 of 400 of the completegenome.) (nt:o287; 28 pct identical (6 gaps) to 87 residues of) (le:804) (re:1667) (di:direct) AE000139 AE000139 g1786512 Escherichia coli 562 -11534208 5000691507 (de:(ecoli_303) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_303 ECOLI_303 Escherichia coli 562 10122772

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841697	9751	31907	372	123

Description

6500730351 yahf:b0320 hypothetical protein:hypothetical 55.6 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0320 b0320 Escherichia coli 562 -11534209
 4000709284 yahf (de:hypothetical 55.6 kd protein in bett-prpr intergenic region) (db:swissprot) YAHF_ECOLI P77187 ESCHERICHIA COLI 562 -11534209
 7000687229 yahf yahf protein (db:pir2.dat) H64758 H64758 Escherichia coli 562 -11534209 7500896185 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to fdra gene of e. coli) (le:44575) (re:46122) (di:direct) ECU73857 U73857 g1657518 Escherichia coli 562 -11534209 239939 yahf putative oxidoreductase subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 29 of 400 of the completegenome.) (nt:o515; 29 pct identical (8 gaps) to 163 residues of) (le:1657) (re:3204) (di:direct) AE000139 AE000139 g1786513 Escherichia coli 562 -11534209 5000691508 (de:(ecoli_304) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_304 ECOLI_304 Escherichia coli 562 10122773

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841706	9752	31908	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841707	9753	31909	1152	383

Description

6500730352 yahg:b0321 hypothetical protein:hypothetical 50.4 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0321 b0321 Escherichia coli 562 -11534210
 4000709285 yahg (de:hypothetical 50.4 kd protein in bett-prpr intergenic region) (db:swissprot) YAHG_ECOLI P77221 ESCHERICHIA COLI 562 -11534210
 7000687230 yahg membrane protein yahg (db:pir2.dat) A64759 A64759 Escherichia coli 562 -11534210 7500896186 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:46122) (re:47540) (di:direct) ECU73857 U73857 g1657519 Escherichia coli 562 -11534210 239940 yahg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 29 of 400 of the completegenome.) (nt:o472; 32 pct identical (7 gaps) to 105 residues of) (le:3204) (re:4622) (di:direct) AE000139 AE000139 g1786514 Escherichia coli 562 -11534210 5000691509 (de:(ecoli_305) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_305 ECOLI_305 Escherichia coli 562 10122774

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841730	9754	31910	2100	699

Description

6500730353 yahh:b0322 hypothetical protein:hypothetical 10.6 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0322 b0322 Escherichia coli 562 -11534211
 4000709286 yahh (de:hypothetical 10.6 kd protein in bett-prpr intergenic region) (db:swissprot) YAHH_ECOLI P75690 ESCHERICHIA COLI 562 -11534211
 7000687231 yahh membrane protein yahh (db:pir2.dat) B64759 B64759 Escherichia coli 562 -11534211 7500896187 yahh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 29 of 400 of the completegenome.) (nt:o106; 34 pct identical (1 gap) to 47 residues of) (le:4648) (re:4968) (di:direct) AE000139 AE000139 g1786515 Escherichia coli 562 -11534211 5000691510 (de:(ecoli_306) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_306 ECOLI_306 Escherichia coli 562 10122775

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841739	9755	31911	1017	338

Description

6500730354 yahi:b0323 hypothetical protein:carbamate kinase-like protein 2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0323 b0323 Escherichia coli 562 -11534212 117485 yahi (de:carbamate kinase-like protein 2) (db:swissprot) ARCM_ECOLI P77624 ESCHERICHIA COLI 562 -11534212 7000684607 yahi probable carbamate kinase:yahi (cl:carbamate kinase) (ec:2.7.2.2) (db:pir2.dat) C64759 C64759 Escherichia coli 562 -11534212 7500877083 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to carbamate kinase of c.perfringens) (le:47962) (re:48912) (di:direct) ECU73857 U73857 g1657521 Escherichia coli 562 -11534212 239942 yahi putative kinase ec 2.7.2.2 . (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 29 of 400 of the completegenome.) (nt:o316; 39 pct identical (12 gaps) to 311 residues of) (le:5044) (re:5994) (di:direct) AE000139 AE000139 g1786516 Escherichia coli 562 -11534212 5000691511 (de:(ecoli_307) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_307 ECOLI_307 Escherichia coli 562 10059309

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841743	9756	31912	1056	351

Description

6500730355 yahj:b0324 hypothetical protein:hypothetical 50.5 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0324 b0324 Escherichia coli 562 -11534213 4000709287 yahj (de:hypothetical 50.5 kd protein in bett-prpr intergenic region) (db:swissprot) YAHJ_ECOLI P77554 ESCHERICHIA COLI 562 -11534213 7000687232 yahj yahj protein (db:pir2.dat) D64759 D64759 Escherichia coli 562 -11534213 7500896188 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:48922) (re:50304) (di:direct) ECU73857 U73857 g1657522 Escherichia coli 562 -11534213 239943 yahj putative deaminase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 29 of 400 of the completegenome.) (nt:o460; 23 pct identical (24 gaps) to 373 residues of) (le:6004) (re:7386) (di:direct) AE000139 AE000139 g1786517 Escherichia coli 562 -11534213 5000691512 (de:(ecoli_308) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_308 ECOLI_308 Escherichia coli 562 10122776

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841763	9757	31913	3078	1025

Description

6500730356 yahk:b0325 hypothetical protein:hypothetical zinc-type alcohol dehydrogenase-like protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0325 b0325 Escherichia coli 562 -11534214 4000707541 yahk (de:intergenic region) (db:swissprot) YAHK_ECOLI P75691 ESCHERICHIA COLI 562 -11534214 7000687233 yahk probable cinnamyl-alcohol dehydrogenase:yahk (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.195) (db:pir2.dat) E64759 E64759 Escherichia coli 562 -11534214 7500896189 yahk putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 29 of 400 of the completegenome.) (nt:o349; residues 23-341 are 44 pct identical to) (le:7763) (re:8812) (di:direct) AE000139 AE000139 g1786518 Escherichia coli 562 -11534214 5000691513 (de:(ecoli_309) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_309 ECOLI_309 Escherichia coli 562 10122777

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841770	9758	31914	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841788	9759	31915	267	88

Description

6500730357 yahl:b0326 hypothetical protein:hypothetical 31.8 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0326 b0326 Escherichia coli 562 -11534215 4000709288 yahl (de:hypothetical 31.8 kd protein in bett-prpr intergenic region) (db:swissprot) YAHL_ECOLI P77393 ESCHERICHIA COLI 562 -11534215 7000687234 yahl membrane protein yahl (db:pir2.dat) F64759 F64759 Escherichia coli 562 -11534215 7500896190 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:51973) (re:52788) (di:direct) ECU73857 U73857 g1657524 Escherichia coli 562 -11534215 239945 yahl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 29 of 400 of the completegenome.) (nt:o271; 28 pct identical (8 gaps) to 88 residues of) (le:9055) (re:9870) (di:direct) AE000139 AE000139 g1786519 Escherichia coli 562 -11534215 5000691514 (de:(ecoli_310) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_310 ECOLI_310 Escherichia coli 562 10122778

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841793	9760	31916	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841797	9761	31917	387	128

Description

6500730358 yahm:b0327 hypothetical protein:hypothetical 9.9 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0327 b0327 Escherichia coli 562 -11534216 7000687235 yahm yahm protein (db:pir2.dat) G64759 G64759 Escherichia coli 562 -11534216 7500896191 yahm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 30 of 400 of the completegenome.) (nt:o91; 43 pct identical (7 gaps) to 65 residues of) (le:222) (re:497) (di:direct) AE000140 AE000140 g1786521 Escherichia coli 562 -11534216 4000709289 yahm (de:hypothetical 9.9 kd protein in bett-prpr intergenic region) (db:swissprot) YAHM_ECOLI P75692 ESCHERICHIA COLI 562 -11534216 5000691515 (de:(ecoli_311) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_311 ECOLI_311 Escherichia coli 562 10122779

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841819	9762	31918	1692	563

Description

6500730359 yahn:b0328 hypothetical protein:hypothetical 24.8 kd protein in bett-prpr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0328 b0328 Escherichia coli 562 -11534217 4000709290 yahn (de:hypothetical 24.8 kd protein in bett-prpr intergenic region) (db:swissprot) YAHN_ECOLI P75693 ESCHERICHIA COLI 562 -11534217 7000687236 yahn membrane protein yahn (cl:hypothetical protein b1798) (db:pir2.dat) H64759 H64759 Escherichia coli 562 -11534217 7500896192 yahn putative cytochrome subunit of dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 30 of 400 of the completegenome.) (nt:f223; 31 pct identical (8 gaps) to 190 residues of) (le:514) (re:1185) (di:complement) AE000140 AE000140 g1786522 Escherichia coli 562 -11534217 5000691516 (de:(ecoli_312) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_312 ECOLI_312 Escherichia coli 562 10122780

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841821	9763	31919	471	156

Description

6500730360 yaho:b0329 hypothetical protein:hypothetical 9.9 kd protein in bett-prpr intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0329 b0329 Escherichia coli 562 -11534218 4000709291 yaho (de:hypothetical 9.9 kd protein in bett-prpr intergenic region precursor) (db:swissprot) YAH0_ECOLI P75694 ESCHERICHIA COLI 562 -11534218 7000687237 yaho yaho protein precursor (db:pir2.dat) A64760 A64760 Escherichia coli 562 -11534218 7500896193 yaho orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 30 of 400 of the complete genome.) (nt:o91; 33 pct identical (2 gaps) to 86 residues of) (le:1332) (re:1607) (di:direct) AE000140 AE000140 g1786523 Escherichia coli 562 -11534218 5000691517 (de:(ecoli_313) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_313 ECOLI_313 Escherichia coli 562 10122781

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841833	9764	31920	327	108

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841838	9765	31921	1560	519

Description

GTC ORF with score 188 to: (sr:mus musculus (strain:129sv/j) embryonic stem cell cell_line:rw) (db:genpept) (ec:2.4.1.80) (de:mus musculus ugcg gene for udp-glucose ceramideglucosyltransferase, exon 9 and complete cds.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841860	9766	31922	1452	483

Description

6500730361 prpr:b0330 hypothetical protein:propionate catabolism operon regulatory protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0330 b0330 Escherichia coli 562 -11534219 1500687353 prpr (de:propionate catabolism operon regulatory protein) (db:swissprot) PRPR_ECOLI P77743 ESCHERICHIA COLI 562 -11534219 7000686188 prpr propionate catabolism operon regulator prpr (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) B64760 B64760 Escherichia coli 562 -11534219 7500888571 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to e. coli hydg) (le:54652) (re:56238) (di:complement) ECU73857 U73857 g1657526 Escherichia coli 562 -11534219 239947 prpr regulator for prp operon (fn:regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 30 of 400 of the completegenome.) (nt:f528; 50 pct identical (12 gaps) to 247 residues of) (le:1705) (re:3291) (di:complement) AE000140 AE000140 g1786524 Escherichia coli 562 -11534219 5000691518 (de:(ecoli_314) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_314 ECOLI_314 Escherichia coli 562 10064718

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841863	9767	31923	687	228

Description

6500730362 yahr:b0332 hypothetical protein:hypothetical 56.5 kd protein in prpb-prpc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0332 b0332 Escherichia coli 562 -11534220 7000687238 yahr yahr protein (db:pir2.dat) D64760 D64760 Escherichia coli 562 -11534220 239949 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:57313) (re:57759) (di:complement) ECU73857 U73857 g1657528 Escherichia coli 562 -11534220 7500959864 b0332 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 30 of 400 of the completegenome.) (nt:f148) (le:4366) (re:4812) (di:complement) AE000140 AE000140 g1786526 Escherichia coli 562 -11534220 1500686253 yahr_ecoli (de:hypothetical 56.5 kd protein in prpb-prpc intergenic region,) P77491 P77491 Escherichia coli 562 -11534220 5000691520 (de:(ecoli_316) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_316 ECOLI_316 Escherichia coli 562 10060996

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841904	9768	31924	480	159

Description

6500730363 prpd:b0334 hypothetical protein:prpd protein (gtcfc:14.1)
 (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0334 b0334
 Escherichia coli 562 -11534221 1500686835 prpd (de:prpd protein)
 (db:swissprot) PRPD_ECOLI P77243 ESCHERICHIA COLI 562 -11534221 7000686186
 prpd membrane protein prpd (db:pir2.dat) F64760 F64760 Escherichia coli 562
 -11534221 7500888569 (db:genpept-bct1) (de:escherichia coli chromosome
 minutes 6-8.) (nt:similar to yqip of b. subtilis) (le:59010) (re:60461)
 (di:direct) ECU73857 U73857 g1657530 Escherichia coli 562 -11534221 239951
 prpd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
 (de:escherichia coli k-12 mg1655 section 30 of 400 of the completegenome.)
 (nt:o483; 70 pct identical to 177 residues of) (le:6063) (re:7514)
 (di:direct) AE000140 AE000140 g1786528 Escherichia coli 562 -11534221
 5000691522 (de:(ecoli_318) (pn:function not assigned) (gtcfc:13.7:14.1)
 (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_318
 ECOLI_318 Escherichia coli 562 10062782

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841909	9769	31925	963	321

Description

6500730364 prpe:b0335 hypothetical protein:prpe protein (gtcfc:14.1)
 (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0335 b0335
 Escherichia coli 562 -11534222 1500685850 prpe (de:prpe protein)
 (db:swissprot) PRPE_ECOLI P77495 ESCHERICHIA COLI 562 -11534222 7000686187
 prpe prpe protein (cl:acetate--coa ligase homology) (db:pir2.dat) G64760
 G64760 Escherichia coli 562 -11534222 7500888570 (db:genpept-bct1)
 (de:escherichia coli chromosome minutes 6-8.) (nt:similar to e. coli acs,
 acetyl-coa synthetase) (le:60501) (re:62387) (di:direct) ECU73857 U73857
 g1657531 Escherichia coli 562 -11534222 239952 prpe putative propionyl-coa
 synthetase (fn:putative enzyme; not classified) (db:genpept-bct2)
 (de:escherichia coli k-12 mg1655 section 30 of 400 of the completegenome.)
 (nt:o628; 40 pct identical (25 gaps) to 612 residues of) (le:7554) (re:9440)
 (di:direct) AE000140 AE000140 g1786529 Escherichia coli 562 -11534222
 5000691523 (de:(ecoli_319) (pn:function not assigned) (gtcfc:13.7:14.1)
 (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_319
 ECOLI_319 Escherichia coli 562 10059280

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841921	9770	31926	912	303
<u>Description</u>				
6500730365 mhpr:b0346 hypothetical protein:mhp operon transcriptional activator (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0346 b0346 Escherichia coli 562 -11534223 239963 mhpr (de:mhp operon transcriptional activator) (db:swissprot) MHPR_ECOLI P77569 ESCHERICHIA COLI 562 -11534223 7000685846 mhpr mhp operon transcription regulator mhpr (db:pir2.dat) B64762 B64762 Escherichia coli 562 -11534223 5000691525 mhpr (fn:activator of the 3-hydroxyphenylpropionate) (db:genpept-bct1) (de:e.coli mhp cluster for 3-hydroxy-phenylpropionic acid degradation.) (le:19) (re:966) (di:complement) ECMHP Y09555 g1702880 Escherichia coli 562 -11534223 7500885614 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:75382) (re:76329) (di:complement) ECU73857 U73857 g1657542 Escherichia coli 562 -11534223 233383 mhpr transcriptional regulator for mhp operon (fn:regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 31 of 400 of the completegenome.) (nt:f315; this 342 aa orf is 27 pct identical (9 gaps)) (le:9995) (re:10942) (di:complement) AE000141 AE000141 g1786541 Escherichia coli 562 -11534223 120049 mhpr (de:mhp operon transcriptional activator) (db:swissprot) MHPR_ECOLI P77569 ESCHERICHIA COLI 562 -11534223				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501841922	9771	31927	582	193
<u>Description</u>				
6500730366 mhp:d0350 hypothetical protein:2-keto-4-pentenoate hydratase (gtcfc:14.1) (ec:4.2.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0350 b0350 Escherichia coli 562 -11534224 7000685843 mhp:d probable hydratase:mhp (cl:2-hydroxypenta-2,4-dienoate hydratase) (ec:4.2.1.-) (db:pir2.dat) F64762 F64762 Escherichia coli 562 -11534224 239967 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to p. putida 2-hydroxypenta-2,4-dienoate) (le:79904) (re:80719) (di:direct) ECU73857 U73857 g1657546 Escherichia coli 562 -11534224 7500959866 mhp:d 2-keto-4-pentenoate hydratase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 32 of 400 of the completegenome.) (nt:o271; this 271 aa orf is 53 pct identical (1 gap)) (le:3567) (re:4382) (di:direct) AE000142 AE000142 g1786546 Escherichia coli 562 -11534224 120052 mhp:d_ecoli (de:2-keto-4-pentenoate hydratase (ec 4.2.-.-).) P77608 P77608 Escherichia coli 562 -11534224 5000691528 (de:(ecoli_334) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_334 ECOLI_334 Escherichia coli 562 10063204				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841929	9772	31928	1266	421

Description

6500730367 mhpt:b0353 hypothetical protein:putative 3-hydroxyphenylpropionic acid transporter (gtcfc:12.2) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0353 b0353 Escherichia coli 562 -11534225 500685314 mhpt (de:putative 3-hydroxyphenylpropionic acid transporter) (db:swissprot) MHPT_ECOLI P77589 ESCHERICHIA COLI 562 -11534225 7000685847 mhpt probable transport protein mhpt (db:pir2.dat) A64763 A64763 Escherichia coli 562 -11534225 7500885615 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to p. putida pcak) (le:83003) (re:84259) (di:direct) ECU73857 U73857 g1657549 Escherichia coli 562 -11534225 239970 mhpt putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 32 of 400 of the completegenome.) (nt:o418; this 418 aa orf is 21 pct identical (13 gaps)) (le:6872) (re:8128) (di:direct) AE000142 AE000142 g1786549 Escherichia coli 562 -11534225 5000691530 (de:(ecoli_337) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_337 ECOLI_337 Escherichia coli 562 10064845

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841954	9773	31929	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841955	9774	31930	2430	810

Description

5000691531 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0354 b0354 Escherichia coli 562 -11534226 7000691010 hypothetical protein b0354 (db:pir2.dat) B64763 B64763 Escherichia coli 562 -11534226 7500959867 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:84244) (re:84900) (di:direct) ECU73857 U73857 g1657550 Escherichia coli 562 -11534226 239971 yail nucleoprotein/polynucleotide-associated enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 32 of 400 of the completegenome.) (nt:o218; this 218 aa orf is 31 pct identical (2 gaps)) (le:8113) (re:8769) (di:direct) AE000142 AE000142 g1786550 Escherichia coli 562 -11534226 6500730368 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0354 b0354 Escherichia coli 562 -11534226

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841963	9775	31931	1257	419

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841994	9776	31932	465	154

Description

6500730369 yaim:b0355 hypothetical protein:hypothetical 31.4 kd protein in mhpt-adhc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0355 b0355 Escherichia coli 562 -11534227 109786 yaim (de:hypothetical 31.4 kd protein in mhpt-adhc intergenic region) (db:swissprot) YAIM_ECOLI P51025 ESCHERICHIA COLI 562 -11534227 7000687242 yaim yaim protein (cl:conserved hypothetical protein yjl068c) (db:pir2.dat) C64763 C64763 Escherichia coli 562 -11534227 7500896202 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to e. coli yeig) (le:85124) (re:85957) (di:complement) ECU73857 U73857 g1657552 Escherichia coli 562 -11534227 239973 yaim putative esterase ec 3.1.1.1 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 32 of 400 of the completegenome.) (nt:f277; this 277 aa orf is 62 pct identical (0 gaps)) (le:8993) (re:9826) (di:complement) AE000142 AE000142 g1786551 Escherichia coli 562 -11534227 5000691532 (de:(ecoli_339) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_339 ECOLI_339 Escherichia coli 562 10122788

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501841996	9777	31933	816	271

Description

5000691533 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0357 b0357 Escherichia coli 562 -11534228 7000691011 hypothetical protein b0357 (cl:hypothetical protein b2105) (db:pir2.dat) E64763 E64763 Escherichia coli 562 -11534228 7500959868 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:87196) (re:87492) (di:complement) ECU73857 U73857 g1657554 Escherichia coli 562 -11534228 239975 yaim putative alpha helix chain (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 32 of 400 of the completegenome.) (nt:f98) (le:11064) (re:11360) (di:complement) AE000142 AE000142 g1786553 Escherichia coli 562 -11534228 6500730370 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0357 b0357 Escherichia coli 562 -11534228

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842016	9778	31934	1683	560

Description

6500730371 yaio:b0358 hypothetical protein:hypothetical 29.0 kd protein in adhC-tauA intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0358 b0358 Escherichia coli 562 -11534229
500684967 yaio (de:hypothetical 29.0 kd protein in adhC-tauA intergenic region) (db:swissprot) YAI0_ECOLI Q47534 ESCHERICHIA COLI 562 -11534229
7000687243 yaio yaio protein (db:pir2.dat) F64763 F64763 Escherichia coli 562 -11534229 239976 29kd protein hypothetical (sr:escherichia coli (strain k12) (library: kohara) dna, clone 8f10) (db:genpept-bct1) (de:escherichia coli hemb gene, complete cds.) (le:5714) (re:6487) (di:complement) ECOPS D85613 g1054572 Escherichia coli 562 -11534229 7500896204 29 kd protein hypothetical (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (le:87659) (re:88432) (di:complement) ECU73857 U73857 g1657555 Escherichia coli 562 -11534229 235575 yaio orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of 400 of the completegenome.) (nt:f257; this 257 aa orf is 25 pct identical (2 gaps)) (le:114) (re:887) (di:complement) AE000143 AE000143 g1786555 Escherichia coli 562 -11534229 5000691534 (de:(ecoli_342) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_342 ECOLI_342 Escherichia coli 562 10060998

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842024	9779	31935	882	293

Description

GTC ORF with score 101 to: (db:genpept-bct1) (de:acinetobacter calcoaceticus malonate decarboxylase alpha subunit(mdca), malonate decarboxylase delta subunit (mdcd), malonatedecarboxylase beta subunit (mdcb), and malonate decarboxylase gammasubunit ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842028	9780	31936	408	135

Description

5000691535 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0359 b0359 Escherichia coli 562 -11534230
7000691012 hypothetical protein b0359 (db:pir2.dat) G64763 G64763 Escherichia coli 562 -11534230 7500959869 b0359 putative transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of 400 of the completegenome.) (nt:f147; this 147 aa orf is 26 pct identical (1 gap)) (le:889) (re:1332) (di:complement) AE000143 AE000143 g1786556 Escherichia coli 562 -11534230 6500730372 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0359 b0359 Escherichia coli 562 -11534230

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842045	9781	31937	1053	350

Description

5000691536 yi21_1:yi21_2:b0360 insertion element is2 hypothetical 13 kd protein:hypothetical protein:insertion element is2 hypothetical 13.4 kd protein:orf1 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0360 b0360 Escherichia coli 562 -11534231 7000690915 yi21_4 hypothetical protein:13.4k (cl:agrobacterium tumefaciens insertion sequence is1312 hypothetical protein) (db:pir2.dat) B65240 B65240 Escherichia coli 562 -11534231 7500959780 is2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #267(31.4-31.7 min.)) (nt:orf_id:o267#10; similar to (pir accession number) (le:12783) (re:13193) (di:complement) D90778 D90778 g1742284 Escherichia coli 562 -11534231 223686 is2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #268(31.6-32.0 min.)) (nt:orf_id:o267#10; similar to (pir accession number) (le:1494) (re:1904) (di:complement) D90779 D90779 g1742292 Escherichia coli 562 -11534231 301145 is2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o348#5; similar to (pir accession number) (le:5381) (re:5791) (di:complement) D90838 D90838 g1736667 Escherichia coli 562 -11534231 301329 is2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #373(49.5-49.9 min.)) (nt:orf_id:o373#12; similar to (pir accession number) (le:17857) (re:18267) (di:complement) D90850 D90850 g1736863 Escherichia coli 562 -11534231 301337 is2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #374(49.8-50.1 min.)) (nt:orf_id:o373#12; similar to (pir accession number) (le:2906) (re:3316) (di:complement) D90851 D90851 g1736872 Escherichia coli 562 -11534231 301360 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min.)) (nt:orf_id:o250#9; similar to (pir accession number) (le:16504) (re:16914) (di:direct) D90852 D90852 g1805519 Escherichia coli 562 -11534231 239258 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:is2 orf; alternate gene name yi21) (le:189061) (re:189471) (di:direct) ECUW93 U14003 g537113 Escherichia coli 562 -11534231 239977 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f136) (le:7052) (re:7462) (di:complement) ECU28375 U28375 g887812 Escherichia coli 562 -11534231 300459 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o136; orf1 of v00279) (le:140530) (re:140940) (di:direct) ECU28377 U28377 g882574 Escherichia coli 562 -11534231 300466 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:orf_o136) (le:88896) (re:89306) (di:direct) ECU73857 U73857 g1657556 Escherichia coli 562 -11534231 224720 yi21_1 is2 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of 400 of the complete genome.)

(de:escherichia coli k-12 mg1655 section 33 of 400 of the completegenome.)
~~(nt:0136; 100 pct identical to yi22_ecoli sw:) (le:1351) (re:1761)~~

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842050	9782	31938	1776	591

Description

5000691537 yi22_1:yi22_2:yi22_3:yi22_4:yi22_5:b0361 hypothetical protein:insertion element is2 hypothetical 34.4 kd protein:orf2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0361 b0361 Escherichia coli 562 -11534232 300463 b0361:b1402:b1996:b2860:b3045:b4273 (de:insertion element is2 hypothetical 34.4 kd protein (orf2)) (db:swissprot) YI22_ECOLI P19777 ESCHERICHIA COLI 562 -11534232 163274 yi22_8 hypothetical protein:34k (db:pir2.dat) C65092 A64764 Escherichia coli 562 -11534232 7500937248 is2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #267(31.4-31.7 min.)) (nt:orf_id:o267#7; similar to (pir accession number) (le:11920) (re:12825) (di:complement) D90778 D90778 g1651641 Escherichia coli 562 -11534232 223683 is2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #268(31.6-32.0 min.)) (nt:orf_id:o267#7; similar to (pir accession number) (le:631) (re:1536) (di:complement) D90779 D90779 g1651645 Escherichia coli 562 -11534232 223690 is2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o348#2; similar to (pir accession number) (le:4518) (re:5423) (di:complement) D90838 D90838 g1736664 Escherichia coli 562 -11534232 224502 is2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #373(49.5-49.9 min.)) (nt:orf_id:o373#9; similar to (pir accession number) (le:16994) (re:17899) (di:complement) D90850 D90850 g1736860 Escherichia coli 562 -11534232 224686 is2 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #374(49.8-50.1 min.)) (nt:orf_id:o373#9; similar to (pir accession number) (le:2043) (re:2948) (di:complement) D90851 D90851 g1736869 Escherichia coli 562 -11534232 301334 (db:genpept-bct1) (de:e. coli gale gene with inserted is2 element.) (nt:orf 2 (aa 1-301)) (le:77) (re:982) (di:complement) ECGALI V00279 g581095 Escherichia coli 562 -11534232 301142 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:is2 orf; alternate gene name yi22) (le:189429) (re:190334) (di:direct) ECOUW93 U14003 g537114 Escherichia coli 562 -11534232 301326 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f301) (le:6189) (re:7094) (di:complement) ECU28375 U28375 g887811 Escherichia coli 562 -11534232 6500730374 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:insertion element is2 hypothetical 34.4 kd protein) (le:89264) (re:90169) (di:direct) ECU73857 U73857 g1657557 Escherichia coli 562 -11534232 224694 yi22_1 is2 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of 400 of the completegenome.) (nt:o301; 100 pct identical to yi22_ecoli sw: p19777) (le:1719) (re:2624) (di:direct) AE000143 AE000143 g1786558 Escherichia coli 562 -11534232 232958 yi22_2 is2 hypothetical protein (fn:is, phage, tn;

232958 yi22_2 is2 hypothetical protein (fn:is, phage, tn;
transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842069	9783	31939	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842073	9784	31940	1854	617

Description

5000691538 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0362 b0362 Escherichia coli 562 -11534233
7000691013 hypothetical protein b0362 (db:pir2.dat) B64764 B64764
Escherichia coli 562 -11534233 7500959870 b0362 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
33 of 400 of the completegenome.) (nt:f128; this 116 aa orf is 44 pct
identical (3 gaps)) (le:2549) (re:2935) (di:complement) AE000143 AE000143
g1786559 Escherichia coli 562 -11534233 6500730375 hypothetical protein
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0362
b0362 Escherichia coli 562 -11534233

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842079	9785	31941	894	297

Description

6500730376 yaip:b0363 hypothetical protein:hypothetical 44.7 kd protein in
adhc-taua intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0363 b0363 Escherichia coli 562 -11534234
500684968 yaip (de:hypothetical 44.7 kd protein in adhc-taua intergenic
region) (db:swissprot) YAIP_ECOLI Q47536 ESCHERICHIA COLI 562 -11534234
7000687244 yaip membrane protein yaip (db:pir2.dat) C64764 C64764
Escherichia coli 562 -11534234 7500896205 (db:genpept-bct1) (de:escherichia
coli chromosome minutes 6-8.) (nt:44.8 kd hypothetical protein) (le:90329)
(re:91525) (di:complement) ECU73857 U73857 g1657558 Escherichia coli 562
-11534234 239979 yaip polysaccharide metabolism (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of
400 of the completegenome.) (nt:f398; this 398 aa orf is 30 pct identical (4
gaps)) (le:2784) (re:3980) (di:complement) AE000143 AE000143 g1786560
Escherichia coli 562 -11534234 5000691539 (de:(ecoli_347) (pn:function not
assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_347 ECOLI_347 Escherichia coli 562 10060999

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842081	9786	31942	1512	503

Description

5000691540 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0364 b0364 Escherichia coli 562 -11534235
 7000691014 hypothetical protein b0364 (db:pir2.dat) D64764 D64764
 Escherichia coli 562 -11534235 7500959871 yais orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of 400 of the completegenome.) (nt:f136) (le:4104) (re:4514) (di:complement) AE000143 AE000143 g1786561 Escherichia coli 562 -11534235
 6500730377 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0364 b0364 Escherichia coli 562 -11534235

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842088	9787	31943	384	127

Description

5000691541 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0365 b0365 Escherichia coli 562 -11534236
 7500959872 substrate-binding protein (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (le:92765) (re:93784) (di:direct) ECU73857 U73857
 g1657560 Escherichia coli 562 -11534236 239981 taua taurine transport system periplasmic protein (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of 400 of the completegenome.) (nt:o339; this 339 aa orf is 28 pct identical (12 gaps)) (le:5220) (re:6239) (di:direct) AE000143 AE000143 g1786562
 Escherichia coli 562 -11534236 7000691015 hypothetical protein b0365 (db:pir) E64764 E64764 Escherichia coli 562 -11534236 6500730378
 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0365 b0365 Escherichia coli 562 -11534236

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842089	9788	31944	1053	350

Description

6500730379 taub:ssib:b0366 hypothetical protein:taurine transport
 atp-binding protein taub (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli) b0366 b0366 Escherichia coli 562 -11534237
 500684751 taub:ssib (de:taurine transport atp-binding protein taub)
 (db:swissprot) TAUB_ECOLI Q47538 ESCHERICHIA COLI 562 -11534237 7000686767
 taub taurine transport protein:sulfate starvation-induced protein:taub
 protein (cl:atp-binding cassette homology) (db:pir2.dat) F64764 S78605
 Escherichia coli 562 -11534237 239982 atp-binding protein (sr:escherichia
 coli (strain k12) (library: kohara) dna, clone 8f10) (db:genpept-bct1)
 (de:escherichia coli hemb gene, complete cds.) (le:11866) (re:12633)
 (di:direct) ECOPS D85613 g1384059 Escherichia coli 562 -11534237 7500892766
 atp-binding protein (db:genpept-bct1) (de:escherichia coli chromosome
 minutes 6-8.) (le:93797) (re:94564) (di:direct) ECU73857 U73857 g1657561
 Escherichia coli 562 -11534237 235579 taub taurine atp-binding component of
 a transport (fn:transport; transport of small molecules: amino)
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of 400 of the
 completegenome.) (nt:o255; this 255 aa orf is 41 pct identical (7 gaps))
 (le:6252) (re:7019) (di:direct) AE000143 AE000143 g1786563 Escherichia coli
 562 -11534237 5000691542 (de:(ecoli_350) (pn:function not assigned)
 (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia
 coli)) ECOLI_350 ECOLI_350 Escherichia coli 562 10059051

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842091	9789	31945	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842100	9790	31946	696	231

Description

6500730380 tauc:ssic:b0367 hypothetical protein:taurine transport permease protein tauc (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0367 b0367 Escherichia coli 562 -11534238 7500955802 membrane component (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (le:94561) (re:95388) (di:direct) ECU73857 U73857 g1657562 Escherichia coli 562 -11534238 239983 tauc taurine transport system permease protein (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of 400 of the completegenome.) (nt:o275; this 275 aa orf is 35 pct identical (5 gaps)) (le:7016) (re:7843) (di:direct) AE000143 AE000143 g1786564 Escherichia coli 562 -11534238 7000689501 hypothetical protein b0367 (cl:hypothetical protein b0934) (db:pir) G64764 G64764 Escherichia coli 562 -11534238 5000691543 (de:(ecoli_351) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_351 ECOLI_351 Escherichia coli 562 10122795

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842112	9791	31947	408	135

Description

6500730381 taud:ssid:b0368 hypothetical protein:probable taurine catabolism dioxygenase:sulfate starvation-induced protein 3:ssi3 (gtcfc:14.1) (ec:1.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0368 b0368 Escherichia coli 562 -11534239 7000691016 taud probable monooxygenase::sulfate starvation-induced protein ssi3:taud protein (ec:1.14.-.-) (db:pir2.dat) H64764 S78607 Escherichia coli 562 -11534239 239984 dioxygenase (sr:escherichia coli (strain k12) (library: kohara) dna, clone 8f10) (db:genpept-bct1) (de:escherichia coli hemb gene, complete cds.) (le:13454) (re:14305) (di:direct) ECOPS D85613 g1054578 Escherichia coli 562 -11534239 7500959873 dioxygenase (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (le:95385) (re:96236) (di:direct) ECU73857 U73857 g1657563 Escherichia coli 562 -11534239 235581 taud taurine dioxygenase:2-oxoglutarate-dependent (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of 400 of the completegenome.) (nt:o283; this 283 aa orf is 32 pct identical (24 gaps)) (le:7840) (re:8691) (di:direct) AE000143 AE000143 g1786565 Escherichia coli 562 -11534239 5000691544 (de:(ecoli_352) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_352 ECOLI_352 Escherichia coli 562 10122796

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842113	9792	31948	570	189

Description

GTC ORF with score 339 to: (sr:lyme disease spirochete) (db:genpept-bct2)
(de:borrelia burgdorferi (section 28 of 70) of the complete genome.)
(nt:similar to sp:p15189 gb:m27221 pid:717082 percent) (le:13517) (re:14989)
(di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842119	9793	31949	363	121

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842124	9794	31950	276	91

Description

5000691545 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0370 b0370 Escherichia coli 562 -11534240
7000691017 hypothetical protein b0370 (db:pir2.dat) B64765 B64765
Escherichia coli 562 -11534240 7500959874 (db:genpept-bct1) (de:escherichia
coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:97487)
(re:97756) (di:complement) ECU73857 U73857 g1657565 Escherichia coli 562
-11534240 239986 b0370 orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 33 of 400 of the
completegenome.) (nt:f89) (le:9942) (re:10211) (di:complement) AE000143
AE000143 g1786567 Escherichia coli 562 -11534240 6500730382 hypothetical
protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)
b0370 b0370 Escherichia coli 562 -11534240

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842130	9795	31951	276	92

Description

6500730383 yait:b0371 hypothetical protein:hypothetical 52.9 kd protein in hemb-sbma intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0371 b0371 Escherichia coli 562 -11534241 4000709292 yait (de:hypothetical 52.9 kd protein in hemb-sbma intergenic region precursor) (db:swissprot) YAIT_ECOLI P77199 ESCHERICHIA COLI 562 -11534241 7000687245 yait yait protein precursor (db:pir2.dat) C64765 C64765 Escherichia coli 562 -11534241 7500896206 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:97841) (re:99301) (di:direct) ECU73857 U73857 gl657566 Escherichia coli 562 -11534241 239987 yait orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 34 of 400 of the completegenome.) (nt:o486; this 486 aa orf is 21 pct identical (36 gaps)) (le:73) (re:1533) (di:direct) AE000144 AE000144 gl786569 Escherichia coli 562 -11534241 5000691546 (de:(ecoli_355) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_355 ECOLI_355 Escherichia coli 562 10122799

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842133	9796	31952	489	162

Description

6500730384 yaiu:b0374 hypothetical protein:hypothetical 50.3 kd protein in hemb-sbma intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0374 b0374 Escherichia coli 562 -11534242 4000709293 yaiu (de:hypothetical 50.3 kd protein in hemb-sbma intergenic region) (db:swissprot) YAIU_ECOLI P75700 ESCHERICHIA COLI 562 -11534242 7000687246 yaiu yaiu protein (db:pir2.dat) F64765 F64765 Escherichia coli 562 -11534242 7500896207 yaiu putative flagellin structural protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 34 of 400 of the completegenome.) (nt:o467; this 467 aa orf is 27 pct identical (28 gaps)) (le:2837) (re:4240) (di:direct) AE000144 AE000144 gl786572 Escherichia coli 562 -11534242 5000691547 (de:(ecoli_358) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_358 ECOLI_358 Escherichia coli 562 10122800

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842152	9797	31953	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842168	9798	31954	816	271

Description

6500730385 yaiv:b0375 hypothetical protein:hypothetical 25.5 kd protein in hemb-sbma intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0375 b0375 Escherichia coli 562 -11534243
 4000709294 yaiv (de:hypothetical 25.5 kd protein in hemb-sbma intergenic region) (db:swissprot) YAIV_ECOLI P77723 ESCHERICHIA COLI 562 -11534243
 7000687247 yaiv yaiv protein (db:pir2.dat) G64765 G64765 Escherichia coli 562 -11534243 7500896208 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:102051) (re:102719) (di:direct) ECU73857 U73857 g1657570 Escherichia coli 562 -11534243 239991 yaiv orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 34 of 400 of the completegenome.) (nt:o222) (le:4283) (re:4951) (di:direct) AE000144 AE000144 g1786573 Escherichia coli 562 -11534243 5000691548 (de:(ecoli_359) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_359 ECOLI_359 Escherichia coli 562 10122801

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842171	9799	31955	579	193

Description

6500730386 yaiw:b0378 hypothetical protein:hypothetical 40.4 kd protein in sbma-ddla intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0378 b0378 Escherichia coli 562 -11534244
 4000709295 yaiw (de:hypothetical 40.4 kd protein in sbma-ddla intergenic region) (db:swissprot) YAIW_ECOLI P77562 ESCHERICHIA COLI 562 -11534244
 7000687248 yaiw yaiw protein (db:pir2.dat) B64766 B64766 Escherichia coli 562 -11534244 7500896209 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:105462) (re:106556) (di:direct) ECU73857 U73857 g1657573 Escherichia coli 562 -11534244 239994 yaiw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 34 of 400 of the completegenome.) (nt:o364) (le:7694) (re:8788) (di:direct) AE000144 AE000144 g1786576 Escherichia coli 562 -11534244 5000691550 (de:(ecoli_362) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_362 ECOLI_362 Escherichia coli 562 10122804

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842174	9800	31956	417	138

Description

5000691551 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0379 b0379 Escherichia coli 562 -11534245
7500896210 yaay (de:hypothetical 11.4 kd protein in sbma-ddla intergenic region) (db:swissprot) YAIY_ECOLI P77669 ESCHERICHIA COLI 562 -11534245
7000691018 yaay membrane protein yaay (db:pir2.dat) C64766 C64766
Escherichia coli 562 -11534245 239995 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:106615) (re:106923) (di:complement) ECU73857 U73857 g1657574 Escherichia coli 562 -11534245 7500896212 b0379 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 34 of 400 of the completegenome.) (nt:f102) (le:8847) (re:9155) (di:complement) AE000144 AE000144 g1786577 Escherichia coli 562 -11534245 6500730387 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0379 b0379 Escherichia coli 562 -11534245

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842176	9801	31957	339	112

Description

5000691552 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0380 b0380 Escherichia coli 562 -11534246
7500896214 yaiz (de:hypothetical 13.0 kd protein in sbma-ddla intergenic region) (db:swissprot) YAIZ_ECOLI P77273 ESCHERICHIA COLI 562 -11534246
7000691019 yaiz membrane protein yaiz (db:pir2.dat) D64766 D64766
Escherichia coli 562 -11534246 239996 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:107051) (re:107395) (di:direct) ECU73857 U73857 g1657575 Escherichia coli 562 -11534246 7500896216 b0380 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 34 of 400 of the completegenome.) (nt:o114) (le:9283) (re:9627) (di:direct) AE000144 AE000144 g1786578 Escherichia coli 562 -11534246 6500730388 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0380 b0380 Escherichia coli 562 -11534246

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842180	9802	31958	450	149

Description

GTC ORF with score 155 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana chromosome 1 bac f508 sequence, completesequences.) (nt:strong similarity to pfam pf|00069 eukaryotic) (le:21143:21479:21726) (re:21388:21640:21873) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842181	9803	31959	963	320

Description

6500730389 yaib:b0382 hypothetical protein fragment in ddla-phoa intergenic region:hypothetical 9.9 kd protein in ddla-phoa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0382 b0382 Escherichia coli 562 -11534247 109776 yaib (de:hypothetical 9.9 kd protein in ddla-phoa intergenic region) (db:swissprot) YAIB_ECOLI P21831 ESCHERICHIA COLI 562 -11534247 7000687239 yaib yaib protein (db:pir2.dat) F64766 F64766 Escherichia coli 562 -11534247 7500896197 yaib (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein in ddla-phoa intergenic) (le:108976) (re:109236) (di:direct) ECU73857 U73857 g1657578 Escherichia coli 562 -11534247 239999 yaib orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completegenome.) (nt:o86; 100 pct identical to fragment yaib_ecoli) (le:262) (re:522) (di:direct) AE000145 AE000145 g1786581 Escherichia coli 562 -11534247 5000691553 (de:(ecoli_366) (pn:hypothetical protein in ddla-phoa intergenic region:fragment) (gn:yaib) (gtcfc:13.7:14.1) (ec:) (yaib_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_366 ECOLI_366 Escherichia coli 562 10122807

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842192	9804	31960	945	314

Description

6500730390 yaia:b0389 hypothetical 7.3 kd protein in arol-arom intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0389 b0389 Escherichia coli 562 -11534248 109774 yaia (de:hypothetical 7.3 kd protein in arol-arom intergenic region) (db:swissprot) YAIA_ECOLI P08366 ESCHERICHIA COLI 562 -11534248 135159 yaia yaia protein (db:pir1.dat) QQECLM B25197 Escherichia coli 562 -11534248 240006 unknown protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli k-12 arol and arom genes encoding shikimate kinaseii and a 26 kd protein respectively, complete cds.) (nt:orf; putative) (le:804) (re:995) (di:direct) ECOAROLM M13045 g1128942 Escherichia coli 562 -11534248 7500896196 yaia (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical 7.3kd protein in arol-arom intergenic) (le:114569) (re:114760) (di:direct) ECU73857 U73857 g1657585 Escherichia coli 562 -11534248 233863 yaia orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completegenome.) (nt:o63; 100 pct identical to yaia_ecoli sw: p08366) (le:5855) (re:6046) (di:direct) AE000145 AE000145 g1786588 Escherichia coli 562 -11534248 5000691556 (de:(ecoli_373) (pn:hypothetical 7) (gn:yaia) (gtcfc:13.7:14.1) (ec:) (yaia_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_373 ECOLI_373 Escherichia coli 562 10051506

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842193	9805	31961	333	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842206	9806	31962	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842210	9807	31963	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842212	9808	31964	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842216	9809	31965	939	312

Description

5000691558 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0392 b0392 Escherichia coli 562 -11534249
7500938531 ykia (de:hypothetical 10.6 kd protein in arom-araj intergenic
region) (db:swissprot) YKIA_ECOLI P75704 ESCHERICHIA COLI 562 -11534249
7000691020 hypothetical protein b0392 (db:pir2.dat) H64767 H64767
Escherichia coli 562 -11534249 7500938533 b0392 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
35 of 400 of the completegenome.) (nt:o93) (le:7545) (re:7826) (di:direct)
AE000145 AE000145 g1786591 Escherichia coli 562 -11534249 6500730391
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0392 b0392 Escherichia coli 562 -11534249

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842222	9810	31966	408	135

Description

6500730392 yajf:b0394 hypothetical protein in araj-arom intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0394 b0394 Escherichia coli 562 -11534250 7000690981 yajf yaif protein (cl:conserved hypothetical protein hi0182:glucose kinase homology) (db:pir2.dat) B64768 B64768 Escherichia coli 562 -11534250 7500959844 yajf possible nagc-like transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completegenome.) (nt:o348; 100 pct identical to yajf_ecoli sw:) (le:8882) (re:9928) (di:direct) AE000145 AE000145 g1786593 Escherichia coli 562 -11534250 5000691560 (de:(ecoli_378) (pn:hypothetical 32) (gn:yajf) (gtcfc:13.7:14.1) (ec:) (yajf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_378 ECOLI_378 Escherichia coli 562 10122814

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842230	9811	31967	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842243	9812	31968	984	327

Description

5000691561 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0395 b0395 Escherichia coli 562 -11534251 7000691021 hypothetical protein b0395 (db:pir2.dat) C64768 C64768 Escherichia coli 562 -11534251 7500959875 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:118621) (re:118863) (di:direct) ECU73857 U73857 g1657591 Escherichia coli 562 -11534251 240012 b0395 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completegenome.) (nt:o80) (le:9907) (re:10149) (di:direct) AE000145 AE000145 g1786594 Escherichia coli 562 -11534251 6500730393 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0395 b0395 Escherichia coli 562 -11534251

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842253	9813	31969	324	107

Description

6500730394 proy:b0402 hypothetical protein:proline-specific permease proy (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0402 b0402 Escherichia coli 562 -11534252 1500685775 proy (de:proline-specific permease proy) (db:swissprot) PROY_ECOLI P77327 ESCHERICHIA COLI 562 -11534252 7000686184 proline transport protein:proline permease:proline-specific permease (cl:arginine permease) (db:pir2.dat) B64769 B64769 Escherichia coli 562 -11534252 7500888563 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to s. typhimurium proy) (le:436) (re:1809) (di:direct) ECU82664 U82664 g1773086 Escherichia coli 562 -11534252 240179 proy proline permease transport protein (fn:transport; transport of small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 36 of 400 of the completegenome.) (nt:o457; 96 pct identical to 246 residues of) (le:8472) (re:9845) (di:direct) AE000146 AE000146 g1786602 Escherichia coli 562 -11534252 5000691563 (de:(ecoli_386) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_386 ECOLI_386 Escherichia coli 562 10059030

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842254	9814	31970	1593	531

Description

6500730395 yajc:b0407 hypothetical 11.9 kd protein in tgt-secd intergenic region:orf12 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0407 b0407 Escherichia coli 562 -11534253 109803 yajc (de:hypothetical 11.9 kd protein in tgt-secd intergenic region (orf12)) (db:swissprot) YAJC_ECOLI P19677 ESCHERICHIA COLI 562 -11534253 7502851992 yajc (de:hypothetical 11.9 kd protein in tgt-secd intergenic region (orf12)) (db:swissprot) YAJC_ECOLI P19677 SHIGELLA FLEXNERI 623 -11534253 164842 yajc preprotein translocase chain yajc (cl:yajc protein) (db:pir2.dat) (mp:9 min) D38530 D38530 Escherichia coli 562 -11534253 240184 (sr:e.coli k-12 dna) (db:genpept-bct1) (de:e.coli trna-guanine-transglycosylase (tgt) gene, complete cds.) (nt:orf) (le:1366) (re:1698) (di:direct) ECOTGT M63939 g147967 Escherichia coli 562 -11534253 258664 yajc hypothetical 11.9 kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:6737) (re:7069) (di:direct) ECU82664 U82664 g1773091 Escherichia coli 562 -11534253 260703 orf (sr:shigella flexneri (strain:2a, isolate:ysh6000) dna) (db:genpept-bct1) (de:shigella flexneri genes for vacc and orf.) (le:1365) (re:1697) (di:direct) SHFVACC D26469 g599589 Shigella flexneri 623 -11534253 236088 yajc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 37 of 400 of the completegenome.) (nt:ol10; 100 pct identical to yajc_ecoli sw: p19677) (le:4880) (re:5212) (di:direct) AE000147 AE000147 g1786608 Escherichia coli 562 -11534253 7500896229 yajc yajc (db:genpept-bct2) (de:tgt=tgt...secd=secd (escherichia coli, genomic, 3 genes, 900 nt).) (nt:this sequence comes from fig. 1.) (le:312) (re:644) (di:direct) S68715 S68715 g545174 Escherichia coli 562 -11534253 5000691565 (de:(ecoli_391) (pn:hypothetical 11) (gn:yajc) (gtcfc:13.7:14.1) (ec:) (yajc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_391 ECOLI_391 Escherichia coli 562 10051535

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842266	9815	31971	573	190

Description

6500730396 ybad:b0413 hypothetical 17.2 kd protein in tsx-ribd intergenic region:hypothetical 17.2 kd protein in tsx-ribg intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0413 b0413 Escherichia coli 562 -11534254 240190 ybad (de:hypothetical 17.2 kd protein in tsx-ribg intergenic region (orf1)) (db:swissprot) YBAD_ECOLI P25538 ESCHERICHIA COLI 562 -11534254 163421 ybad ybad protein (cl:conserved hypothetical protein hi0943) (db:pir2.dat) S26200 S26200 Escherichia coli 562 -11534254 5000691568 (db:genpept-bct1) (de:e.coli genes nusB (ssyb) and 3 orfs.) (nt:orf1) (le:391) (re:840) (di:direct) ECNUB X64395 g42148 Escherichia coli 562 -11534254 7500896531 ybad hypothetical 17.2kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:12452) (re:12901) (di:direct) ECU82664 U82664 g1773097 Escherichia coli 562 -11534254 233536 ybad orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the complete genome.) (nt:o149; 100 pct identical to ybad_ecoli sw: p25538) (le:76) (re:525) (di:direct) AE000148 AE000148 g1786615 Escherichia coli 562 -11534254 110172 ybad (de:hypothetical 17.2 kd protein in tsx-ribg intergenic region (orf1)) (db:swissprot) YBAD_ECOLI P25538 ESCHERICHIA COLI 562 -11534254

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842268	9816	31972	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842276	9817	31973	1833	610

Description

6500730397 yajo:b0419 hypothetical protein:hypothetical oxidoreductase in pgpa-ispA intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0419 b0419 Escherichia coli 562 -11534255
7000687252 yajo probable oxidoreductase:yajo (cl:conserved hypothetical protein ypl088w) (ec:1.-.-.-) (db:pir2.dat) C64771 C64771 Escherichia coli 562 -11534255 7500896236 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to s. cerevisiae lpg20p) (le:16611) (re:17657) (di:complement) ECU82664 U82664 g1773103 Escherichia coli 562 -11534255 240196 yajo putative nad p h-dependent xylose reductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the complete genome.) (nt:f348; 37 pct identical (8 gaps) to 335 residues of) (le:4235) (re:5281) (di:complement) AE000148 AE000148 g1786621 Escherichia coli 562 -11534255 4000707546 yajo (de:hypothetical oxidoreductase in pgpa-ispA intergenic region) (db:swissprot) YAJO_ECOLI P77735 ESCHERICHIA COLI 562 -11534255 5000691571 (de:(ecoli_403) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_403 ECOLI_403 Escherichia coli 562 10122822

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842298	9818	31974	285	94

Description

6500730398 yajp:b0420 hypothetical protein:hypothetical 67.6 kd protein in pgpa-ispa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0420 b0420 Escherichia coli 562 -11534256 7000687253 dxs dxs protein (cl:hypothetical protein c2814) (db:pir2.dat) D64771 D64771 Escherichia coli 562 -11534256 240197 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to h. influenzae hi1439) (le:17765) (re:19627) (di:complement) ECU82664 U82664 g1773104 Escherichia coli 562 -11534256 7500959877 dxs 1-deoxyxylulose-5-phosphate synthase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completegenome.) (nt:f620; 73 pct identical (4 gaps) to 620 residues of) (le:5389) (re:7251) (di:complement) AE000148 AE000148 g1786622 Escherichia coli 562 -11534256 7000687254 dxs d-1-deoxyxylulose 5-phosphate synthase (db:genpept-bct2) (de:escherichia coli d-1-deoxyxylulose 5-phosphate synthase (dxs) gene,complete cds.) (nt:transketolase-like) (le:1) (re:1863) (di:direct) AF035440 AF035440 g2665586 Escherichia coli 562 -11534256 4000709886 yajp_ecoli (de:(gn:yajp) (de:hypothetical 67.6 kd protein in pgpa-ispa intergenic region) (sp:p77488)) P77488 P77488 Escherichia coli 562 -11534256 5000691572 (de:(ecoli_404) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_404 ECOLI_404 Escherichia coli 562 10122823

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842300	9819	31975	303	100

Description

6500730399 yajk:b0423 hypothetical protein:hypothetical 55.0 kd protein in xseb-thij intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0423 b0423 Escherichia coli 562 -11534257 121759 thii (de:thiamin biosynthesis protein thii) (db:swissprot) THII_ECOLI P77718 ESCHERICHIA COLI 562 -11534257 7000687251 yajk yajk protein (db:pir2.dat) G64771 G64771 Escherichia coli 562 -11534257 7500896235 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to m. jannaschii mg372) (le:20999) (re:22447) (di:direct) ECU82664 U82664 g1773107 Escherichia coli 562 -11534257 240200 yajk putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completegenome.) (nt:o482; 65 pct identical to 365 aa of gb:) (le:8623) (re:10071) (di:direct) AE000148 AE000148 g1786625 Escherichia coli 562 -11534257 5000691573 (de:(ecoli_407) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_407 ECOLI_407 Escherichia coli 562 10065227

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842301	9820	31976	504	167

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842303	9821	31977	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842307	9822	31978	1212	403

Description

6500730400 yajq:b0426 hypothetical protein: hypothetical 19.0 kd protein in abpa-cyoe intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0426 b0426 Escherichia coli 562 -11534258 4000708169 yajq (de: hypothetical 19.0 kd protein in abpa-cyoe intergenic region) (db:swissprot) YAJQ_ECOLI P77482 ESCHERICHIA COLI 562 -11534258 7000687255 yajq yajq protein: protein b0426 (cl: hypothetical protein b0426) (db:pir2.dat) B64772 B64772 Escherichia coli 562 -11534258 7500896237 (db:genpept-bct1) (de: escherichia coli minutes 9 to 11 genomic sequence.) (nt: similar to h. influenzae hi1034) (le:24115) (re:24624) (di: direct) ECU82664 U82664 g1773110 Escherichia coli 562 -11534258 240203 yajq orf: hypothetical protein (fn: orf; unknown) (db:genpept-bct2) (de: escherichia coli k-12 mgl655 section 39 of 400 of the complete genome.) (nt: o169; 61 pct identical to all 163 residues of) (le:105) (re:614) (di: direct) AE000149 AE000149 g1786629 Escherichia coli 562 -11534258 5000691576 (de: (ecoli_410) (pn: function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_410 ECOLI_410 Escherichia coli 562 10122824

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842313	9823	31979	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842319	9824	31980	405	134
<u>Description</u>				

6500730401 yajr:b0427 hypothetical protein:hypothetical 49.0 kd protein in abpa-cyoe intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0427 b0427 Escherichia coli 562 -11534259
4000709843 yajr (de:hypothetical 49.0 kd protein in abpa-cyoe intergenic region) (db:swissprot) YAJR_ECOLI P77726 ESCHERICHIA COLI 562 -11534259
7000687256 yajr probable transport protein yajr (db:pir2.dat) C64772 C64772 Escherichia coli 562 -11534259 7500896239 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:hypothetical protein) (le:24752) (re:26122) (di:complement) ECU82664 U82664 gl773111 Escherichia coli 562 -11534259 240204 yajr putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 39 of 400 of the completegenome.) (nt:f456; this 456 aa orf is 26 pct identical (16 gaps)) (le:742) (re:2112) (di:complement) AE000149 AE000149 g1786630 Escherichia coli 562 -11534259 5000691577 (de:(ecoli_411) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_411 ECOLI_411 Escherichia coli 562 10122825

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842338	9825	31981	255	84
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842348	9826	31982	321	106
<u>Description</u>				

6500730402 yajg:b0434 hypothetical lipoprotein in ampg 5 region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0434 b0434 Escherichia coli 562 -11534260 7000690979 yajg lipoprotein yajg precursor (db:pir2.dat) B64773 B64773 Escherichia coli 562 -11534260 7500959841 yajg hypothetical 20.9 kd lipoprotein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:33039) (re:33719) (di:complement) ECU82664 U82664 gl773118 Escherichia coli 562 -11534260 240211 yajg putative polymerase/proteinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 39 of 400 of the completegenome.) (nt:f226; 100 pct identical to yajg_ecoli sw: p36671) (le:9029) (re:9709) (di:complement) AE000149 AE000149 g1786637 Escherichia coli 562 -11534260 5000691578 (de:(ecoli_418) (pn:hypothetical 20) (gn:yajg) (gtcfc:13.7:14.1) (ec:) (yajg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_418 ECOLI_418 Escherichia coli 562 10122826

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842355	9827	31983	258	85

Description

6500730403 ybau:b0441 hypothetical protein:hypothetical 68.2 kd protein in hupb-cof intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0441 b0441 Escherichia coli 562 -11534261 4000709462 ppid (ec:5.2.1.8) (de:(rotamase d)) (db:swissprot) CYPD_ECOLI P77241 ESCHERICHIA COLI 562 -11534261 7000687272 ybau ybau protein (cl:hypothetical protein hi1004) (db:pir2.dat) A64774 A64774 Escherichia coli 562 -11534261 222824 ybau ybau (sr:escherichia coli (strain:w3110) dna, clone_lib:kohara clone:3b) (db:genpept-bct1) (de:escherichia coli genes for beta-subunit of hu, ybau, ybav, ybaw,ybax, ybae, cof, ybao, complete cds, and for hupb, partial cds.) (nt:hypothetical gene; strong sim... D82943 D82943 g1580712 Escherichia coli 562 -11534261 7500879880 similar to h. influenzae hi1004 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:41365) (re:43236) (di:direct) ECU82664 U82664 g1773125 Escherichia coli 562 -11534261 240218 ybau putative protease maturation protein (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 40 of 400 of the completegenome.) (nt:o623; this 623 aa orf is 34 pct identical (18 gaps)) (le:6984) (re:8855) (di:direct) AE000150 AE000150 g1786645 Escherichia coli 562 -11534261 5000691579 (de:(ecoli_425) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_425 ECOLI_425 Escherichia coli 562 10119130

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842357	9828	31984	786	261

Description

6500730404 ybav:b0442 hypothetical protein:hypothetical 12.7 kd protein in hupb-cof intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0442 b0442 Escherichia coli 562 -11534262 4000708173 ybav (de:hypothetical 12.7 kd protein in hupb-cof intergenic region) (db:swissprot) YBAV_ECOLI P77415 ESCHERICHIA COLI 562 -11534262 7000687273 ybav ybav protein (cl:hypothetical protein hi1008) (db:pir2.dat) B64774 B64774 Escherichia coli 562 -11534262 222825 ybav ybav (sr:escherichia coli (strain:w3110) dna, clone_lib:kohara clone:3b) (db:genpept-bct1) (de:escherichia coli genes for beta-subunit of hu, ybau, ybav, ybaw,ybax, ybae, cof, ybao, complete cds, and for hupb, partial cds.) (nt:a hypothetical gene; strong s... D82943 D82943 g1580713 Escherichia coli 562 -11534262 7500896546 similar to h. influenzae hi1008 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:43387) (re:43758) (di:direct) ECU82664 U82664 g1773126 Escherichia coli 562 -11534262 240219 ybav orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 40 of 400 of the completegenome.) (nt:o123; this 123 aa orf is 37 pct identical (1 gap)) (le:9006) (re:9377) (di:direct) AE000150 AE000150 g1786646 Escherichia coli 562 -11534262 5000691580 (de:(ecoli_426) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_426 ECOLI_426 Escherichia coli 562 10119131

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842365	9829	31985	414	138

Description

6500730405 ybaw:b0443 hypothetical protein:hypothetical 15.1 kd protein in hupb-cof intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0443 b0443 Escherichia coli 562 -11534263 4000708175 ybaw (de:hypothetical 15.1 kd protein in hupb-cof intergenic region) (db:swissprot) YBAW_ECOLI P77712 ESCHERICHIA COLI 562 -11534263 7000687274 ybaw ybaw protein (db:pir2.dat) C64774 C64774 Escherichia coli 562 -11534263 222826 ybaw ybaw (sr:escherichia coli (strain:w3110) dna, clone_lib:kohara clone:3b) (db:genpept-bct1) (de:escherichia coli genes for beta-subunit of hu, ybau, ybav, ybaw,ybax, ybae, cof, ybao, complete cds, and for hupb, partial cds.) (nt:a hypothetical gene) (le:2844... D82943 D82943 g1580714 Escherichia coli 562 -11534263 7500896548 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:hypothetical protein) (le:43852) (re:44250) (di:direct) ECU82664 U82664 g1773127 Escherichia coli 562 -11534263 240220 ybaw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 40 of 400 of the completegenome.) (nt:ol32) (le:9471) (re:9869) (di:direct) AE000150 AE000150 g1786647 Escherichia coli 562 -11534263 5000691581 (de:(ecoli_427) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_427 ECOLI_427 Escherichia coli 562 10119132

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842376	9830	31986	1404	467

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842382	9831	31987	582	193

Description

6500730406 ybax:b0444 hypothetical protein:hypothetical 25.5 kd protein in hupb-cof intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0444 b0444 Escherichia coli 562 -11534264
 4000708176 ybax (de:hypothetical 25.5 kd protein in hupb-cof intergenic region) (db:swissprot) YBAX_ECOLI P77756 ESCHERICHIA COLI 562 -11534264
 7000687275 ybax ybax protein (cl:conserved hypothetical protein hil191) (db:pir2.dat) D64774 D64774 Escherichia coli 562 -11534264 222827 ybax ybax (sr:escherichia coli (strain:w3110) dna, clone_lib:kohara clone:3b) (db:genpept-bct1) (de:escherichia coli genes for beta-subunit of hu, ybau, ybav, ybaw,ybax, ybae, cof, ybao, complete cds, and for hupb, partial cds.) (nt:a hypothetical gene; strong s... D82943 D82943 g1580715 Escherichia coli 562 -11534264 7500896549 similar to h. influenzae hil191 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:44302) (re:44997) (di:complement) ECU82664 U82664 g1773128 Escherichia coli 562 -11534264 240221 ybax orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 40 of 400 of the completegenome.) (nt:f231; this 231 aa orf is 46 pct identical (7 gaps)) (le:9921) (re:10616) (di:complement) AE000150 AE000150 g1786648 Escherichia coli 562 -11534264 5000691582 (de:(ecoli_428) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_428 ECOLI_428 Escherichia coli 562 10119133

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842386	9832	31988	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842393	9833	31989	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842394	9834	31990	795	264

Description

GTC ORF with score 560 to: (fn:putative enzyme; not classified)
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completegenome.) (nt:f348; 37 pct identical (8 gaps) to 335 residues of) (le:4235) (re:5281) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842410	9835	31991	186	61
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842415	9836	31992	201	66
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842424	9837	31993	348	115
<u>Description</u>				

5000691585 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0447 b0447 Escherichia coli 562 -11534265
7000691022 regulatory protein b0447 (db:pir2.dat) G64774 G64774 Escherichia
coli 562 -11534265 7500959878 similar to z. mobilis glutamate uptake
(db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.)
(le:47746) (re:48291) (di:direct) ECU82664 U82664 g1773131 Escherichia coli
562 -11534265 240224 ybao putative lrp-like transcriptional regulator
(fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 41 of 400 of the completegenome.) (nt:0181; this
181 aa orf is 34 pct identical (1 gap)) (le:2747) (re:3292) (di:direct)
AE000151 AE000151 g1786652 Escherichia coli 562 -11534265 6500730407
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0447 b0447 Escherichia coli 562 -11534265

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842433	9838	31994	561	186
<u>Description</u>				
6500730408 amtb:b0451 hypothetical protein in mdl-tesb intergenic region:probable ammonium transporter (gtcfc:12.5) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) b0451 b0451 Escherichia coli 562 -11534266 59427 amtb (de:probable ammonium transporter) (db:swissprot) AMTB_ECOLI P37905 ESCHERICHIA COLI 562 -11534266 7000684577 amtb ammonium transport protein amtb (cl:ammonium transporter nrga) (db:pir2.dat) C64775 Escherichia coli 562 -11534266 240228 amtb putative ammonium transporter (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:52416) (re:53702) (di:direct) ECU82664 U82664 g1773135 Escherichia coli 562 -11534266 239576 amtb probable ammonium transporter (fn:putative transport; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 41 of 400 of the completegenome.) (nt:o428; 100 pct identical to 46 aa of) (le:7417) (re:8703) (di:direct) AE000151 AE000151 g1786656 Escherichia coli 562 -11534266 7500876884 amtb amtb (sr:escherichia coli strain=k12) (db:genpept-bct2) (de:escherichia coli pii-homolog (glnk) gene, complete cds, putativeammonium transporter (amtb) gene, complete cds, and thioesterase ii(tesb) gene, partial cds.) (nt:formerly known as ybag; putative am... ECU40429 U40429 g1103924 Escherichia coli 562 -11534266 5000691587 (de:(ecoli_435) (pn:probable ammonium transporter) (gn:amtb) (gtcfc:13.7:14.1) (ec:) (amtb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_435 ECOLI_435 Escherichia coli 562 10002164				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842435	9839	31995	291	96
<u>Description</u>				
6500730409 ybay:b0453 hypothetical protein:hypothetical 19.4 kd lipoprotein in tesb-hha intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0453 b0453 Escherichia coli 562 -11534267 4000709298 ybay (de:precursor) (db:swissprot) YBAY_ECOLI P77717 ESCHERICHIA COLI 562 -11534267 7000687276 ybay probable lipoprotein ybay precursor (db:pir2.dat) E64775 E64775 Escherichia coli 562 -11534267 7500896551 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:hypothetical protein) (le:54829) (re:55401) (di:direct) ECU82664 U82664 g1773137 Escherichia coli 562 -11534267 240230 ybay glycoprotein/polysaccharide metabolism (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 41 of 400 of the completegenome.) (nt:o190; this 190 aa orf is 24 pct identical (7 gaps)) (le:9830) (re:10402) (di:direct) AE000151 AE000151 g1786658 Escherichia coli 562 -11534267 5000691588 (de:(ecoli_437) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_437 ECOLI_437 Escherichia coli 562 10122833				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842447	9840	31996	1563	520

Description

6500730410 ybaz:b0454 hypothetical protein:hypothetical 14.4 kd protein in tesb-hha intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0454 b0454 Escherichia coli 562 -11534268 4000707879 ybaz (de:hypothetical 14.4 kd protein in tesb-hha intergenic region) (db:swissprot) YBAZ_ECOLI P75707 ESCHERICHIA COLI 562 -11534268 7000687277 ybaz ybaz protein (cl:methylated-dna--protein-cysteine s-methyltransferase homology) (db:pir2.dat) F64775 F64775 Escherichia coli 562 -11534268 7500896552 ybaz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 41 of 400 of the completegenome.) (nt:f129; residues 37-112 are 45 pct identical to) (le:10433) (re:10822) (di:complement) AE000151 AE000151 g1786659 Escherichia coli 562 -11534268 5000691589 (de:(ecoli_438) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_438 ECOLI_438 Escherichia coli 562 10122834

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842453	9841	31997	420	139

Description

6500730411 ybaa:b0456 hypothetical 13.3 kd protein in ffs 3region:hypothetical 13.3 kd protein in tesb-hha intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0456 b0456 Escherichia coli 562 -11534269 240232 ybaa (de:hypothetical 13.3 kd protein in tesb-hha intergenic region) (db:swissprot) YBAA_ECOLI P09161 ESCHERICHIA COLI 562 -11534269 163300 ybaa ybaa protein (db:pir2.dat) S07261 S07261 Escherichia coli 562 -11534269 5000691590 (db:genpept-bct1) (de:e. coli 4.5s rrna gene.) (nt:urf (pot. 4.5s protein)) (le:386) (re:739) (di:direct) ECRNA45 X01074 g42759 Escherichia coli 562 -11534269 7500896529 hypothetical 13.3kd protein in ffs 3 region (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:56120) (re:56473) (di:direct) ECU82664 U82664 g1773139 Escherichia coli 562 -11534269 238095 ybaa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 42 of 400 of the completegenome.) (nt:o117; 100 pct identical to ybaa_ecoli sw: p09161) (le:86) (re:439) (di:direct) AE000152 AE000152 g1786661 Escherichia coli 562 -11534269 110167 ybaa (de:hypothetical 13.3 kd protein in tesb-hha intergenic region) (db:swissprot) YBAA_ECOLI P09161 ESCHERICHIA COLI 562 -11534269

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842464	9842	31998	1437	478

Description

6500730412 ylab:b0457 hypothetical protein:hypothetical 58.9 kd protein in tesb-hha intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0457 b0457 Escherichia coli 562 -11534270
4000709299 ylab (de:hypothetical 58.9 kd protein in tesb-hha intergenic region) (db:swissprot) YLAB_ECOLI P77473 ESCHERICHIA COLI 562 -11534270
7000688114 ylab probable membrane protein ylab (cl:probable membrane protein ylab) (db:pir2.dat) H64775 H64775 Escherichia coli 562 -11534270
7500950931 similar to the 60.8kd protein in ssb-soxs (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:56515) (re:58071) (di:complement) ECU82664 U82664 g1773140 Escherichia coli 562 -11534270 240233 ylab orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 42 of 400 of the completegenome.) (nt:f518; this 518 aa orf is 33 pct identical (6 gaps)) (le:481) (re:2037) (di:complement) AE000152 AE000152 g1786662 Escherichia coli 562 -11534270 5000691591 (de:(ecoli_440) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_440 ECOLI_440 Escherichia coli 562 10122835

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842468	9843	31999	279	92

Description

6500730413 ylac:b0458 hypothetical protein:hypothetical 19.8 kd protein in tesb-hha intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0458 b0458 Escherichia coli 562 -11534271
4000709300 ylac (de:hypothetical 19.8 kd protein in tesb-hha intergenic region) (db:swissprot) YLAC_ECOLI P77523 ESCHERICHIA COLI 562 -11534271
7000688115 ylac probable membrane protein ylac (db:pir2.dat) A64776 A64776 Escherichia coli 562 -11534271 7500950932 hypothetical (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:58229) (re:58738) (di:complement) ECU82664 U82664 g1773141 Escherichia coli 562 -11534271 240234 ylac orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 42 of 400 of the completegenome.) (nt:f169; this 169 aa orf is 32 pct identical (0 gaps)) (le:2195) (re:2704) (di:complement) AE000152 AE000152 g1786663 Escherichia coli 562 -11534271 5000691592 (de:(ecoli_441) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_441 ECOLI_441 Escherichia coli 562 10122836

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842471	9844	32000	789	263

Description

GTC ORF with score 181 to: (fn:binds to orip to permit replication of the) (db:genpept-vrl) (de:herpesvirus papio brrf2 homolog gene, partial cds, ebna1, bkrf2homolog and bkrf3 homolog genes, complete cds, and bkrf4 homologene, partial cds.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842477	9845	32001	243	80

Description

GTC ORF with score 110 to: (sr:human) (db:genpept-pri2) (de:human dna from overlapping chromosome 19-specific cosmids r29515and r28253, genomic sequence, complete sequence.) (nt:hypothetical 16.6kda protein most similar to) (le:14570) (re:14992) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842484	9846	32002	378	125

Description

6500730414 ylad:b0459 hypothetical protein:20.0 kd protein in tesb-hha intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0459 b0459 Escherichia coli 562 -11534272 7000691023 ylad acetyltransferase homolog ylad (cl:galactoside acetyltransferase) (db:pir2.dat) B64776 B64776 Escherichia coli 562 -11534272 7000691024 maa maltose transacetylase (fn:acetylates maltose and other sugars) (db:genpept-bct1) (ec:2.3.1.79) (de:escherichia coli maltose transacetylase orf (maa).) (le:1) (re:552) (di:direct) ECAJ3173 AJ223173 g2826839 Escherichia coli 562 -11534272 7500959879 similar to the 20.2kd protein in tetb-exoa (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:58815) (re:59366) (di:complement) ECU82664 U82664 g1773142 Escherichia coli 562 -11534272 240235 ylad putative transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 42 of 400 of the completegenome.) (nt:f183; this 183 aa orf is 65 pct identical (2 gaps)) (le:2781) (re:3332) (di:complement) AE000152 AE000152 g1786664 Escherichia coli 562 -11534272 5000691593 (de:(ecoli_442) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_442 ECOLI_442 Escherichia coli 562 10122837

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842485	9847	32003	456	151

Description

6500730415 aefa:b0465 hypothetical protein:aefa protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0465 b0465 Escherichia coli 562 -11534273 4000709932 aefa (de:aefa protein) (db:swissprot) AEFA_ECOLI P77338 ESCHERICHIA COLI 562 -11534273 7000684531 aefa probable membrane protein aefa (db:pir2.dat) H64776 H64776 Escherichia coli 562 -11534273 240240 membrane protein (db:genpept-bct1) (de:e.coli gene encoding large membrane protein.) (le:128) (re:3490) (di:direct) ECMEMPR Y07802 g1707458 Escherichia coli 562 -11534273 7500876629 similar to h. influenzae hi0195.1 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:65984) (re:69346) (di:direct) ECU82664 U82664 g1773147 Escherichia coli 562 -11534273 233368 aefa putative alpha helix protein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 42 of 400 of the completegenome.) (nt:ol120; this 1120 aa orf is 28 pct identical) (le:9950) (re:13312) (di:direct) AE000152 AE000152 g1786670 Escherichia coli 562 -11534273 5000691596 (de:(ecoli_448) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_448 ECOLI_448 Escherichia coli 562 10122839

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842489	9848	32004	255	84

Description

6500730416 ybam:b0466 hypothetical 6.0 kd protein in acrr-pric intergenic region:hypothetical 6.0 kd protein in aefa-pric intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0466 b0466 Escherichia coli 562 -11534274 110182 ybam (de:hypothetical 6.0 kd protein in aefa-pric intergenic region) (db:swissprot) YBAM_ECOLI P45807 ESCHERICHIA COLI 562 -11534274 7000687267 ybam ybam protein (db:pir2.dat) A64777 A64777 Escherichia coli 562 -11534274 7500896540 ybam hypothetical 6.0kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:69558) (re:69719) (di:complement) ECU82664 U82664 g1773148 Escherichia coli 562 -11534274 240241 ybam orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 43 of 400 of the completegenome.) (nt:f53; 100 pct identical to ybam_ecoli sw: p45807) (le:136) (re:297) (di:complement) AE000153 AE000153 g1786672 Escherichia coli 562 -11534274 5000691597 (de:(ecoli_449) (pn:hypothetical 6) (gn:ybam) (gtcfc:13.7:14.1) (ec:) (ybam_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_449 ECOLI_449 Escherichia coli 562 10051914

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842518	9849	32005	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842522	9850	32006	387	128

Description

6500730417 yban:b0468 hypothetical 14.8 kd protein in pric-apt intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0468 b0468 Escherichia coli 562 -11534275 110184 yban (de:hypothetical 14.8 kd protein in pric-apt intergenic region) (db:swissprot) YBAN_ECOLI P45808 ESCHERICHIA COLI 562 -11534275 7000687268 yban probable membrane protein yban (db:pir2.dat) C64777 C64777 Escherichia coli 562 -11534275 7500896541 yban hypothetical 14.8kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:70330) (re:70707) (di:direct) ECU82664 U82664 g1773150 Escherichia coli 562 -11534275 240243 yban putative gene 58 (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 43 of 400 of the completegenome.) (nt:ol25; 99 pct identical to yban_ecoli sw: p45808) (le:908) (re:1285) (di:direct) AE000153 AE000153 g1786674 Escherichia coli 562 -11534275 5000691598 (de:(ecoli_451) (pn:hypothetical 14) (gn:yban) (gtcfc:13.7:14.1) (ec:) (yban_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_451 ECOLI_451 Escherichia coli 562 10122840

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842524	9851	32007	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842527	9852	32008	291	96

Description

6500730418 ybab:b0471 hypothetical 12.0 kd protein in dnax-recr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0471 b0471 Escherichia coli 562 -11534276 110169 ybab (de:hypothetical 12.0 kd protein in dnax-recr intergenic region) (db:swissprot) YBAB_ECOLI P17577 ESCHERICHIA COLI 562 -11534276 135224 ybab ybab protein (db:pir1.dat) (mp:11 min) QQECZG A30371 Escherichia coli 562 -11534276 7500896530 (sr:e.coli dna) (db:genpept-bct1) (de:e.coli sequence of the apt-adk region.) (nt:orf12 orf) (le:2854) (re:3183) (di:direct) ECOAPTADK M38777 g145298 Escherichia coli 562 -11534276 233817 ybab orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 43 of 400 of the completegenome.) (nt:ol09; 100 pct identical to ybab_ecoli sw: p17577) (le:4102) (re:4431) (di:direct) AE000153 AE000153 g1786677 Escherichia coli 562 -11534276 5000691599 (de:(ecoli_454) (pn:hypothetical 12) (gn:ybab) (gtcfc:13.7:14.1) (ec:) (ybab_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_454 ECOLI_454 Escherichia coli 562 10051901

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842528	9853	32009	366	121

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842529	9854	32010	270	89

Description

6500730419 ybac:b0476 hypothetical protein in hemh-gsk intergenic region:hypothetical 36.0 kd protein in hemh-gsk intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0476 b0476 Escherichia coli 562 -11534277 110171 aes (ec:3.1.1.-) (de:acetyl esterase,) (db:swissprot) AES_ECOLI P23872 ESCHERICHIA COLI 562 -11534277 7000687260 ybac probable carboxylesterase:ybac (cl:probable lipolytic protein ybac) (ec:3.1.1.1) (db:pir2.dat) (mp:11 min) C64778 C64778 Escherichia coli 562 -11534277 7500876632 ybac hypothetical 36.0kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:78462) (re:79421) (di:complement) ECU82664 U82664 g1773158 Escherichia coli 562 -11534277 240251 ybac putative lipase ec 3.1.1.- (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 43 of 400 of the completegenome.) (nt:f319; 98 pct identical to ybac_ecoli sw: p23872;) (le:9040) (re:9999) (di:complement) AE000153 AE000153 g1786682 Escherichia coli 562 -11534277 5000691601 (de:(ecoli_459) (pn:hypothetical 36) (gn:ybac) (gtcfc:13.7:14.1) (ec:) (ybac_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_459 ECOLI_459 Escherichia coli 562 10122841

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842533	9855	32011	426	141

Description

6500730420 ybal:b0478 hypothetical protein in gsk 3region:hypothetical 59.4 kd protein in gsk-fsr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0478 b0478 Escherichia coli 562 -11534278 110181 ybal (de:hypothetical 59.4 kd protein in gsk-fsr intergenic region) (db:swissprot) YBAL_ECOLI P39830 ESCHERICHIA COLI 562 -11534278 7000687266 ybal probable membrane protein ybal (db:pir2.dat) E64778 E64778 Escherichia coli 562 -11534278 7500896539 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to y. enterocolitica rosb) (le:81010) (re:82686) (di:complement) ECU82664 U82664 g1773160 Escherichia coli 562 -11534278 240253 ybal putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 44 of 400 of the completegenome.) (nt:f558; 100 pct identical to fragment ybal_ecoli) (le:1543) (re:3219) (di:complement) AE000154 AE000154 g1786685 Escherichia coli 562 -11534278 5000691602 (de:(ecoli_461) (pn:hypothetical protein in gsk:3"region:fragment) (gn:ybal) (gtcfc:13.7:14.1) (ec:) (ybal_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_461 ECOLI_461 Escherichia coli 562 10122842

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842535	9856	32012	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842537	9857	32013	204	67

Description

6500730421 ybak:b0481 hypothetical protein:hypothetical 17.1 kd protein in usha-tesa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0481 b0481 Escherichia coli 562 -11534279 110177 ybak (de:hypothetical 17.1 kd protein in usha-tesa intergenic region) (db:swissprot) YBAK_ECOLI P37175 ESCHERICHIA COLI 562 -11534279 7000687264 ybak ybak protein (cl:conserved hypothetical protein hil434) (db:pir2.dat) H64778 H64778 Escherichia coli 562 -11534279 7500896536 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to h. influenzae hil434) (le:86051) (re:86530) (di:complement) ECU82664 U82664 g1773163 Escherichia coli 562 -11534279 240256 ybak orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 44 of 400 of the completegenome.) (nt:f159; 90 pct identical amino acid sequence and) (le:6584) (re:7063) (di:complement) AE000154 AE000154 g1786688 Escherichia coli 562 -11534279 5000691604 (de:(ecoli_464) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_464 ECOLI_464 Escherichia coli 562 10122844

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842554	9858	32014	1482	493

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842555	9859	32015	522	173

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842558	9860	32016	489	162

Description

6500730422 ybap:b0482 hypothetical protein:hypothetical 29.9 kd protein in usha-tesa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0482 b0482 Escherichia coli 562 -11534280
 4000709296 ybap (de:hypothetical 29.9 kd protein in usha-tesa intergenic region) (db:swissprot) YBAP_ECOLI P77301 ESCHERICHIA COLI 562 -11534280
 7000687269 ybap ybap protein (db:pir2.dat) A64779 A64779 Escherichia coli 562 -11534280 7500896542 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:hypothetical protein) (le:86734) (re:87528) (di:complement) ECU82664 U82664 g1773164 Escherichia coli 562 -11534280
 240257 ybap putative ligase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 44 of 400 of the completegenome.) (nt:f264; this 264 aa orf is 25 pct identical (10 gaps)) (le:7267) (re:8061) (di:complement) AE000154 AE000154 g1786689 Escherichia coli 562 -11534280 5000691605 (de:(ecoli_465) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_465 ECOLI_465 Escherichia coli 562 10122845

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842560	9861	32017	279	92

Description

5000691606 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0483 b0483 Escherichia coli 562 -11534281
 7000689399 hypothetical protein b0483 (cl:virulence-associated protein vapa) (db:pir2.dat) B64779 B64779 Escherichia coli 562 -11534281 7500955354 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to d. nodosus vapi gene) (le:87612) (re:88007) (di:direct) ECU82664 U82664 g1773165 Escherichia coli 562 -11534281 240258 ybaq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 44 of 400 of the completegenome.) (nt:o131; this 131 aa orf is 38 pct identical (0 gaps)) (le:8145) (re:8540) (di:direct) AE000154 AE000154 g1786690 Escherichia coli 562 -11534281 6500730423 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0483 b0483 Escherichia coli 562 -11534281

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842568	9862	32018	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842570	9863	32019	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842571	9864	32020	555	184

Description

6500730424 ybar:b0484 hypothetical protein:probable copper-transporting atpase (gtcfc:12.6) (ec:3.6.1.36) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0484 b0484 Escherichia coli 562 -11534282 1500685878 ybar (ec:3.6.1.36) (de:probable copper-transporting atpase,) (db:swissprot) ATCU_ECOLI_Q59385 ESCHERICHIA COLI 562 -11534282 7000684653 ybar probable copper-transporting atpase (cl:escherichia coli probable copper-transporting atpase b0484:atpase nucleotide-binding domain homology:atpase transduction domain homology:heavy-metal-associated homology) (ec:3.6.1.-) (db:pir1.dat) C64779 C64779 Escherichia coli 562 -11534282 7500877288 probable copper-transporting atpase (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:88323) (re:90827) (di:complement) ECU82664 U82664 g1773166 Escherichia coli 562 -11534282 240259 ybar putative atpase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 44 of 400 of the completegenome.) (nt:f834; this 834 aa orf is 44 pct identical (16 gaps)) (le:8856) (re:11360) (di:complement) AE000154 AE000154 g1786691 Escherichia coli 562 -11534282 5000691607 (de:(ecoli_467) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_467 ECOLI_467 Escherichia coli 562 10059367

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842572	9865	32021	1116	371

Description

6500730425 ybas:b0485 hypothetical protein:hypothetical 32.9 kd protein in usha-tesa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0485 b0485 Escherichia coli 562 -11534283
4000709297 ybas (de:hypothetical 32.9 kd protein in usha-tesa intergenic region) (db:swissprot) YBAS_ECOLI P77454 ESCHERICHIA COLI 562 -11534283
7000687270 ybas probable membrane protein ybas (cl:hypothetical protein b1524) (db:pir2.dat) D64779 D64779 Escherichia coli 562 -11534283
7500896544 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to rat mitochondrial glutaminase) (le:91089) (re:92021) (di:direct) ECU82664 U82664 g1773167 Escherichia coli 562 -11534283 240260 ybas putative glutaminase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:o310; this 310 aa orf is 39 pct identical (6 gaps)) (le:161) (re:1093) (di:direct) AE000155 AE000155 g1786693 Escherichia coli 562 -11534283 5000691608 (de:(ecoli_468) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_468 ECOLI_468 Escherichia coli 562 10122847

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842595	9866	32022	447	148

Description

6500730426 ybat:b0486 hypothetical protein:hypothetical 45.7 kd protein in usha-tesa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0486 b0486 Escherichia coli 562 -11534284
4000708172 ybat (de:hypothetical 45.7 kd protein in usha-tesa intergenic region) (db:swissprot) YBAT_ECOLI P77400 ESCHERICHIA COLI 562 -11534284
7000687271 ybat probable membrane protein ybat (cl:probable membrane protein ybat) (db:pir2.dat) E64779 E64779 Escherichia coli 562 -11534284
7500896545 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to m. jannaschii amino acid transporter) (le:92024) (re:93316) (di:direct) ECU82664 U82664 g1773168 Escherichia coli 562 -11534284 240261 ybat putative amino acid/amine transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:o430; this 430 aa orf is 23 pct identical (19 gaps)) (le:1096) (re:2388) (di:direct) AE000155 AE000155 g1786694 Escherichia coli 562 -11534284 5000691609 (de:(ecoli_469) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_469 ECOLI_469 Escherichia coli 562 10122848

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842598	9867	32023	417	138

Description

6500730427 ybbi:b0487 hypothetical protein:hypothetical transcriptional regulator in usha-tesa intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0487 b0487 Escherichia coli 562 -11534285 4000708157 ybbi (de:hypothetical transcriptional regulator in usha-tesa intergenic region) (db:swissprot) YBBI_ECOLI P77565 ESCHERICHIA COLI 562 -11534285 7000687286 ybbi probable transcription regulator ybbi (cl:transcription repressor glnr) (db:pir2.dat) F64779 F64779 Escherichia coli 562 -11534285 7500896570 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to h. influenzae hi0293) (le:93441) (re:93848) (di:direct) ECU82664 U82664 g1773169 Escherichia coli 562 -11534285 240262 ybbi putative transcriptional regulator (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:o135; this 135 aa orf is 39 pct identical (0 gaps)) (le:2513) (re:2920) (di:direct) AE000155 AE000155 g1786695 Escherichia coli 562 -11534285 5000691610 (de:(ecoli_470) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_470 ECOLI_470 Escherichia coli 562 10122849

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842599	9868	32024	1035	344

Description

6500730428 ybbj:b0488 hypothetical protein:hypothetical 16.8 kd protein in usha-tesa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0488 b0488 Escherichia coli 562 -11534286 4000709301 ybbj (de:hypothetical 16.8 kd protein in usha-tesa intergenic region) (db:swissprot) YBBJ_ECOLI P75709 ESCHERICHIA COLI 562 -11534286 7000687287 ybbj probable membrane protein ybbj (db:pir2.dat) G64779 G64779 Escherichia coli 562 -11534286 7500896572 ybbj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:f151; this 151 aa orf is 28 pct identical (9 gaps)) (le:2921) (re:3376) (di:complement) AE000155 AE000155 g1786696 Escherichia coli 562 -11534286 5000691611 (de:(ecoli_471) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_471 ECOLI_471 Escherichia coli 562 10122850

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842600	9869	32025	723	240

Description

6500730429 ybbk:b0489 hypothetical protein:hypothetical 33.7 kd protein in usha-tesa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0489 b0489 Escherichia coli 562 -11534287
 4000707623 ybbk (de:hypothetical 33.7 kd protein in usha-tesa intergenic region) (db:swissprot) YBBK_ECOLI P77367 ESCHERICHIA COLI 562 -11534287
 7000687288 ybbk probable membrane protein ybbk (cl:erythrocyte band 7 integral membrane protein) (db:pir2.dat) H64779 H64779 Escherichia coli 562 -11534287 7500896573 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to m. tuberculosis mtcy277.09) (le:94304) (re:95221) (di:complement) ECU82664 U82664 g1773171 Escherichia coli 562 -11534287 240264 ybbk putative protease (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:f305; this 305 aa orf is 33 pct identical (5 gaps)) (le:3376) (re:4293) (di:complement) AE000155 AE000155 g1786697 Escherichia coli 562 -11534287 5000691612 (de:(ecoli_472) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_472 ECOLI_472 Escherichia coli 562 10122851

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842623	9870	32026	2085	694

Description

6500730430 ybbl:b0490 hypothetical protein:hypothetical abc transporter atp-binding protein in usha-tesa intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0490 b0490 Escherichia coli 562 -11534288 4000707501 ybbl (de:hypothetical abc transporter atp-binding protein ybbl) (db:swissprot) YBBL_ECOLI P77279 ESCHERICHIA COLI 562 -11534288 7000687289 ybbl probable abc-type transport protein ybbl:probable abc transporter:atp-binding protein ybbl (cl:atp-binding cassette homology) (db:pir2.dat) A64780 A64780 Escherichia coli 562 -11534288 7500896574 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:hypothetical protein) (le:95367) (re:96044) (di:direct) ECU82664 U82664 g1773172 Escherichia coli 562 -11534288 240265 ybbl putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:o225; this 225 aa orf is 32 pct identical (7 gaps)) (le:4439) (re:5116) (di:direct) AE000155 AE000155 g1786698 Escherichia coli 562 -11534288 5000691613 (de:(ecoli_473) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_473 ECOLI_473 Escherichia coli 562 10122852

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842628	9871	32027	1227	408

Description

6500730431 ybbm:b0491 hypothetical protein:hypothetical 29.2 kd protein in usha-tesa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0491 b0491 Escherichia coli 562 -11534289
7000687290 ybbm probable transport protein ybbm:probable permease ybbm:probable transporter ybbm (cl:conserved hypothetical protein mj0938) (db:pir2.dat) B64780 B64780 Escherichia coli 562 -11534289 7500896575 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to m. jannaschii mj0938) (le:96004) (re:96810) (di:direct) ECU82664 U82664 g1773173 Escherichia coli 562 -11534289 240266 ybbm putative metal resistance protein (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:o268; this 268 aa orf is 27 pct identical (9 gaps)) (le:5076) (re:5882) (di:direct) AE000155 AE000155 g1786699 Escherichia coli 562 -11534289 4000709939 ybbm (de:hypothetical 29.2 kd protein in usha-tesa intergenic region) (db:swissprot) YBBM_ECOLI P77307 ESCHERICHIA COLI 562 -11534289 5000691614 (de:(ecoli_474) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_474 ECOLI_474 Escherichia coli 562 10122853

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842651	9872	32028	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842678	9873	32029	1833	611

Description

6500730432 ybbn:b0492 hypothetical protein:hypothetical 33.1 kd protein in usha-tesa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0492 b0492 Escherichia coli 562 -11534290
4000708177 ybbn (de:hypothetical 33.1 kd protein in usha-tesa intergenic region) (db:swissprot) YBBN_ECOLI P77395 ESCHERICHIA COLI 562 -11534290
7000687291 ybbn ybbn protein (db:pir2.dat) C64780 C64780 Escherichia coli 562 -11534290 7500896576 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to h. influenzae h1159) (le:96873) (re:97763) (di:complement) ECU82664 U82664 g1773174 Escherichia coli 562 -11534290 240267 ybbn putative thioredoxin-like protein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:f296; this 296 aa orf is 54 pct identical (2 gaps)) (le:5945) (re:6835) (di:complement) AE000155 AE000155 g1786700 Escherichia coli 562 -11534290 5000691615 (de:(ecoli_475) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_475 ECOLI_475 Escherichia coli 562 10122854

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842687	9874	32030	693	230

Description

6500730433 ybbo:b0493 hypothetical protein:hypothetical oxidoreductase in usha-tesa intergenic region (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0493 b0493 Escherichia coli 562 -11534291 4000707534 ybbo (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YBBO_ECOLI P77388 ESCHERICHIA COLI 562 -11534291 7000687292 ybbo probable retinol dehydrogenase (cl:retinol dehydrogenase:short-chain alcohol dehydrogenase homology) (ec:1.1.1.-) (db:pir2.dat) D64780 D64780 Escherichia coli 562 -11534291 7500896578 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to human protein that oxidizes 11-cis) (le:97788) (re:98597) (di:complement) ECU82664 U82664 g1773175 Escherichia coli 562 -11534291 240268 ybbo putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:f269; this 269 aa orf is 36 pct identical (11 gaps)) (le:6860) (re:7669) (di:complement) AE000155 AE000155 g1786701 Escherichia coli 562 -11534291 5000691616 (de:(ecoli_476) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_476 ECOLI_476 Escherichia coli 562 10122855

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842688	9875	32031	507	168

Description

6500730434 ybba:b0495 hypothetical abc transporter:hypothetical abc transporter atp-binding protein in usha-tesa intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0495 b0495 Escherichia coli 562 -11534292 110198 ybba (de:hypothetical abc transporter atp-binding protein ybba) (db:swissprot) YBBA_ECOLI P31219 ESCHERICHIA COLI 562 -11534292 7000687278 ybba probable abc-type transport protein ybba:probable abc transporter:atp-binding protein ybba (cl:atp-binding cassette homology) (db:pir2.dat) F64780 F64780 Escherichia coli 562 -11534292 7500896560 ybba hypothetical abc transporter (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:99181) (re:99867) (di:direct) ECU82664 U82664 g1773177 Escherichia coli 562 -11534292 240270 ybba putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:o228; 98 pct identical to fragment ybba_ecoli) (le:8253) (re:8939) (di:direct) AE000155 AE000155 g1786703 Escherichia coli 562 -11534292 5000691617 (de:(ecoli_478) (pn:hypothetical abc transporter atp-binding protein in tesa 5"region:fragment) (gn:ybba) (gtcfc:13.7:14.1) (ec:) (ybba_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_478 ECOLI_478 Escherichia coli 562 10122856

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842690	9876	32032	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842691	9877	32033	669	222

Description

6500730435 ybbp:b0496 hypothetical protein:hypothetical 89.3 kd protein in tesa-rhsd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0496 b0496 Escherichia coli 562 -11534293
4000709302 ybbp (de:hypothetical 89.3 kd protein in tesa-rhsd intergenic region) (db:swissprot) YBBP_ECOLI P77504 ESCHERICHIA COLI 562 -11534293
7000687293 ybbp probable membrane protein ybbp (db:pir2.dat) G64780 Escherichia coli 562 -11534293 7500896579 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:hypothetical protein) (le:99864) (re:102278) (di:direct) ECU82664 U82664 g1773178 Escherichia coli 562 -11534293 240271 ybbp putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 45 of 400 of the completegenome.) (nt:o804; this 804 aa orf is 24 pct identical (13 gaps)) (le:8936) (re:11350) (di:direct) AE000155 AE000155 g1786704 Escherichia coli 562 -11534293 5000691618 (de:(ecoli_479) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_479 ECOLI_479 Escherichia coli 562 10122857

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842692	9878	32034	408	135

Description

6500730436 ybbc:b0498 hypothetical 14.2 kd protein in rhsd 3region:hypothetical 14.2 kd protein in rhsd-gcl intergenic region precursor:orfd2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0498 b0498 Escherichia coli 562 -11534294 110203 ybbc (de:(orfd2)) (db:swissprot) YBBC_ECOLI P33668 ESCHERICHIA COLI 562 -11534294 7000687282 ybbc ybbc protein precursor (cl:yhhh protein) (db:pir2.dat) A64781 A64781 Escherichia coli 562 -11534294 240273 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli rhsd genetic element; core protein (rhsd) gene,complete cds; complete orf-d2; complete orf-d3.) (nt:orfd2) (le:4875) (re:5243) (di:direct) ECORHSDX L19084 g304942 Escherichia coli 562 -11534294 7500896565 ybbc hypothetical 14.2 kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:107029) (re:107397) (di:direct) ECU82664 U82664 g1773180 Escherichia coli 562 -11534294 235824 ybbc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 46 of 400 of the completegenome.) (nt:ol22; 100 pct identical to ybbc_ecoli sw: p33668) (le:4566) (re:4934) (di:direct) AE000156 AE000156 g1786707 Escherichia coli 562 -11534294 5000691620 (de:(ecoli_481) (pn:hypothetical 14) (gn:ybbc) (gtcfc:13.7:14.1) (ec:) (ybbc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_481 ECOLI_481 Escherichia coli 562 10051935

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842694	9879	32035	183	60

Description

5000691621 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0499 b0499 Escherichia coli 562 -11534295
 7000691025 hypothetical protein b0499 (db:pir2.dat) B64781 B64781
 Escherichia coli 562 -11534295 7500959880 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to rhsd) (le:107397) (re:108107) (di:direct) ECU82664 U82664 g1773181 Escherichia coli 562 -11534295 240274 b0499 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 46 of 400 of the completegenome.) (nt:o236; this 236 aa orf is 57 pct identical (12 gaps)) (le:4934) (re:5644) (di:direct) AE000156 AE000156 g1786708 Escherichia coli 562 -11534295 6500730437 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0499 b0499 Escherichia coli 562 -11534295

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842711	9880	32036	411	136

Description

GTC ORF with score 208 to: (db:genpept-bct2) (de:myxococcus xanthus saframycin mx1 synthetase b (safb), saframycinmx1 synthetase a (safa), and safc genes, complete cds.) (nt:contains two putative amino acid activating) (le:5491) (re:13308) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842714	9881	32037	288	95

Description

5000691623 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0501 b0501 Escherichia coli 562 -11534296
 7000691026 hypothetical protein b0501 (db:pir2.dat) D64781 D64781
 Escherichia coli 562 -11534296 7500959881 b0501 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 46 of 400 of the completegenome.) (nt:o63; o63; phage stats; this 63 aa orf is 34 pct) (le:5924) (re:6115) (di:direct) AE000156 AE000156 g1786710
 Escherichia coli 562 -11534296 6500730438 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0501 b0501
 Escherichia coli 562 -11534296

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842717	9882	32038	1326	442

Description

5000691624 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0502 b0502 Escherichia coli 562 -11534297
7000691027 hypothetical protein b0502 (db:pir2.dat) E64781 E64781
Escherichia coli 562 -11534297 7500959882 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to a. pleuropneumoniae orf1) (le:109093) (re:109500) (di:complement) ECU82664 U82664 g1773183
Escherichia coli 562 -11534297 240276 b0502 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 46 of 400 of the completegenome.) (nt:fl35; residues 18-128 are 68 pct identical to) (le:6630) (re:7037) (di:complement) AE000156 AE000156 g1786711
Escherichia coli 562 -11534297 6500730439 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0502 b0502
Escherichia coli 562 -11534297

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842719	9883	32039	366	121

Description

6500730440 ybbs:b0504 hypothetical protein:hypothetical transcriptional regulator in rhd-gcl intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0504 b0504 Escherichia coli 562 -11534298 4000708148 ybbs:glxa1 (de:hypothetical transcriptional regulator in rhd-gcl intergenic region) (db:swissprot) YBBS_ECOLI P77702 ESCHERICHIA COLI 562 -11534298 7000687296 ybbs probable transcription regulator ybbs (cl:probable transcription regulator ybbs) (db:pir2.dat) G64781 G64781
Escherichia coli 562 -11534298 7000687297 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to e. coli ydhh) (le:110743) (re:111669) (di:complement) ECU82664 U82664 g1773185 Escherichia coli 562 -11534298 7500896581 glxa1 hypothetical transcriptional regulator (db:genpept-bct1) (de:escherichia coli hypothetical transcriptional regulator (glxa1),glyoxylate induced protein (glxa2) and glyoxylate regulatoryprotein (glxa3) genes, complete cds.) (le:23) (re:949) (di:complement) ECU89024 U89024 g2735226 Escherichia coli 562 -11534298
240278 ybbs putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 46 of 400 of the completegenome.) (nt:f308; 30 pct identical (1 gap) to 275 residues of) (le:8280) (re:9206) (di:complement) AE000156 AE000156 g1786713 Escherichia coli 562 -11534298 5000691626 (de:(ecoli_487) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_487 ECOLI_487 Escherichia coli 562 10122864

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842720	9884	32040	432	143

Description

6500730441 ybbt:b0505 hypothetical protein:hypothetical 18.2 kd protein in rhsd-gcl intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0505 b0505 Escherichia coli 562 -11534299 4000709303 ybbt:glxa2 (de:hypothetical 18.2 kd protein in rhsd-gcl intergenic region) (db:swissprot) YBBT_ECOLI P77731 ESCHERICHIA COLI 562 -11534299 7000687298 ybbt probable membrane protein ybbt (db:pir2.dat) H64781 H64781 Escherichia coli 562 -11534299 7000687299 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to s. cerevisiae dal3) (le:111899) (re:112381) (di:direct) ECU82664 U82664 g1773186 Escherichia coli 562 -11534299 7500896582 glxa2 glyoxylate induced protein (db:genpept-bct1) (de:escherichia coli hypothetical transcriptional regulator (glxa1),glyoxylate induced protein (glxa2) and glyoxylate regulatoryprotein (glxa3) genes, complete cds.) (nt:similar to ureidoglycolate hydrolase from yeast) (le:1179) (re:1... ECU89024 U89024 g2735227 Escherichia coli 562 -11534299 240279 ybbt orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 46 of 400 of the completegenome.) (nt:ol60; this 160 aa orf is 55 pct identical (7 gaps)) (le:9436) (re:9918) (di:direct) AE000156 AE000156 g1786714 Escherichia coli 562 -11534299 5000691627 (de:(ecoli_488) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_488 ECOLI_488 Escherichia coli 562 10122865

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842724	9885	32041	333	110

Description

GTC ORF with score 276 to: (sr:fusarium oxysporum (sub_species:f. sp. lycopersici, strain:race 2) (db:genpept-pln2) (de:fusarium oxysporum dna for endopolygalacturonase, complete cds.) (le:372:479:689:888:1399) (re:431:637:837:1344:1689) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842744	9886	32042	1368	455
<u>Description</u>				
6500730442 ybbu:b0506 hypothetical protein:hypothetical transcriptional regulator in rhd-gcl intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0506 b0506 Escherichia coli 562 -11534300 4000708138 ybbu:glxa3 (de:hypothetical transcriptional regulator in rhd-gcl intergenic region) (db:swissprot) YBBU_ECOLI P77734 ESCHERICHIA COLI 562 -11534300 7000687300 ybbu probable transcription regulator ybbu (cl:acetate operon repressor) (db:pir2.dat) A64782 A64782 Escherichia coli 562 -11534300 7000687301 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to e. coli iclr) (le:112459) (re:113274) (di:direct) ECU82664 U82664 g1773187 Escherichia coli 562 -11534300 7500896583 glxa3 glyoxylate regulatory protein (db:genpept-bct1) (de:escherichia coli hypothetical transcriptional regulator (glxa1),glyoxylate induced protein (glxa2) and glyoxylate regulatoryprotein (glxa3) genes, complete cds.) (le:1739) (re:2554) (di:direct) ECU89024 U89024 g2735228 Escherichia coli 562 -11534300 240280 ybbu putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 46 of 400 of the completegenome.) (nt:o271; this 271 aa orf is 42 pct identical (3 gaps)) (le:9996) (re:10811) (di:direct) AE000156 AE000156 g1786715 Escherichia coli 562 -11534300 5000691628 (de:(ecoli_489) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_489 ECOLI_489 Escherichia coli 562 10122866				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842756	9887	32043	903	300

Description

6500730443 ybbq:b0509 hypothetical protein:hypothetical 30.8 kd protein in gip-fdra intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0509 b0509 Escherichia coli 562 -11534301 4000707848 ybbq:glxb1 (de:hypothetical 30.8 kd protein in gip-fdra intergenic region) (db:swissprot) YBBQ_ECOLI P77161 ESCHERICHIA COLI 562 -11534301 7000687294 3-hydroxyisobutyrate dehydrogenase homolog b0509 (cl:3-hydroxyisobutyrate dehydrogenase:3-hydroxyisobutyrate dehydrogenase homology) (db:pir2.dat) D64782 D64782 Escherichia coli 562 -11534301 7000687295 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to e. coli yhae) (le:116034) (re:116912) (di:direct) ECU82664 U82664 g1773190 Escherichia coli 562 -11534301 7500896580 glxb1 glxb1 (db:genpept-bct1) (de:escherichia coli glyoxylate induced proteins glxb1, glxb2, glxb3,glxb4, glxb6, glxb7 and glxb8, and glycerate kinase glxb5 genes,complete cds.) (nt:glyoxylate induced protein) (le:116) (re:994) (di:direct) ECU89279 U89279 g2735236 Escherichia coli 562 -11534301 240283 ybbq putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 47 of 400 of the completegenome.) (nt:o292; this 292 aa orf is 44 pct identical (1 gap)) (le:2745) (re:3623) (di:direct) AE000157 AE000157 g1786719 Escherichia coli 562 -11534301 5000691630 (de:(ecoli_492) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_492 ECOLI_492 Escherichia coli 562 10122867

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842759	9888	32044	1029	343

Description

6500730444 ybbv:b0510 hypothetical protein:hypothetical 10.8 kd protein in gip-fdra intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0510 b0510 Escherichia coli 562 -11534302 4000709304 ybbv (de:hypothetical 10.8 kd protein in gip-fdra intergenic region) (db:swissprot) YBBV_ECOLI P75711 ESCHERICHIA COLI 562 -11534302 7000687302 hypothetical protein b0510 (db:pir2.dat) E64782 E64782 Escherichia coli 562 -11534302 7500896584 ybbv orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 47 of 400 of the completegenome.) (nt:o92; 27 pct identical (3 gaps) to 54 residues) (le:3655) (re:3933) (di:direct) AE000157 AE000157 g1786720 Escherichia coli 562 -11534302 5000691631 (de:(ecoli_493) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_493 ECOLI_493 Escherichia coli 562 10122868

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842776	9889	32045	369	122

Description

5000691632 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0511 b0511 Escherichia coli 562 -11534303
7000691028 probable transport protein b0511 (cl:escherichia coli probable transport protein b0511) (db:pir2.dat) F64782 F64782 Escherichia coli 562 -11534303 7500959883 ybbw putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 47 of 400 of the completegenome.) (nt:o437; 27 pct identical (26 gaps) to 433 residues) (le:3933) (re:5246) (di:direct) AE000157 AE000157 g1786721 Escherichia coli 562 -11534303 6500730445 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0511 b0511 Escherichia coli 562 -11534303

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842784	9890	32046	807	268

Description

5000691634 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0513 b0513 Escherichia coli 562 -11534304
7500896585 ybby:glxb4 (de:hypothetical 47.5 kd protein in gip-fdra intergenic region) (db:swissprot) YBBY_ECOLI P77328 ESCHERICHIA COLI 562 -11534304 7000691029 probable membrane protein b0513 (db:pir2.dat) H64782 H64782 Escherichia coli 562 -11534304 240286 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to b. subtilis ywdj) (le:120007) (re:121314) (di:direct) ECU82664 U82664 g1773193 Escherichia coli 562 -11534304 7500896587 ybby putative transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 47 of 400 of the completegenome.) (nt:o435; this 435 aa orf is 27 pct identical (19 gaps)) (le:6718) (re:8025) (di:direct) AE000157 AE000157 g1786723 Escherichia coli 562 -11534304 6500730446 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0513 b0513 Escherichia coli 562 -11534304

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842785	9891	32047	1227	408

Description

6500730447 ybbz:b0514 hypothetical protein:hypothetical 38.7 kd protein in gip-fdra intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0514 b0514 Escherichia coli 562 -11534305 4000708178 ybbz:glxb5 (de:hypothetical 38.7 kd protein in gip-fdra intergenic region) (db:swissprot) YBBZ_ECOLI P77364 ESCHERICHIA COLI 562 -11534305 7000687303 ybbz ybbz protein (cl:yhad protein) (db:pir2.dat) A64783 A64783 Escherichia coli 562 -11534305 7000687304 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to e. coli yhad) (le:121336) (re:122481) (di:direct) ECU82664 U82664 g1773194 Escherichia coli 562 -11534305 7500896589 glxb5 glycerate kinase glxb5 (db:genpept-bct1) (de:escherichia coli glyoxylate induced proteins glxb1, glxb2, glxb3, glxb4, glxb6, glxb7 and glxb8, and glycerate kinase glxb5 genes, complete cds.) (le:5418) (re:6563) (di:direct) ECU89279 U89279 g2735240 Escherichia coli 562 -11534305 240287 ybbz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 47 of 400 of the complete genome.) (nt:o381; this 381 aa orf is 56 pct identical (0 gaps)) (le:8047) (re:9192) (di:direct) AE000157 AE000157 g1786724 Escherichia coli 562 -11534305 5000691635 (de:(ecoli_497) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_497 ECOLI_497 Escherichia coli 562 10122872

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842796	9892	32048	387	128

Description

6500730448 ylba:b0515 hypothetical protein:hypothetical 28.7 kd protein in gip-fdra intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0515 b0515 Escherichia coli 562 -11534306 1500686254 ylba:glxb6 (de:hypothetical 28.7 kd protein in gip-fdra intergenic region) (db:swissprot) YLBA_ECOLI P75713 ESCHERICHIA COLI 562 -11534306 7000688118 hypothetical protein b0515 (db:pir2.dat) B64783 B64783 Escherichia coli 562 -11534306 7500950935 ylba orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 47 of 400 of the complete genome.) (nt:f261; this 261 aa orf is 21 pct identical (8 gaps)) (le:9420) (re:10205) (di:complement) AE000157 AE000157 g1786725 Escherichia coli 562 -11534306 5000691636 (de:(ecoli_498) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_498 ECOLI_498 Escherichia coli 562 10061001

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842797	9893	32049	486	162

Description

6500730449 ylb:b0516 hypothetical protein:hypothetical 45.7 kd protein in gip-fdra intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0516 b0516 Escherichia coli 562 -11534307 1500685832 ylb:glxb7 (de:hypothetical 45.7 kd protein in gip-fdra intergenic region) (db:swissprot) YLBB_ECOLI P77425 ESCHERICHIA COLI 562 -11534307 7000688119 ylb ylb protein (cl:n-carbamyl-l-amino acid amidohydrolase) (db:pir2.dat) C64783 C64783 Escherichia coli 562 -11534307 7000688120 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to b. stearothermophilus n-carbamyl-l-amino) (le:123506) (re:124741) (di:complement) ECU82664 U82664 g1773196 Escherichia coli 562 -11534307 7500950936 glxb7 glxb7 (db:genpept-bct1) (de:escherichia coli glyoxylate induced proteins glxb1, glxb2, glxb3,glxb4, glxb6, glxb7 and glxb8, and glycerate kinase glxb5 genes,complete cds.) (nt:glyoxylate induced protein) (le:7586) (re:8821) (di:complement) ECU89279 U89279 g2735242 Escherichia coli 562 -11534307 240289 ylb putative hydantoin utilization protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 47 of 400 of the completegenome.) (nt:f411; this 411 aa orf is 32 pct identical (10 gaps)) (le:10216) (re:11451) (di:complement) AE000157 AE000157 g1786726 Escherichia coli 562 -11534307 5000691637 (de:(ecoli_499) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_499 ECOLI_499 Escherichia coli 562 10059233

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842825	9894	32050	315	104

Description

6500730450 ylbcb0517 hypothetical protein: hypothetical 38.0 kd protein in gip-fdra intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0517 b0517 Escherichia coli 562 -11534308 4000708868 ylbcbglxb8 (de: hypothetical 38.0 kd protein in gip-fdra intergenic region) (db:swissprot) YLBC_ECOLI P77555 ESCHERICHIA COLI 562 -11534308 7000688121 ylbcbmalate dehydrogenase homolog ylbcb (cl:malate dehydrogenase ylbcb) (db:pir2.dat) D64783 D64783 Escherichia coli 562 -11534308 7000688122 (db:genpept-bct1) (de: escherichia coli minutes 9 to 11 genomic sequence.) (nt: similar to m. fervidus malate dehydrogenase) (le:124763) (re:125812) (di:complement) ECU82664 U82664 g1773197 Escherichia coli 562 -11534308 7500950937 glxb8 glxb8 (db:genpept-bct1) (de: escherichia coli glyoxylate induced proteins glxb1, glxb2, glxb3, glxb4, glxb6, glxb7 and glxb8, and glycerate kinase glxb5 genes, complete cds.) (nt: glyoxylate induced protein) (le:8843) (re:9892) (di:complement) ECU89279 U89279 g2735243 Escherichia coli 562 -11534308 240290 ylbcbputative malate dehydrogenase ec 1.1.1.37 (fn: putative enzyme; not classified) (db:genpept-bct2) (de: escherichia coli k-12 mg1655 section 47 of 400 of the complete genome.) (nt: f349; this 349 aa orf is 35 pct identical (11 gaps)) (le:11473) (re:12522) (di:complement) AE000157 AE000157 g1786727 Escherichia coli 562 -11534308 5000691638 (de: (ecoli_500) (pn: function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_500 ECOLI_500 Escherichia coli 562 10122873

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842858	9895	32051	258	85

Description

Hypothetical protein .

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842874	9896	32052	618	205

Description

6500730451 fdra:b0518 hypothetical protein:fdra protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0518 b0518 Escherichia coli 562 -11534309 500685118 fdra (de:fdra protein) (db:swissprot) FDRA_ECOLI Q47208 ESCHERICHIA COLI 562 -11534309 164109 fdra multicopy suppressor fdra (db:pir2.dat) (mp:12 min) S60201 S60201 Escherichia coli 562 -11534309 240291 fdra fdra protein (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli gene for fdra protein, complete cds.) (nt:a multicopy suppressor of dominant negative ftsh) (le:127) (re:1794) (di:direct) ECOFDRAP D42020 g565641 Escherichia coli 562 -11534309 7500881384 fdra (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:126129) (re:127796) (di:direct) ECU82664 U82664 g1773198 Escherichia coli 562 -11534309 234311 fdra involved in protein transport:multicopy (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 48 of 400 of the completegenome.) (nt:o555; o555; was o533p (partial); this 555 aa orf is) (le:189) (re:1856) (di:direct) AE000158 AE000158 g1786729 Escherichia coli 562 -11534309 5000691639 (de:(ecoli_501) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_501 ECOLI_501 Escherichia coli 562 10063087

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842877	9897	32053	615	204

Description

5000691640 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0519 b0519 Escherichia coli 562 -11534310 7000691030 hypothetical protein b0519 (db:pir2.dat) F64783 F64783 Escherichia coli 562 -11534310 7500959884 ylbe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 48 of 400 of the completegenome.) (nt:o333 was o419; this 419 aa orf is 26 pct identical) (le:2123) (re:3124) (di:direct) AE000158 AE000158 g1786730 Escherichia coli 562 -11534310 6500730452 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0519 b0519 Escherichia coli 562 -11534310

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842890	9898	32054	741	246

Description

6500730453 ylbfb0520 hypothetical protein:hypothetical 29.6 kd protein in fdra-arcc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0520 b0520 Escherichia coli 562 -11534311
4000708179 ylbfb (de:hypothetical 29.6 kd protein in fdra-arcc intergenic region) (db:swissprot) YLBF_ECOLI P77518 ESCHERICHIA COLI 562 -11534311
7000688123 ylbfb ylbfb protein (db:pir2.dat) G64783 G64783 Escherichia coli 562 -11534311 7500950938 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:hypothetical protein) (le:129076) (re:129891) (di:direct) ECU82664 U82664 g1773200 Escherichia coli 562 -11534311 240293 ylbfb putative carboxylase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 48 of 400 of the completegenome.) (nt:o271; o271; internal frameshift; this 271 aa orf is) (le:3135) (re:3950) (di:direct) AE000158 AE000158 g1786731 Escherichia coli 562 -11534311 5000691641 (de:(ecoli_503) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_503 ECOLI_503 Escherichia coli 562 10122875

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842894	9899	32055	825	274

Description

6500730454 ybcib0527 hypothetical protein in cyss-fold intergenic region:hypothetical 19.5 kd protein in cyss-fold intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0527 b0527 Escherichia coli 562 -11534312 110216 ybcib (de:hypothetical 19.5 kd protein in cyss-fold intergenic region) (db:swissprot) YBCI_ECOLI P45570 ESCHERICHIA COLI 562 -11534312 7000687305 ybcib ybcib protein (db:pir2.dat) F64784 F64784 Escherichia coli 562 -11534312 7500896594 ybcib hypothetical 19.5 kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:135481) (re:136002) (di:complement) ECU82664 U82664 g1773208 Escherichia coli 562 -11534312 240301 ybcib orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 48 of 400 of the completegenome.) (nt:f173; 100 pct identical to ybcib_ecoli sw: p45570) (le:9540) (re:10061) (di:complement) AE000158 AE000158 g1786738 Escherichia coli 562 -11534312 5000691644 (de:(ecoli_510) (pn:hypothetical 19) (gn:ybcib) (gtcfc:13.7:14.1) (ec:) (ybcib_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_510 ECOLI_510 Escherichia coli 562 10051948

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842898	9900	32056	306	101

Description

GTC ORF with score 113 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842901	9901	32057	402	133

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842918	9902	32058	483	160

Description

6500730455 ybcj:b0528 hypothetical 7.4 kd protein in cyss-fold intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0528 b0528 Escherichia coli 562 -11534313 7000690969 ybcj ybcj protein (db:pir2.dat) G64784 G64784 Escherichia coli 562 -11534313 7500959828 ybcj hypothetical 7.4kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:136110) (re:136343) (di:complement) ECU82664 U82664 g1773209 Escherichia coli 562 -11534313 240302 ybcj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 49 of 400 of the completegenome.) (nt:f77; 98 pct identical to ybcj_ecoli sw: p45571 but) (le:84) (re:317) (di:complement) AE000159 AE000159 g1786740 Escherichia coli 562 -11534313 5000691645 (de:(ecoli_511) (pn:hypothetical 7) (gn:ybcj) (gtcfc:13.7:14.1) (ec:) (ybcj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_511 ECOLI_511 Escherichia coli 562 10122879

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501842922	9903	32059	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842924	9904	32060	615	204

Description

6500730456 sfma:b0530 hypothetical protein:sfm fimbrial protein:a chain precursor:type-1a pilin (gtcfc:11.3:12.8) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0530 b0530 Escherichia coli 562 -11534314 4000707940 sfma (de:sfm fimbrial protein, a chain precursor (type-1a pilin)) (db:swissprot) SFMA_ECOLI P77660 ESCHERICHIA COLI 562 -11534314 7000686592 sfma type 1 fimbrial protein sfaa precursor:sfm fimbrial protein chain a:type 1a pilin (cl:type 1 fimbrial protein) (db:pir2.dat) A64785 A64785 Escherichia coli 562 -11534314 7500891568 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to s. typhimurium fmla) (le:137628) (re:138203) (di:direct) ECU82664 U82664 g1773211 Escherichia coli 562 -11534314 240304 sfma putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 49 of 400 of the completegenome.) (nt:o191; this 191 aa orf is 66 pct identical (5 gaps)) (le:1602) (re:2177) (di:direct) AE000159 AE000159 g1786742 Escherichia coli 562 -11534314 5000691646 (de:(ecoli_513) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_513 ECOLI_513 Escherichia coli 562 10122880

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842934	9905	32061	1428	475

Description

6500730457 sfmc:b0531 hypothetical protein:chaperone protein sfmc precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0531 b0531 Escherichia coli 562 -11534315 4000707942 sfmc (de:chaperone protein sfmc precursor) (db:swissprot) SFMC_ECOLI P77249 ESCHERICHIA COLI 562 -11534315 7000686593 smfc molecular chaperone smfc precursor (cl:chaperone protein papd) (db:pir2.dat) B64785 B64785 Escherichia coli 562 -11534315 7500891569 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to s. typhimurium fimc) (le:138423) (re:139115) (di:direct) ECU82664 U82664 g1773212 Escherichia coli 562 -11534315 240305 sfmc putative chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 49 of 400 of the completegenome.) (nt:o230 was o215; this 230 aa orf is 62 pct identical) (le:2397) (re:3089) (di:direct) AE000159 AE000159 g1786743 Escherichia coli 562 -11534315 5000691647 (de:(ecoli_514) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_514 ECOLI_514 Escherichia coli 562 10122881

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842937	9906	32062	1479	493

Description

6500730458 sfmh:b0533 hypothetical protein:sfmh protein precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0533 b0533 Escherichia coli 562 -11534316 4000707941 sfmh (de:sfmh protein precursor) (db:swissprot) SFMH_ECOLI P75715 ESCHERICHIA COLI 562 -11534316 7000686596 sfmh sfmh protein precursor (db:pir2.dat) D64785 D64785 Escherichia coli 562 -11534316 7500891572 sfmh involved in fimbrial assembly (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 49 of 400 of the completegenome.) (nt:o325; 69 pct identical to fimh_salty sw: p37925) (le:5765) (re:6742) (di:direct) AE000159 AE000159 g1786745 Escherichia coli 562 -11534316 5000691648 (de:(ecoli_516) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_516 ECOLI_516 Escherichia coli 562 10122883

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842942	9907	32063	687	228

Description

6500730459 ybcg:sfmf:b0534 hypothetical fimbrial-like protein in fimz 5 region:fimbrial-like protein sfmf precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0534 b0534 Escherichia coli 562 -11534317 110214 sfmf (de:fimbrial-like protein sfmf precursor) (db:swissprot) SFMF_ECOLI P38052 ESCHERICHIA COLI 562 -11534317 7000686595 sfmf:ybcg fimbrial protein-like protein sfmf (db:pir2.dat) E64785 E64785 Escherichia coli 562 -11534317 7500891571 sfmf putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 49 of 400 of the completegenome.) (nt:o171; formerly designated ybcg; 57 pct identical (1) (le:6753) (re:7268) (di:direct) AE000159 AE000159 g1786746 Escherichia coli 562 -11534317 5000691649 (de:(ecoli_517) (pn:hypothetical fimbrial-like protein in fimz 5"region:fragment) (gn:ybcg) (gtcfc:13.7:14.1) (ec:) (ybcg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_517 ECOLI_517 Escherichia coli 562 10122884

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842948	9908	32064	318	105

Description

5000691651 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0538 b0538 Escherichia coli 562 -11534318
 7000691031 hypothetical protein b0538 (db:pir2.dat) H64785 H64785
 Escherichia coli 562 -11534318 7500959885 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:6603) (re:7163) (di:direct) ECU82598 U82598 g1778452 Escherichia coli 562 -11534318 240048 b0538 putative sensory transduction regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 49 of 400 of the completegenome.) (nt:o186; this 186 aa orf is 29 pct identical (4 gaps)) (le:9395) (re:9955) (di:direct) AE000159 AE000159 g1786749 Escherichia coli 562 -11534318 6500730460 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0538 b0538 Escherichia coli 562 -11534318

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842970	9909	32065	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842976	9910	32066	1401	467

Description

5000691652 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0539 b0539 Escherichia coli 562 -11534319
 7000691032 hypothetical protein b0539 (db:pir2.dat) A64786 A64786
 Escherichia coli 562 -11534319 7500959886 b0539 putative exonuclease ec 3.1.11.3 similar to (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 49 of 400 of the completegenome.) (nt:f87; this 87 aa orf is 96 pct identical to) (le:9521) (re:9784) (di:complement) AE000159 AE000159 g1786750 Escherichia coli 562 -11534319 6500730461 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0539 b0539 Escherichia coli 562 -11534319

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842988	9911	32067	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842989	9912	32068	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501842992	9913	32069	357	118

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843003	9914	32070	705	234

Description

5000691653 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0542 b0542 Escherichia coli 562 -11534320
7000689454 phage lambda ren protein homolog b0542 (cl:phage lambda ren
protein) (db:pir2.dat) (mp:12.3 min) D64786 D64786 Escherichia coli 562
-11534320 7500955726 b0542 orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the
completegenome.) (nt:o45; phage stats) (le:1458) (re:1595) (di:direct)
AE000160 AE000160 g1786754 Escherichia coli 562 -11534320 6500730462
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0542 b0542 Escherichia coli 562 -11534320

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843006	9915	32071	597	198

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843018	9916	32072	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843029	9917	32073	1065	354

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843040	9918	32074	1215	404

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843045	9919	32075	1287	428

Description

6500730463 emre:mvr:eb:b0543 hypothetical protein:emre protein:methyl
viologen resistance protein c:ethidium resistance protein (gtcfc:13.3:13.4)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0543 b0543
Escherichia coli 562 -11534321 235209 emre:mvr:eb (de:resistance protein))
(db:swissprot) EMRE_ECOLI P23895 ESCHERICHIA COLI 562 -11534321 163000
emre:mvr ethidium efflux protein eb:ethidium resistance protein:methyl
viologen resistance protein c (cl:suge protein) (db:pir2.dat) (mp:12.3 min)
JN0329 JN0329 Escherichia coli 562 -11534321 240053 eb ethidium resistance
(fn:ethidium efflux) (db:genpept-bct1) (de:e.coli ethidium efflux gene for
ethidium resistance protein.) (le:486) (re:818) (di:direct) ECETHRES Z11877
g49282 Escherichia coli 562 -11534321 5000691654 mvr (sr:e.coli dna)
(db:genpept-bct1) (de:e.coli mvr gene, complete cds.) (nt:membrane protein
(predicted by hydropathy)) (le:486) (re:818) (di:direct) ECOMVRC M62732
g146910 Escherichia coli 562 -11534321 7500881007 emre methyl viologen
resistance protein c (db:genpept-bct1) (de:escherichia coli genomic sequence
of minutes 9 to 12.) (le:8946) (re:9278) (di:direct) ECU82598 U82598
g1778457 Escherichia coli 562 -11534321 232780 emre methylviologen
resistance (fn:transport; drug/analog sensitivity) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 50 of 400 of the completegenome.)
(nt:ol10; phage stats) (le:1663) (re:1995) (di:direct) AE000160 AE000160
g1786755 Escherichia coli 562 -11534321 70133 emre:mvr:eb (de:resistance
protein)) (db:swissprot) EMRE_ECOLI P23895 ESCHERICHIA COLI 562 -11534321

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843056	9920	32076	696	231

Description

6500730464 ybck:b0544 hypothetical protein:hypothetical 57.5 kd protein in emre-rus intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0544 b0544 Escherichia coli 562 -11534322
 4000709305 ybck (de:hypothetical 57.5 kd protein in emre-rus intergenic region) (db:swissprot) YBCK_ECOLI P77698 ESCHERICHIA COLI 562 -11534322
 7000687306 ybck ybck protein (db:pir2.dat) F64786 F64786 Escherichia coli 562 -11534322 7500896595 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:9533) (re:11059) (di:direct) ECU82598 U82598 g1778458 Escherichia coli 562 -11534322 240054 ybck orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the completegenome.) (nt:o508; phage stats) (le:2250) (re:3776) (di:direct) AE000160 AE000160 g1786756 Escherichia coli 562 -11534322 5000691655 (de:(ecoli_526) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_526 ECOLI_526 Escherichia coli 562 10122888

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843062	9921	32077	195	64

Description

6500730465 ybcl:b0545 hypothetical protein:hypothetical 19.5 kd protein in emre-rus intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0545 b0545 Escherichia coli 562 -11534323
 4000709306 ybcl (de:hypothetical 19.5 kd protein in emre-rus intergenic region) (db:swissprot) YBCL_ECOLI P77368 ESCHERICHIA COLI 562 -11534323
 7000687307 ybcl ybcl protein (cl:conserved hypothetical protein ybhb) (db:pir2.dat) G64786 G64786 Escherichia coli 562 -11534323 7500896596 ybhb homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to e. coli ybhb) (le:11524) (re:12075) (di:direct) ECU82598 U82598 g1778459 Escherichia coli 562 -11534323 240055 ybcl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the completegenome.) (nt:o183; phage stats) (le:4241) (re:4792) (di:direct) AE000160 AE000160 g1786757 Escherichia coli 562 -11534323 5000691656 (de:(ecoli_527) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_527 ECOLI_527 Escherichia coli 562 10122889

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843075	9922	32078	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843083	9923	32079	273	90

Description

6500730466 ybcm:b0546 hypothetical protein:hypothetical transcriptional regulator in emre-rus intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0546 b0546 Escherichia coli 562 -11534324 4000708134 ybcm (de:hypothetical transcriptional regulator in emre-rus intergenic region) (db:swissprot) YBCM_ECOLI P77634 ESCHERICHIA COLI 562 -11534324 7000687308 ybcm ybcm protein (db:pir2.dat) H64786 H64786 Escherichia coli 562 -11534324 7500896597 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:12085) (re:12882) (di:direct) ECU82598 U82598 g1778460 Escherichia coli 562 -11534324 240056 ybcm putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the completegenome.) (nt:o265; phage stats; 28 pct identical (8 gaps) to 171) (le:4802) (re:5599) (di:direct) AE000160 AE000160 g1786758 Escherichia coli 562 -11534324 5000691657 (de:(ecoli_528) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_528 ECOLI_528 Escherichia coli 562 10122890

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843094	9924	32080	264	87

Description

6500730467 ybcn:b0547 hypothetical protein:hypothetical 17.4 kd protein in emre-rus intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0547 b0547 Escherichia coli 562 -11534325 4000709307 ybcn (de:hypothetical 17.4 kd protein in emre-rus intergenic region) (db:swissprot) YBCN_ECOLI Q47269 ESCHERICHIA COLI 562 -11534325 205539 ybcn ybcn protein:protein 151 (db:pir2.dat) (mp:12 min) S66587 S66587 Escherichia coli 562 -11534325 240057 (db:genpept-bct1) (de:e.coli orf33, orf151, orf56, orf96, rus, orf45, orf8, orf127, andnmpc genes.) (nt:orf151) (le:232) (re:687) (di:direct) ECHOLL X92587 g1051138 Escherichia coli 562 -11534325 7500896598 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:13097) (re:13552) (di:direct) ECU82598 U82598 g1778461 Escherichia coli 562 -11534325 233133 ybcn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the completegenome.) (nt:o151; this 151 aa orf is 21 pct identical (3 gaps)) (le:5814) (re:6269) (di:direct) AE000160 AE000160 g1786759 Escherichia coli 562 -11534325 5000691658 (de:(ecoli_529) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_529 ECOLI_529 Escherichia coli 562 10086939

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843097	9925	32081	2262	753

Description

5000691659 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0548 b0548 Escherichia coli 562 -11534326
7500886470 nine (de:nine protein) (db:swissprot) NINE_ECOLI Q47270
ESCHERICHIA COLI 562 -11534326 205545 nine nine protein:protein 56
(db:pir2.dat) (mp:12 min) S66588 S66588 Escherichia coli 562 -11534326
233134 (db:genpept-bct1) (de:e.coli orf33, orf151, orf56, orf96, rus,
orf45, orf8, orf127, andnmpc genes.) (nt:orf56; related to nin60 (nine) of
bacteriophage) (le:687) (re:857) (di:direct) ECHOLL X92587 g1051139
Escherichia coli 562 -11534326 7500886472 nine similar to phage 82 and
lambda proteins (fn:is, phage, tn; phage-related functions and)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the
completegenome.) (nt:o56; this 56 aa orf is 47 pct identical (1 gap) to)
(le:6269) (re:6439) (di:direct) AE000160 AE000160 g1786760 Escherichia coli
562 -11534326 6500730468 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b0548 b0548 Escherichia coli 562
-11534326

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843120	9926	32082	327	108

Description

6500730469 ybco:b0549 hypothetical protein:hypothetical 10.3 kd protein in emre-rus intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0549 b0549 Escherichia coli 562 -11534327
4000709309 ybco (de:hypothetical 10.3 kd protein in emre-rus intergenic region) (db:swissprot) YBCO_ECOLI Q47271 ESCHERICHIA COLI 562 -11534327
7502851993 ybco (de:hypothetical 10.3 kd protein in emre-rus intergenic region) (db:swissprot) YBCO_ECOLI Q47271 BACTERIOPHAGE 82 10705 -11534327
7500896599 hypothetical protein 96 (db:pir2.dat) S66582 S66582 phage 82 10705 -11534327 7000687309 ybco ybco protein (db:pir2.dat) (mp:12 min) C64787 C64787 Escherichia coli 562 -11534327 233135 (db:genpept-bct1) (de:e.coli orf33, orf151, orf56, orf96, rus, orf45, orf8, orf127, andnmpc genes.) (nt:orf96) (le:850) (re:1140) (di:direct) ECHOLL X92587 g1051140 Escherichia coli 562 -11534327 240058 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:13715) (re:14005) (di:direct) ECU82598 U82598 g1778462 Escherichia coli 562 -11534327 7500896600 ybco orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the completegenome.) (nt:o96; this 96 aa orf is 36 pct identical (5 gaps) to) (le:6432) (re:6722) (di:direct) AE000160 AE000160 g1786761 Escherichia coli 562 -11534327 326301 (db:genpept-phg) (de:bacteriophage 82 orf33, orf151, orf56, orf96, rus, orf45, and ggenes.) (nt:orf96) (le:850) (re:1140) (di:direct) BAC82HOLL X92588 g1051115 Bacteriophage 82 10705 -11534327
4000709310 ybco (de:hypothetical 10.3 kd protein in emre-rus intergenic region) (db:swissprot) YBCO_ECOLI Q37872 ESCHERICHIA COLI 562 -11534327
7502851994 ybco (de:hypothetical 10.3 kd protein in emre-rus intergenic region) (db:swissprot) YBCO_ECOLI Q37872 BACTERIOPHAGE 82 10705 -11534327
204824 hypothetical protein b0549 (db:pir) C64787 C64787 Escherichia coli 562 -11534327 5000691660 (de:(ecoli_531) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_531 ECOLI_531 Escherichia coli 562 10084353

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843129	9927	32083	636	211

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843135	9928	32084	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843137	9929	32085	198	65

Description

GTC ORF with score 106 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843159	9930	32086	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843161	9931	32087	216	71

Description

6500730470 rus:b0550 hypothetical protein:crossover junction
endodeoxyribonuclease:holliday junction nuclease rus:holliday junction
resolvase rus (gtcfc:14.1) (ec:3.1.22.-) (keggfc:14.1) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0550 b0550 Escherichia coli 562 -11534328 97678
rus (ec:3.1.22.-) (de:junction nuclease rus) (holliday junction resolvase
rus)) (db:swissprot) RUS_ECOLI P40116 ESCHERICHIA COLI 562 -11534328 205531
rusa holliday junction-specific endonuclease rusa::crossover junction
endodeoxyribonuclease rus:holliday junction resolvase:rus endonuclease
(ec:3.1.22.-) (db:pir2.dat) (mp:12 min) S66590 S66590 Escherichia coli 562
-11534328 240059 rus (fn:holliday junction specific endonuclease)
(db:genpept-bct1) (de:e.coli orf33, orf151, orf56, orf96, rus, orf45, orf8,
orf127, andnmpc genes.) (nt:improved expression of rus suppresses the dna)
(le:1137) (re:1499) (di:direct) ECHOLL X92587 g1051141 Escherichia coli 562
-11534328 7500891217 rus holliday junction specific endonuclease
(db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.)
(le:14002) (re:14364) (di:direct) ECU82598 U82598 g1778463 Escherichia coli
562 -11534328 233136 rus endodeoxyribonuclease rus holliday junction
(fn:enzyme; degradation of dna) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 50 of 400 of the completegenome.) (nt:ol20; this 120 aa orf
is 36 pct identical (5 gaps)) (le:6719) (re:7081) (di:direct) AE000160
AE000160 g1786762 Escherichia coli 562 -11534328 5000691661 (de:(ecoli_532)
(pn:with recg processes holliday junctions) (gn:suppressor of ruv mutants)
(gtcfc:13.7:14.1) (ec:3.1.22.-) (rus_ecoli) (keggfc:11.1) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_532 ECOLI_532 Escherichia coli 562 10086804

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843164	9932	32088	966	321

Description

6500730471 ybcq:b0551 hypothetical protein: hypothetical 14.2 kd protein in rus-nmpc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0551 b0551 Escherichia coli 562 -11534329
 4000709311 ybcq (de: hypothetical 14.2 kd protein in rus-nmpc intergenic region) (db:swissprot) YBCQ_ECOLI Q47274 ESCHERICHIA COLI 562 -11534329
 205573 ybcq probable antiterminator ybcq:protein b0551 (db:pir2.dat) (mp:12 min) S66593 S66593 Escherichia coli 562 -11534329 240060 (fn:probable q antiterminator) (db:genpept-bct1) (de:e.coli orf33, orf151, orf56, orf96, rus, orf45, orf8, orf127, andnmpc genes.) (nt:orf127; similar to phage 21 q gene) (le:1722) (re:2105) (di:direct) ECHOLL X92587 g1051144 Escherichia coli 562 -11534329 7500896601 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:14587) (re:14970) (di:direct) ECU82598 U82598 g1778464 Escherichia coli 562 -11534329 233139 ybcq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the completegenome.) (nt:o127; this 127 aa orf is 36 pct identical (1 gap)) (le:7304) (re:7687) (di:direct) AE000160 AE000160 g1786763 Escherichia coli 562 -11534329 5000691662 (de:(ecoli_533) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_533 ECOLI_533 Escherichia coli 562 10087303

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843165	9933	32089	633	210

Description

6500730472 ybcr:b0554 hypothetical protein: putative lysis protein s (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0554 b0554 Escherichia coli 562 -11534330 4000707647 ybcr (de:putative lysis protein s) (db:swissprot) VLYS_ECOLI P77242 ESCHERICHIA COLI 562 -11534330 7000686970 ybcr lysis protein s.ybcr (db:pir2.dat) (mp:12 min) H64787 H64787 Escherichia coli 562 -11534330 7500894287 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:18029) (re:18244) (di:direct) ECU82598 U82598 g1778467 Escherichia coli 562 -11534330 240063 ybcr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:o71; 85 pct identical amino acid sequence and equal) (le:287) (re:502) (di:direct) AE000161 AE000161 g1786767 Escherichia coli 562 -11534330 5000691663 (de:(ecoli_536) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_536 ECOLI_536 Escherichia coli 562 10122892

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843168	9934	32090	189	62
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843171	9935	32091	327	108
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843178	9936	32092	306	101
<u>Description</u>				

6500730473 ybcv:b0558 hypothetical protein: hypothetical 18.1 kd protein in nmmpc-nohb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0558 b0558 Escherichia coli 562 -11534331 4000708180 ybcv (de: hypothetical 18.1 kd protein in nmmpc-nohb intergenic region) (db:swissprot) YBCV_ECOLI P77598 ESCHERICHIA COLI 562 -11534331 7000687310 ybcv ybcv protein (cl:ydfp protein) (db:pir2.dat) D64788 D64788 Escherichia coli 562 -11534331 7500896602 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt: hypothetical protein) (le:19815) (re:20267) (di:complement) ECU82598 U82598 g1778471 Escherichia coli 562 -11534331 240067 ybcv putative an envelop protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:f150; phage stats; 24 pct identical (6 gaps) to) (le:2073) (re:2525) (di:complement) AE000161 AE000161 g1786771 Escherichia coli 562 -11534331 5000691666 (de:(ecoli_540) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_540 ECOLI_540 Escherichia coli 562 10122896

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843179	9937	32093	366	121
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843182	9938	32094	846	281

Description

6500730474 ybcw:b0559 hypothetical protein:hypothetical 7.6 kd protein in nmpc-nohb intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0559 b0559 Escherichia coli 562 -11534332 4000709312 ybcw (de:hypothetical 7.6 kd protein in nmpc-nohb intergenic region precursor) (db:swissprot) YBCW_ECOLI P75720 ESCHERICHIA COLI 562 -11534332 7000687311 ybcw ybcw protein (db:pir2.dat) E64788 E64788 Escherichia coli 562 -11534332 7500896603 ybcw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:o68; 28 pct identical (3 gaps) to 57 residues of) (le:2769) (re:2975) (di:direct) AE000161 AE000161 g1786772 Escherichia coli 562 -11534332 5000691667 (de:(ecoli_541) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_541 ECOLI_541 Escherichia coli 562 10122897

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843184	9939	32095	444	147

Description

6500730475 ybcx:b0561 hypothetical protein:hypothetical 28.3 kd protein in nohb-appy intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0561 b0561 Escherichia coli 562 -11534333 4000708181 ybcx (de:hypothetical 28.3 kd protein in nohb-appy intergenic region) (db:swissprot) YBCX_ECOLI P77699 ESCHERICHIA COLI 562 -11534333 7000687312 ybcx ybcx protein:phage protein-related (db:pir2.dat) G64788 G64788 Escherichia coli 562 -11534333 7500896604 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:21985) (re:22728) (di:direct) ECU82598 U82598 g1778474 Escherichia coli 562 -11534333 240070 ybcx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:o247; residues 1-103 are 100 pct identical to) (le:4243) (re:4986) (di:direct) AE000161 AE000161 g1786774 Escherichia coli 562 -11534333 5000691669 (de:(ecoli_543) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_543 ECOLI_543 Escherichia coli 562 10122899

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843189	9940	32096	522	173

Description

6500730476 ybcy:b0562 hypothetical protein:hypothetical 15.5 kd protein in nohb-appy intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0562 b0562 Escherichia coli 562 -11534334 4000709313 ybcy (de:hypothetical 15.5 kd protein in nohb-appy intergenic region precursor) (db:swissprot) YBCY_ECOLI P77460 ESCHERICHIA COLI 562 -11534334 7000687313 ybcy ybcy protein (db:pir2.dat) H64788 H64788 Escherichia coli 562 -11534334 7500896605 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:22783) (re:23214) (di:complement) ECU82598 U82598 g1778475 Escherichia coli 562 -11534334 240071 ybcy orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:f143; this 143 aa orf is 30 pct identical (7 gaps)) (le:5041) (re:5472) (di:complement) AE000161 AE000161 g1786775 Escherichia coli 562 -11534334 5000691670 (de:(ecoli_544) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_544 ECOLI_544 Escherichia coli 562 10122900

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843210	9941	32097	396	131

Description

6500730477 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0563 b0563 Escherichia coli 562 -11534335 7500950952 ylce (de:hypothetical 7.1 kd protein in nohb-appy intergenic region) (db:swissprot) YLCE_ECOLI P77087 ESCHERICHIA COLI 562 -11534335 7000691033 ylce ylce protein (db:pir2.dat) A64789 A64789 Escherichia coli 562 -11534335 240072 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:23506) (re:23691) (di:direct) ECU82598 U82598 g1778476 Escherichia coli 562 -11534335 7500950954 ylce orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:o61; 100 pct identical to hypothetical e. coli) (le:5764) (re:5949) (di:direct) AE000161 AE000161 g2367110 Escherichia coli 562 -11534335

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843221	9942	32098	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843226	9943	32099	978	325

Description

6500730478 ybcz:b0570 hypothetical protein:probable sensor protein ybcz (gtcfc:14.1) (ec:2.7.3.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0570 b0570 Escherichia coli 562 -11534336 4000709729 ybcz (ec:2.7.3.-) (de:probable sensor protein ybcz,) (db:swissprot) YBCZ_ECOLI P77485 ESCHERICHIA COLI 562 -11534336 7000687314 ybcz probable sensor protein ybcz (db:pir2.dat) H64789 H64789 Escherichia coli 562 -11534336 7500896606 pcos homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to e. coli pcos) (le:33959) (re:35401) (di:complement) ECU82598 U82598 g1778485 Escherichia coli 562 -11534336 240081 ybcz putative 2-component sensor protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 52 of 400 of the completegenome.) (nt:f480; this 480 aa orf is 33 pct identical (22 gaps)) (le:105) (re:1547) (di:complement) AE000162 AE000162 g1786783 Escherichia coli 562 -11534336 5000691672 (de:(ecoli_551) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_551 ECOLI_551 Escherichia coli 562 10122902

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843242	9944	32100	1239	412

Description

GTC ORF with score 1231 to: (db:genpept-pln1) (ec:3.2.1.28) (de:emericeella nidulans acid trehalase precursor (trea) gene, completecds.) (nt:alpha, alpha-trehalose glucohydrolase) (le:769:837:2620) (re:780:2570:4038) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843245	9945	32101	861	286

Description

6500730479 ylca:b0571 hypothetical protein:probable transcriptional regulatory protein ylca (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0571 b0571 Escherichia coli 562 -11534337 4000709723 ylca (de:probable transcriptional regulatory protein ylca) (db:swissprot) YLCA_ECOLI P77380 ESCHERICHIA COLI 562 -11534337 7000688127 ycla probable transcription regulator ycla:probable transcription regulation protein ycla (cl:ompr protein:response regulator homology) (db:pir2.dat) A64790 A64790 Escherichia coli 562 -11534337 7500950948 copr homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to p. syringae copr) (le:35391) (re:36074) (di:complement) ECU82598 U82598 g1778486 Escherichia coli 562 -11534337 240082 ylca putative 2-component transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 52 of 400 of the complete genome.) (nt:f227; this 227 aa orf is 61 pct identical (0 gaps)) (le:1537) (re:2220) (di:complement) AE000162 AE000162 g1786784 Escherichia coli 562 -11534337 5000691673 copr transcriptional activator protein copr. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #162) (db:genpept) (de:escherichia coli genomic dna. (12.6 - 12.9 min).) (nt:orf_id:o163#1; similar to pir accession number) (le:9175) (re:9858) (di:complement) D90699 D90699 g4062195 Escherichia coli 562 -11534337 7502851995 copr transcriptional activator protein copr. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf_id:o163#1; similar to pir accession number) (le:98) (re:781) (di:complement) D90700 D90700 g4062201 Escherichia coli 562 -11534337

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843246	9946	32102	474	158

Description

6500730480 ylc b:b0572 hypothetical protein:hypothetical 50.3 kd protein in nfrb-phep intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0572 b0572 Escherichia coli 562 -11534338 4000709314 ylc b (de:precursor) (db:swissprot) YLCB_ECOLI P77211 ESCHERICHIA COLI 562 -11534338 7000688128 ylc b ylc b protein (cl:nodulation protein nodt) (db:pir2.dat) B64790 B64790 Escherichia coli 562 -11534338 7500950949 outer membrane protein oprk homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to p. aeruginosa oprk) (le:36231) (re:37604) (di:direct) ECU82598 U82598 g1778487 Escherichia coli 562 -11534338 240083 ylc b putative resistance protein (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 52 of 400 of the complete genome.) (nt:o457; this 457 aa orf is 26 pct identical (12 gaps)) (le:2377) (re:3750) (di:direct) AE000162 AE000162 g1786785 Escherichia coli 562 -11534338 5000691674 50k outer membrane protein oprk (sr:escherichia coli(strain:k12) dna, clone:kohara clone #162) (db:genpept) (de:escherichia coli genomic dna. (12.6 - 12.9 min).) (nt:orf_id:o163#2; similar to pir accession number) (le:10015) (re:11388) (di:direct) D90699 D90699 g4062196 Escherichia coli 562 -11534338 7502851996 50k outer membrane protein oprk (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf_id:o163#2; similar to pir accession number) (le:938) (re:2311) (di:direct) D90700 D90700 g4062202 Escherichia coli 562 -11534338

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843247	9947	32103	459	152

Description

6500730481 ylcc:b0573 hypothetical protein:hypothetical 12.3 kd protein in nfrb-phep intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0573 b0573 Escherichia coli 562 -11534339 4000709315 ylcc (de:hypothetical 12.3 kd protein in nfrb-phep intergenic region precursor) (db:swissprot) YLCC_ECOLI P77214 ESCHERICHIA COLI 562 -11534339 7000688129 yclc yclc protein (db:pir2.dat) C64790 C64790 Escherichia coli 562 -11534339 7500950950 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:37762) (re:38094) (di:direct) ECU82598 U82598 g1778488 Escherichia coli 562 -11534339 240084 ylcc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 52 of 400 of the completegenome.) (nt:o110; this 110 aa orf is 25 pct identical (1 gap)) (le:3908) (re:4240) (di:direct) AE000162 AE000162 g1786786 Escherichia coli 562 -11534339 5000691675 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #162) (db:genpept) (de:escherichia coli genomic dna. (12.6 - 12.9 min).) (nt:orf_id:o163#3) (le:11546) (re:11878) (di:direct) D90699 D90699 g4062197 Escherichia coli 562 -11534339 7502851997 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf_id:o163#3) (le:2469) (re:2801) (di:direct) D90700 D90700 g4062203 Escherichia coli 562 -11534339

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843253	9948	32104	330	109

Description

6500730482 ylcd:b0574 hypothetical protein:hypothetical 44.3 kd protein in nfrb-phep intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0574 b0574 Escherichia coli 562 -11534340 4000709316 ylcd (de:hypothetical 44.3 kd protein in nfrb-phep intergenic region precursor) (db:swissprot) YLCD_ECOLI P77239 ESCHERICHIA COLI 562 -11534340 7000688130 yclcd yclcd protein (db:pir2.dat) D64790 D64790 Escherichia coli 562 -11534340 7500950951 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:38110) (re:39333) (di:direct) ECU82598 U82598 g1778489 Escherichia coli 562 -11534340 240085 ylcd putative resistance protein (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 52 of 400 of the completegenome.) (nt:o407; this 407 aa orf is 24 pct identical (37 gaps)) (le:4256) (re:5479) (di:direct) AE000162 AE000162 g1786787 Escherichia coli 562 -11534340 5000691676 mtrc membrane fusion protein mtrc precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #162) (db:genpept) (de:escherichia coli genomic dna. (12.6 - 12.9 min).) (nt:orf_id:o163#4; similar to swissprot accession) (le:11894) (re:13117) (di:direct) D90699 D90699 g4062198 Escherichia coli 562 -11534340 7502851998 mtrc membrane fusion protein mtrc precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf_id:o163#4; similar to swissprot accession) (le:2817) (re:4040) (di:direct) D90700 D90700 g4062204 Escherichia coli 562 -11534340

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843284	9949	32105	534	177

Description

GTC ORF with score 114 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843286	9950	32106	1212	403

Description

6500730483 ybde:b0575 hypothetical protein in phep 5 region:hypothetical 114.7 kd protein in nfrb-phep intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0575 b0575 Escherichia coli 562 -11534341 110228 ybde (de:hypothetical 114.7 kd protein in nfrb-phep intergenic region) (db:swissprot) YBDE_ECOLI P38054 ESCHERICHIA COLI 562 -11534341 7000687315 ybde ybde protein (cl:cation efflux system membrane protein czca) (db:pir2.dat) E64790 E64790 Escherichia coli 562 -11534341 7500896616 hela homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to l. pneumophila hela) (le:39345) (re:42488) (di:direct) ECU82598 U82598 g1778490 Escherichia coli 562 -11534341 240086 ybde putative inner membrane component for iron (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 52 of 400 of the completegenome.) (nt:o1047; 98 pct identical to fragment ybde_ecoli sw:) (le:5491) (re:8634) (di:direct) AE000162 AE000162 g1786788 Escherichia coli 562 -11534341 5000691677 ybde hypothetical protein in phep 5region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf_id:o163#5; similar to swissprot accession) (le:4052) (re:7195) (di:direct) D90700 D90700 g4062205 Escherichia coli 562 -11534341

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843288	9951	32107	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843298	9952	32108	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843302	9953	32109	837	278

Description

6500730484 ybdg:b0577 hypothetical protein in phep-entd intergenic region:hypothetical 46.6 kd protein in phep-nfnb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0577 b0577 Escherichia coli 562 -11534342 110231 ybdg (de:hypothetical 46.6 kd protein in phep-nfnb intergenic region) (db:swissprot) YBDG_ECOLI P39455 ESCHERICHIA COLI 562 -11534342 7000687317 ybdg ybdg protein (db:pir2.dat) G64790 G64790 Escherichia coli 562 -11534342 7500896618 ybdg (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:44047) (re:45294) (di:complement) ECU82598 U82598 g1778492 Escherichia coli 562 -11534342 240088 ybdg putative transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 53 of 400 of the completegenome.) (nt:f415; 100 pct identical to fragment ybdg_ecoli) (le:71) (re:1318) (di:complement) AE000163 AE000163 g1786791 Escherichia coli 562 -11534342 5000691678 ybdg hypothetical protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf_id:o163#7; similar to pir accession number) (le:8754) (re:10001) (di:complement) D90700 D90700 g4062206 Escherichia coli 562 -11534342

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843319	9954	32110	570	190

Description

6500730485 ybdf:b0579 hypothetical protein in nfnb-entd intergenic region:hypothetical 14.1 kd protein in nfnb-entd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0579 b0579 Escherichia coli 562 -11534343 110229 ybdf (de:hypothetical 14.1 kd protein in nfnb-entd intergenic region) (db:swissprot) YBDF_ECOLI P39454 ESCHERICHIA COLI 562 -11534343 7000687316 ybdf ybdf protein (db:pir2.dat) A64791 A64791 Escherichia coli 562 -11534343 7500896617 ybdf (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:46149) (re:46517) (di:complement) ECU82598 U82598 g1778494 Escherichia coli 562 -11534343 240090 ybdf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 53 of 400 of the completegenome.) (nt:f122; 97 pct identical to fragment ybdf_ecoli) (le:2173) (re:2541) (di:complement) AE000163 AE000163 g1786793 Escherichia coli 562 -11534343 5000691679 (de:(ecoli_560) (pn:hypothetical protein in nfnb 5"region:fragment) (gn:ybdf) (gtcfc:13.7:14.1) (ec:) (ybdf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_560 ECOLI_560 Escherichia coli 562 10122909

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843334	9955	32111	429	142

Description

6500730486 ybdj:b0580 hypothetical protein:hypothetical 9.4 kd protein in nfnb-entd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0580 b0580 Escherichia coli 562 -11534344
 4000709317 ybdj (de:hypothetical 9.4 kd protein in nfnb-entd intergenic region) (db:swissprot) YBDJ_ECOLI P77506 ESCHERICHIA COLI 562 -11534344
 7000687319 ybdj ybdj protein (db:pir2.dat) B64791 B64791 Escherichia coli 562 -11534344 7500896620 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to k. pneumoniae orf82 product) (le:46582) (re:46830) (di:complement) ECU82598 U82598 g1778495 Escherichia coli 562 -11534344 240091 ybdj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 53 of 400 of the completgenome.) (nt:f82; this 82 aa orf is 32 pct identical (1 gap)) (le:2606) (re:2854) (di:complement) AE000163 AE000163 g1786794 Escherichia coli 562 -11534344 5000691680 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf_id:o164#2) (le:11289) (re:11537) (di:complement) D90700 D90700 g4062208 Escherichia coli 562 -11534344

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843335	9956	32112	762	253

Description

6500730487 ybdk:b0581 hypothetical protein:hypothetical 41.7 kd protein in nfnb-entd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0581 b0581 Escherichia coli 562 -11534345
 4000709318 ybdk (de:hypothetical 41.7 kd protein in nfnb-entd intergenic region) (db:swissprot) YBDK_ECOLI P77213 ESCHERICHIA COLI 562 -11534345
 7000687320 ybdk ybdk protein (db:pir2.dat) C64791 C64791 Escherichia coli 562 -11534345 7500896621 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:46896) (re:48014) (di:complement) ECU82598 U82598 g1778496 Escherichia coli 562 -11534345 240092 ybdk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 53 of 400 of the completgenome.) (nt:f372; this 372 aa orf is 26 pct identical (3 gaps)) (le:2920) (re:4038) (di:complement) AE000163 AE000163 g1786795 Escherichia coli 562 -11534345 5000691681 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #163) (db:genpept) (de:escherichia coli genomic dna. (12.8 - 13.2 min).) (nt:orf_id:o164#3) (le:11603) (re:12721) (di:complement) D90700 D90700 g4062209 Escherichia coli 562 -11534345

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843342	9957	32113	264	87

Description

6500730488 ybda:b0591 hypothetical membrane protein p43 (gtcfc:11.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0591 b0591 Escherichia coli 562 -11534346 240103 ybda (de:hypothetical membrane protein p43) (db:swissprot) YBDA_ECOLI P24077 ESCHERICHIA COLI 562 -11534346 164055 ybda membrane protein p43 (db:pir2.dat) S16306 S16306 Escherichia coli 562 -11534346 5000691682 orf43 p43 (db:genpept-bct1) (de:e.coli fepd & orf43 genes for fepd & p43 membrane proteins offerrienterobactin permease.) (le:1131) (re:2381) (di:direct) ECFEPD43 X59402 g41435 Escherichia coli 562 -11534346 7500896613 ybda (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical membrane protein p43) (le:62931) (re:64181) (di:direct) ECU82598 U82598 g1778507 Escherichia coli 562 -11534346 232854 ybda putative transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 54 of 400 of the completegenome.) (nt:o416; 99 pct identical to ybda_ecoli sw: p24077) (le:8282) (re:9532) (di:direct) AE000164 AE000164 g1786806 Escherichia coli 562 -11534346 110223 ybda (de:hypothetical membrane protein p43) (db:swissprot) YBDA_ECOLI P24077 ESCHERICHIA COLI 562 -11534346

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843356	9958	32114	738	245

Description

GTC ORF with score 280 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f10n7 (essaiproject).) (nt:similarity to synaptobrevin-like protein, mus) (le:11598:12077:12387:12755) (re:11814:12267:12550:12842) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843357	9959	32115	426	141

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843375	9960	32116	1497	498

Description

6500730489 ybdb:b0597 hypothetical 15.0 kd protein in enta-csta intergenic region:p15 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0597 b0597 Escherichia coli 562 -11534347 110224 ybdb (de:hypothetical 15.0 kd protein in enta-csta intergenic region (p15)) (db:swissprot) YBDB_ECOLI P15050 ESCHERICHIA COLI 562 -11534347 135165 ybdb ybdb protein (db:pir1.dat) (mp:13 min) Q3ECEA B91904 Escherichia coli 562 -11534347 234244 p15 15 kda protein (sr:escherichia coli (individual_isolate mc4100, strain k-12) (clone) (db:genpept-bct1) (de:escherichia coli enterobactin biosynthesis-associated protein (entaand entb), and 15-kda protein (p15) genes, complete cds.) (le:1682) (re:2095) (di:direct) ECOENTAB M24143 g522184 Escherichia coli 562 -11534347 240110 (sr:escherichia coli dna) (db:genpept-bct1) (de:e. coli enterobactin biosynthesis genes ente, partial cds, entb,enta, and p15, complete cds.) (nt:p15) (le:2055) (re:2468) (di:direct) ECOENTEBA M24148 g450383 Escherichia coli 562 -11534347 7500896614 ybdb (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:69931) (re:70344) (di:direct) ECU82598 U82598 g1778514 Escherichia coli 562 -11534347 234238 ybdb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 55 of 400 of the completegenome.) (nt:ol37; 100 pct identical to ybdb_ecoli sw: p15050) (le:4633) (re:5046) (di:direct) AE000165 AE000165 g1786813 Escherichia coli 562 -11534347 5000691683 (de:(ecoli_578) (pn:hypothetical 15) (gn:ybdb) (gtcfc:13.7:14.1) (ec:) (ybdb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_578 ECOLI_578 Escherichia coli 562 10051956

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843394	9961	32117	654	217

Description

6500730490 csta:b0598 hypothetical protein:carbon starvation protein a (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0598 b0598 Escherichia coli 562 -11534348 66698 csta (de:carbon starvation protein a) (db:swissprot) CSTA_ECOLI P15078 ESCHERICHIA COLI 562 -11534348 7000684931 csta carbon starvation protein a:protein b0598 (cl:carbon starvation protein) (db:pir1.dat) (mp:13 min) Q0ECNA D64793 Escherichia coli 562 -11534348 7500879505 csta carbon starvation protein (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:70525) (re:72630) (di:direct) ECU82598 U82598 g1778515 Escherichia coli 562 -11534348 240111 csta carbon starvation protein (fn:phenotype; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 55 of 400 of the completegenome.) (nt:o701; 99 pct identical to 544 n-term residues of) (le:5227) (re:7332) (di:direct) AE000165 AE000165 g1786814 Escherichia coli 562 -11534348 5000691684 (de:(ecoli_579) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_579 ECOLI_579 Escherichia coli 562 10122917

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843410	9962	32118	768	255

Description

6500730491 ybdh:b0599 hypothetical protein in csta 3 region:hypothetical 39.1 kd protein in csta-ahpc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0599 b0599 Escherichia coli 562 -11534349 110232 ybdh (de:hypothetical oxidoreductase in csta-ahpc intergenic region) (db:swissprot) YBDH_ECOLI P45579 ESCHERICHIA COLI 562 -11534349 7000687318 ybdh ybdh protein (cl:lactaldehyde reductase homology) (db:pir2.dat) E64793 E64793 Escherichia coli 562 -11534349 7500896619 glycerol dehydrogenase homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to synechocystis sp. glycerol) (le:73020) (re:74108) (di:complement) ECU82598 U82598 g1778517 Escherichia coli 562 -11534349 240113 ybdh putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 55 of 400 of the completegenome.) (nt:f362; 100 pct identical to 81 aa fragment) (le:7722) (re:8810) (di:complement) AE000165 AE000165 g1786815 Escherichia coli 562 -11534349 5000691685 ybdh hypothetical protein in csta 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #166) (db:genpept) (de:escherichia coli genomic dna. (13.6 - 14.0 min).) (nt:orf_id:o166#2; similar to swissprot accession) (le:2146) (re:3234) (di:complement) D90701 D90701 g4062216 Escherichia coli 562 -11534349

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843411	9963	32119	516	171

Description

5000691686 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0600 b0600 Escherichia coli 562 -11534350
7500896622 ybd1 (ec:2.6.1.-) (de:hypothetical aminotransferase ybd1,) (db:swissprot) YBDL_ECOLI P77806 ESCHERICHIA COLI 562 -11534350 7000691034 ybd1 ybd1 protein (db:pir2.dat) F64793 F64793 Escherichia coli 562 -11534350 240114 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:74217) (re:75377) (di:direct) ECU82598 U82598 g1778518 Escherichia coli 562 -11534350 7500896624 ybd1 putative aminotransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 55 of 400 of the complete genome.) (nt:o386; this 386 aa orf is 31 pct identical (32 gaps)) (le:8919) (re:10079) (di:direct) AE000165 AE000165 g1786816 Escherichia coli 562 -11534350 7502851999 aspartate transaminase ec 2.6.1.1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #166) (db:genpept) (de:escherichia coli genomic dna. (13.6 - 14.0 min).) (nt:orf_id:o166#3; similar to pir accession number) (le:3343) (re:4503) (di:direct) D90701 D90701 g4062217 Escherichia coli 562 -11534350 6500730492 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0600 b0600 Escherichia coli 562 -11534350

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843422	9964	32120	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843426	9965	32121	531	176

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843438	9966	32122	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843460	9967	32123	666	221

Description

GTC ORF with score 220 to: (fn:may catalyze the formation of)
(db:genpept-bct1) (de:rhodopseudomonas palustris
cyclohex-1-ene-1-carboxyl-coa hydratase(badk), cyclohex-1-ene-1-carboxylate
coa ligase (alia),cyclohexanecarboxyl-coa dehydrogenase ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843472	9968	32124	1791	596

Description

5000691687 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0601 b0601 Escherichia coli 562 -11534351
7500896626 ybdm (de:hypothetical 23.9 kd protein in csta-dsbg intergenic
region) (db:swissprot) YBDM_ECOLI P77174 ESCHERICHIA COLI 562 -11534351
7000691035 ybdm ybdm protein (db:pir2.dat) G64793 G64793 Escherichia coli
562 -11534351 240115 (db:genpept-bct1) (de:escherichia coli genomic
sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:75378)
(re:76007) (di:complement) ECU82598 U82598 g1778519 Escherichia coli 562
-11534351 7500896628 ybdm orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 55 of 400 of the
completegenome.) (nt:f209; this 209 aa orf is 33 pct identical (2 gaps))
(le:10080) (re:10709) (di:complement) AE000165 AE000165 g1786817 Escherichia
coli 562 -11534351 6500730493 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0601 b0601
Escherichia coli 562 -11534351

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843496	9969	32125	237	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843501	9970	32126	252	83

Description

5000691688 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0602 b0602 Escherichia coli 562 -11534352
7500896630 ybdn (de:hypothetical 47.8 kd protein in csta-dsbg intergenic region) (db:swissprot) YBDN_ECOLI P77216 ESCHERICHIA COLI 562 -11534352
7000691036 ybdn ybdn protein (db:pir2.dat) H64793 H64793 Escherichia coli 562 -11534352 240116 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:75980) (re:77200) (di:complement) ECU82598 U82598 g1778520 Escherichia coli 562 -11534352 7500896632 ybdn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 55 of 400 of the completegenome.) (nt:f406) (le:10682) (re:11902) (di:complement) AE000165 AE000165 g1786818 Escherichia coli 562 -11534352 7502852000 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #166) (db:genpept) (de:escherichia coli genomic dna. (13.6 - 14.0 min).) (nt:orf_id:o166#5) (le:5106) (re:6326) (di:complement) D90701 D90701 g4062219 Escherichia coli 562 -11534352
6500730494 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0602 b0602 Escherichia coli 562 -11534352

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843502	9971	32127	543	180

Description

5000691689 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0603 b0603 Escherichia coli 562 -11534353
7500896634 ybdo (de:hypothetical transcriptional regulator in csta-dsbg intergenic region) (db:swissprot) YBDO_ECOLI P77746 ESCHERICHIA COLI 562 -11534353 7000691037 ybdo ybdo protein (db:pir2.dat) A64794 A64794 Escherichia coli 562 -11534353 240117 ybef homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to e. coli ybef) (le:77347) (re:78249) (di:complement) ECU82598 U82598 g1778521 Escherichia coli 562 -11534353 7500896636 ybdo putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f300; this 300 aa orf is 29 pct identical (5 gaps)) (le:104) (re:1006) (di:complement) AE000166 AE000166 g1786820 Escherichia coli 562 -11534353 7502852001 hypothetical transcriptional regulator in (sr:escherichia coli(strain:k12) dna, clone:kohara clone #166) (db:genpept) (de:escherichia coli genomic dna. (13.6 - 14.0 min).) (nt:orf_id:o166#6; similar to swissprot accession) (le:6473) (re:7375) (di:complement) D90701 D90701 g4062220 Escherichia coli 562 -11534353 6500730495 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0603 b0603 Escherichia coli 562 -11534353

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843504	9972	32128	360	119

Description

5000691690 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0604 b0604 Escherichia coli 562 -11534354
7000691038 hypothetical protein b0604 (db:pir2.dat) B64794 B64794
Escherichia coli 562 -11534354 7500959887 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:78458) (re:79264) (di:complement) ECU82598 U82598 g1778522 Escherichia coli 562 -11534354 240118 dsbg thiol:disulfide interchange protein (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f268; this 268 aa orf is 30 pct identical (31 gaps)) (le:1215) (re:2021) (di:complement) AE000166 AE000166 g1786821 Escherichia coli 562 -11534354 7502852002 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #166) (db:genpept) (de:escherichia coli genomic dna. (13.6 - 14.0 min).) (nt:orf_id:o166#7) (le:7584) (re:8390) (di:complement) D90701 D90701 g4062221 Escherichia coli 562 -11534354 6500730496 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0604 b0604 Escherichia coli 562 -11534354

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843511	9973	32129	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843515	9974	32130	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843531	9975	32131	228	75

Description

6500730497 ybdq:b0607 hypothetical protein:unknown protein from 2d-page:spots pr25/lm16/2d_000lr3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0607 b0607 Escherichia coli 562 -11534355 103751 ybdq (de:unknown protein from 2d-page (spots pr25/lm16/2d_000lr3)) (db:swissprot) UP12_ECOLI P39177 ESCHERICHIA COLI 562 -11534355 7000686894 ybdq ybdq protein (cl:escherichia coli ybdq protein) (db:pir2.dat) E64794 E64794 Escherichia coli 562 -11534355 7500893821 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:82069) (re:82497) (di:complement) ECU82598 U82598 g1778525 Escherichia coli 562 -11534355 240121 ybdq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f142; this 142 aa orf is 30 pct identical (4 gaps)) (le:4827) (re:5255) (di:complement) AE000166 AE000166 g1786824 Escherichia coli 562 -11534355 5000691691 yzzu unknown protein from 2d-page spots (sr:escherichia coli(strain:k12) dna, clone:kohara clone #166) (db:genpept) (de:escherichia coli genomic dna. (13.6 - 14.0 min).) (nt:orf_id:ol67#3; similar to swissprot accession) (le:11196) (re:11624) (di:complement) D90701 D90701 g4062223 Escherichia coli 562 -11534355 7502852003 yzzu unknown protein from 2d-page spots (sr:escherichia coli(strain:k12) dna, clone:kohara clone #167) (db:genpept) (de:escherichia coli genomic dna. (13.7 - 14.1 min).) (nt:orf_id:ol67#3; similar to swissprot accession) (le:3380) (re:3808) (di:complement) D90702 D90702 g4062229 Escherichia coli 562 -11534355

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843544	9976	32132	942	313

Description

5000691692 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0608 b0608 Escherichia coli 562 -11534356
7500896638 ybdr (de:intergenic region) (db:swissprot) YBDR_ECOLI P77316
ESCHERICHIA COLI 562 -11534356 7000691039 ybdr probable alcohol
dehydrogenase:ybdr (cl:alcohol dehydrogenase:long-chain alcohol
dehydrogenase homology) (ec:1.1.1.1) (db:pir1.dat) F64794 F64794 Escherichia
coli 562 -11534356 240122 fadh homolog (db:genpept-bct1) (de:escherichia
coli genomic sequence of minutes 9 to 12.) (nt:similar to e. coli fadh)
(le:82718) (re:83956) (di:direct) ECU82598 U82598 g1778526 Escherichia coli
562 -11534356 7500896640 ybdr putative oxidoreductase (fn:putative enzyme;
not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
56 of 400 of the completegenome.) (nt:o412; this 412 aa orf is 47 pct
identical (8 gaps)) (le:5476) (re:6714) (di:direct) AE000166 AE000166
g1786825 Escherichia coli 562 -11534356 7502852004 fadh
glutathione-dependent formaldehyde dehydrogenase (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #166) (db:genpept) (de:escherichia
coli genomic dna. (13.6 - 14.0 min).) (nt:orf_id:o167#4; similar to
swissprot accession) (le:11845) (re:13083) (di:direct) D90701 D90701
g4062224 Escherichia coli 562 -11534356 7502852005 fadh
glutathione-dependent formaldehyde dehydrogenase (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #167) (db:genpept) (de:escherichia
coli genomic dna. (13.7 - 14.1 min).) (nt:orf_id:o167#4; similar to
swissprot accession) (le:4029) (re:5267) (di:direct) D90702 D90702 g4062230
Escherichia coli 562 -11534356 6500730498 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0608 b0608
Escherichia coli 562 -11534356

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843550	9977	32133	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843567	9978	32134	723	240

Description

GTC ORF with score 161 to: (or:Caenorhabditis elegans) (db:genpept-inv)
(de:caenorhabditis elegans cosmid c18b12b, complete sequence.) (nt:similar
to zinc finger, c3hc4 type (ring finger);) (le:12212:12778:13089)
(re:12367:13034:13263) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843568	9979	32135	396	132

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843572	9980	32136	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843575	9981	32137	1518	505

Description

5000691693 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0609 b0609 Escherichia coli 562 -11534357
 7000691040 hypothetical protein b0609 (db:pir2.dat) G64794 G64794
 Escherichia coli 562 -11534357 7500959888 b0609 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:o153; this 153 aa orf is 27 pct identical (0 gaps)) (le:6795) (re:7256) (di:direct) AE000166 AE000166 g1786826 Escherichia coli 562 -11534357 6500730499 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0609 b0609 Escherichia coli 562 -11534357

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843590	9982	32138	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843597	9983	32139	663	221

Description

6500730500 ybds:b0612 hypothetical protein:hypothetical 53.1 kd protein in rna-citg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0612 b0612 Escherichia coli 562 -11534358 4000709414 citt (de:citrate carrier (citrate transporter) (citrate/succinate antiporter)) (db:swissprot) CITT_ECOLI P77405 ESCHERICHIA COLI 562 -11534358 7000687321 ybds ybds protein (cl:2-oxoglutarate/malate translocator) (db:pir2.dat) B64795 B64795 Escherichia coli 562 -11534358 7500896642 ygje homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to e. coli ygje) (le:85747) (re:87210) (di:complement) ECU82598 U82598 g1778529 Escherichia coli 562 -11534358 240125 ybds putative a membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f487 was f477; this 477 aa orf is 41 pct identical) (le:8505) (re:9968) (di:complement) AE000166 AE000166 g1786829 Escherichia coli 562 -11534358 5000691695 hypothetical 32.2 kd protein in ttldb-rpsu (sr:escherichia coli(strain:k12) dna, clone:kohara clone #166) (db:genpept) (de:escherichia coli genomic dna. (13.6 - 14.0 min).) (nt:orf_id:ol67#7; similar to swissprot accession) (le:14874) (re:16337) (di:complement) D90701 D90701 g4062225 Escherichia coli 562 -11534358 7502852006 hypothetical 32.2 kd protein in ttldb-rpsu (sr:escherichia coli(strain:k12) dna, clone:kohara clone #167) (db:genpept) (de:escherichia coli genomic dna. (13.7 - 14.1 min).) (nt:orf_id:ol67#7; similar to swissprot accession) (le:7058) (re:8521) (di:complement) D90702 D90702 g4062231 Escherichia coli 562 -11534358

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843609	9984	32140	351	116

Description

6500730501 citg:b0613 hypothetical protein:citg protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0613 b0613 Escherichia coli 562 -11534359 1500686912 citg (de:citg protein) (db:swissprot) CITG_ECOLI P77231 ESCHERICHIA COLI 562 -11534359 7000684829 citg citg protein (cl:citg protein) (db:pir2.dat) C64795 C64795 Escherichia coli 562 -11534359 7500878778 citg homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to k. pneumoniae citg) (le:87261) (re:88139) (di:complement) ECU82598 U82598 g1778530 Escherichia coli 562 -11534359 240126 citg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f292; this 292 aa orf is 51 pct identical (1 gap)) (le:10019) (re:10897) (di:complement) AE000166 AE000166 g1786830 Escherichia coli 562 -11534359 5000691696 (de:(ecoli_594) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_594 ECOLI_594 Escherichia coli 562 10062987

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843612	9985	32141	549	182

Description

5000691697 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0614 b0614 Escherichia coli 562 -11534360 7500896643 citx (de:citx protein) (db:swissprot) CITX_ECOLI P77563 ESCHERICHIA COLI 562 -11534360 7000691041 ybdu ybdu protein (db:pir2.dat) D64795 D64795 Escherichia coli 562 -11534360 240127 hi0021 homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to h. influenzae hi0021) (le:88114) (re:88665) (di:complement) ECU82598 U82598 g1778531 Escherichia coli 562 -11534360 7500896645 ybdu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f183; this 183 aa orf is 33 pct identical (0 gaps)) (le:10872) (re:11423) (di:complement) AE000166 AE000166 g1786831 Escherichia coli 562 -11534360 6500730502 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0614 b0614 Escherichia coli 562 -11534360

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843615	9986	32142	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843617	9987	32143	1215	404

Description

6500730503 citd:b0617 hypothetical protein:citrate lyase acyl carrier protein:citrate lyase gamma chain (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0617 b0617 Escherichia coli 562 -11534361
1500686911 citd (de:citrate lyase acyl carrier protein (citrate lyase gamma chain)) (db:swissprot) CILG_ECOLI P77618 ESCHERICHIA COLI 562 -11534361
7000684816 citd citrate pro-3s -lyase:gamma chain:citrate lyase acyl carrier protein (cl:citrate lyase acyl carrier protein) (ec:4.1.3.6) (db:pir2.dat) G64795 G64795 Escherichia coli 562 -11534361 7500878748 hi0024 homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to h. influenzae hi0024) (le:91117) (re:91413) (di:complement) ECU82598 U82598 g1778534 Escherichia coli 562 -11534361
240130 citd citrate lyase acyl carrier protein gamma (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f98; residues 9-86 are 51 pct identical to 9-86) (le:13875) (re:14171) (di:complement) AE000166 AE000166 g1786834 Escherichia coli 562 -11534361 5000691700 citd citrate pro-3s -lyase ec 4.1.3.6 gamma chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #167) (db:genpept) (de:escherichia coli genomic dna. (13.7 - 14.1 min).) (nt:orf_id:o168#1; similar to pir accession number) (le:12428) (re:12724) (di:complement) D90702 D90702 g4062234 Escherichia coli 562 -11534361 7502852007 citd citrate pro-3s -lyase ec 4.1.3.6 gamma chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf_id:o168#1; similar to pir accession number) (le:351) (re:647) (di:complement) D90703 D90703 g4062240 Escherichia coli 562 -11534361

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843619	9988	32144	1005	334

Description

5000691701 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0618 b0618 Escherichia coli 562 -11534362
 7000691042 citc citrate pro-3s -lyase ligase::citrate lyase ligase (cl:citrate (pro-3s)-lyase ligase) (ec:6.2.1.22) (db:pir2.dat) H64795 H64795 Escherichia coli 562 -11534362 7500959891 hi0025 homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to h. influenzae hi0025) (le:91428) (re:92573) (di:complement) ECU82598 U82598 g1778535 Escherichia coli 562 -11534362 240131 citc citrate lyase synthetase citrate pro-3s -lyase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f381; this 381 aa orf is 53 pct identical (2 gaps)) (le:14186) (re:15331) (di:complement) AE000166 AE000166 g1786835 Escherichia coli 562 -11534362 6500730504 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0618 b0618 Escherichia coli 562 -11534362

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843641	9989	32145	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843646	9990	32146	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843665	9991	32147	900	300

Description

6500730505 cita:b0619 hypothetical protein:sensor kinase cita (gtcfc:14.1) (ec:2.7.3.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0619 b0619 Escherichia coli 562 -11534363 4000709727 cita:mpdb (ec:2.7.3.-) (de:sensor kinase cita,) (db:swissprot) CITA_ECOLI P77510 ESCHERICHIA COLI 562 -11534363 7000684826 signal-transducing histidine kinase homolog b0619 (cl:two-component sensor histidine kinase:sensor histidine kinase homolog) (db:pir2.dat) A64796 A64796 Escherichia coli 562 -11534363 7500878774 sensor kinase cita homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to k. pneumoniae sensor kinase cita) (le:92865) (re:94523) (di:direct) ECU82598 U82598 g1778536 Escherichia coli 562 -11534363 240132 cita putative sensor-type protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 57 of 400 of the completegenome.) (nt:o552 was o455; this 455 aa orf is 29 pct identical) (le:176) (re:1834) (di:direct) AE000167 AE000167 g1786837 Escherichia coli 562 -11534363 5000691702 cita sensor kinase cita (sr:escherichia coli(strain:k12) dna, clone:kohara clone #167) (db:genpept) (de:escherichia coli genomic dna. (13.7 - 14.1 min).) (nt:orf_id:o168#3; similar to pir accession number) (le:14176) (re:15834) (di:direct) D90702 D90702 g4062236 Escherichia coli 562 -11534363 7502852008 cita sensor kinase cita (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf_id:o168#3; similar to pir accession number) (le:2099) (re:3757) (di:direct) D90703 D90703 g4062242 Escherichia coli 562 -11534363

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843677	9992	32148	1248	415

Description

6500730506 dcuc:b0621 hypothetical protein:c4-dicarboxylate anaerobic carrier (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0621 b0621 Escherichia coli 562 -11534364 500685117 dcuc (de:c4-dicarboxylate anaerobic carrier) (db:swissprot) DCUC_ECOLI Q47134 ESCHERICHIA COLI 562 -11534364 7000684993 dcuc dcuc protein:c4-dicarboxylate anaerobic carrier (cl:dcuc protein) (db:pir2.dat) C64796 C64796 Escherichia coli 562 -11534364 240134 dcuc dcuc protein (fn:anaerobic carrier for c4, dicarboxylates) (db:genpept-bct1) (de:e.coli dcuc gene.) (le:261) (re:1646) (di:complement) ECDCUCGEN X99112 g1429374 Escherichia coli 562 -11534364 7500880096 dcuc anaerobic carrier for c4:dicarboxylates (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:95213) (re:96598) (di:complement) ECU82598 U82598 g1778538 Escherichia coli 562 -11534364 232653 dcuc transport of dicarboxylates (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 57 of 400 of the completegenome.) (nt:f461; this 461 aa orf is 36 pct identical (6 gaps)) (le:2524) (re:3909) (di:complement) AE000167 AE000167 g1786839 Escherichia coli 562 -11534364 5000691704 (de:(ecoli_602) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_602 ECOLI_602 Escherichia coli 562 10063024

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843681	9993	32149	861	286

Description

6500730507 ybeg:crca:b0622 hypothetical protein in cspe 5region:crca protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0622 b0622 Escherichia coli 562 -11534365 110250 crca (de:crca protein) (db:swissprot) CRCA_ECOLI P37001 ESCHERICHIA COLI 562 -11534365 7000684907 crca:ybeg crca protein (db:pir2.dat) D64796 D64796 Escherichia coli 562 -11534365 240135 (sr:escherichia coli (sub_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli (strain: k-12) gica gene, complete cds.) (nt:putative) (le:542) (re:1102) (di:direct) ECOGICA L29054 g786003 Escherichia coli 562 -11534365 7500879389 ybeg (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:97187) (re:97747) (di:direct) ECU82598 U82598 g1778539 Escherichia coli 562 -11534365 234480 crca orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 57 of 400 of the completegenome.) (nt:o186; 100 pct identical to gb: ecogica_1 accession:) (le:4498) (re:5058) (di:direct) AE000167 AE000167 g1786840 Escherichia coli 562 -11534365 5000691705 (de:(ecoli_603) (pn:hypothetical 18) (gn:ybeg) (gtcfc:13.7:14.1) (ec:) (ybeg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_603 ECOLI_603 Escherichia coli 562 10122933

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843686	9994	32150	1242	413

Description

6500730508 ybei:b0624 hypothetical 13.8 kd protein in cspe-lipa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0624 b0624 Escherichia coli 562 -11534366 110252 crcb (de:crcb protein) (db:swissprot) CRCB_ECOLI P37002 ESCHERICHIA COLI 562 -11534366 7000687324 crcb:ybei crcb protein (cl:hypothetical protein mj1523) (db:pir2.dat) F64796 F64796 Escherichia coli 562 -11534366 7500879390 ybei (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:98185) (re:98568) (di:complement) ECU82598 U82598 g1778541 Escherichia coli 562 -11534366 240137 crcb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 57 of 400 of the completegenome.) (nt:f127; formerly designated ybei) (le:5496) (re:5879) (di:complement) AE000167 AE000167 g1786842 Escherichia coli 562 -11534366 5000691707 ybei hypothetical 13.8 kd protein in cspe-lipa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf_id:o168#9; similar to swissprot accession) (le:8618) (re:9001) (di:complement) D90703 D90703 g4062247 Escherichia coli 562 -11534366

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843689	9995	32151	432	144

Description

6500730509 ybeh:b0625 hypothetical protein in cspe-lipa intergenic region:hypothetical 8.0 kd protein in cspe-lipa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0625 b0625 Escherichia coli 562 -11534367 110251 ybeh (de:hypothetical 8.0 kd protein in crcb-lipa intergenic region) (db:swissprot) YBEH_ECOLI P39874 ESCHERICHIA COLI 562 -11534367 7000687323 ybeh ybeh protein (db:pir2.dat) G64796 G64796 Escherichia coli 562 -11534367 7500896667 ybeh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 57 of 400 of the completegenome.) (nt:o75; 100 pct identical to ybeh_ecoli sw: p39874) (le:5972) (re:6199) (di:direct) AE000167 AE000167 g1786843 Escherichia coli 562 -11534367 5000691708 ybeh hypothetical 8.0 kd protein in cspe-lipa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf_id:o168#10; similar to swissprot accession) (le:9094) (re:9321) (di:direct) D90703 D90703 g4062248 Escherichia coli 562 -11534367

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843715	9996	32152	300	99

Description

6500730510 ybem:b0626 hypothetical protein:hypothetical 20.5 kd protein in cspe-lipa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0626 b0626 Escherichia coli 562 -11534368
 1500687482 ybem (de:hypothetical 20.5 kd protein in crcb-lipa intergenic region) (db:swissprot) YBEM_ECOLI P77192 ESCHERICHIA COLI 562 -11534368
 7000687328 ybem ybem protein (db:pir2.dat) H64796 H64796 Escherichia coli 562 -11534368 7500896671 mtcy20g9.06c homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to m. tuberculosis mtcy20g9.06c) (le:98885) (re:99448) (di:direct) ECU82598 U82598 g1778543 Escherichia coli 562 -11534368 240139 ybem putative amidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 57 of 400 of the completegenome.) (nt:o187; this 187 aa orf is 40 pct identical (33 gaps)) (le:6196) (re:6759) (di:direct) AE000167 AE000167 g1786844 Escherichia coli 562 -11534368 5000691709 hypothetical 30.2 kd protein sll0601. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf_id:o168#11; similar to swissprot accession) (le:9318) (re:9881) (di:direct) D90703 D90703 g4062249 Escherichia coli 562 -11534368

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843717	9997	32153	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843726	9998	32154	477	159

Description

6500730511 ybec:b0627 hypothetical 7.0 kd protein in cspe-lipa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0627 b0627 Escherichia coli 562 -11534369 110245 ybec (de:hypothetical 7.0 kd protein in crcb-lipa intergenic region) (db:swissprot) YBEC_ECOLI P25895 ESCHERICHIA COLI 562 -11534369 163326 ybec ybec protein (cl:conserved hypothetical secreted protein hp0320) (db:pir2.dat) JN0256 JN0256 Escherichia coli 562 -11534369 7500896664 ybec hi0187 homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to h. influenzae hi0187) (le:99577) (re:99780) (di:direct) ECU82598 U82598 g1778544 Escherichia coli 562 -11534369 240140 ybec orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 57 of 400 of the completegenome.) (nt:o67; 98 pct identical to ybec_ecoli sw: p25895) (le:6888) (re:7091) (di:direct) AE000167 AE000167 g1786845 Escherichia coli 562 -11534369 5000691710 ybec hypothetical protein lip 3 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf_id:o168#12; similar to pir accession number) (le:10010) (re:10213) (di:direct) D90703 D90703 g4062250 Escherichia coli 562 -11534369

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843727	9999	32155	789	262

Description

6500730512 ybef:b0629 hypothetical transcriptional regulator in lipa-lipb intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0629 b0629 Escherichia coli 562 -11534370 7000691849 ybef probable transcription regulator ybef (db:pir2.dat) C64797 C64797 Escherichia coli 562 -11534370 7500960366 ybef putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 57 of 400 of the completegenome.) (nt:f266; this 266 aa orf is 99 pct identical (1 gap)) (le:8366) (re:9166) (di:complement) AE000167 AE000167 g1786847 Escherichia coli 562 -11534370 5000691711 (de:(ecoli_610) (pn:hypothetical transcriptional regulator in lipa-lipb intergenic region:orf2) (gn:ybef) (gtcfc:13.7:14.1) (ec:) (ybef_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_610 ECOLI_610 Escherichia coli 562 10122934

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843733	10000	32156	801	266

Description

6500730513 ybeb:b0637 hypothetical 7.7 kd protein in mrda/pbpa 3region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0637 b0637 Escherichia coli 562 -11534371 135161 ybeb ybeb protein (cl:escherichia coli ybeb protein) (db:pir1.dat) (mp:15 min) QQECP7 A24995 Escherichia coli 562 -11534371 7500953692 (db:genpept-bct1) (de:e. coli pbpa gene for penicillin-binding protein (pbp)2.) (nt:orf1 (aa 1-69)) (le:324) (re:533) (di:direct) ECPBPA X04516 g42314 Escherichia coli 562 -11534371 237724 ybeb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 58 of 400 of the completegenome.) (nt:f69; 100 pct identical to ybeb_ecoli sw: p05848) (le:6454) (re:6663) (di:complement) AE000168 AE000168 g1786856 Escherichia coli 562 -11534371 5000691714 ybeb hypothetical 7.6k protein pbpa 5 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:ol69#5; similar to pir accession number) (le:4967) (re:5176) (di:complement) D90704 D90704 g4062255 Escherichia coli 562 -11534371

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843736	10001	32157	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843756	10002	32158	396	131

Description

6500730514 yben:b0639 hypothetical protein:hypothetical 24.5 kd protein in phpb-hola intergenic region:orfuu (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0639 b0639 Escherichia coli 562 -11534372 110257 yben (de:hypothetical 24.5 kd protein in phpb-hola intergenic region (orfuu)) (db:swissprot) YBEN_ECOLI P52085 ESCHERICHIA COLI 562 -11534372 7000687329 hypothetical protein b0639 (db:pir2.dat) E64798 E64798 Escherichia coli 562 -11534372 240153 orfuu orfuu (fn:unknown, but appears to be essential for) (db:genpept-bct1) (de:escherichia coli orfuu (orfuu) gene and putative cobalaminsynthesis phpb (phpb) gene, complete cds.) (le:2) (re:643) (di:direct) ECU23163 U23163 g727430 Escherichia coli 562 -11534372 7500896672 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:orfuu; hypothetical protein) (le:110561) (re:111202) (di:complement) ECU82598 U82598 g1778557 Escherichia coli 562 -11534372 238774 yben orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 58 of 400 of the completegenome.) (nt:f213; this 213 aa orf is 36 pct identical (2 gaps)) (le:7666) (re:8307) (di:complement) AE000168 AE000168 g1786858 Escherichia coli 562 -11534372 5000691716 yben hypothetical 24.5 kd protein in phpb-hola (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:o169#7; similar to swissprot accession) (le:6179) (re:6820) (di:complement) D90704 D90704 g4062257 Escherichia coli 562 -11534372

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843763	10003	32159	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843780	10004	32160	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843783	10005	32161	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843786	10006	32162	534	177

Description

5000691718 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0644 b0644 Escherichia coli 562 -11534373
7500896673 ybeq (de:hypothetical 37.3 kd protein in leus-glrl intergenic region) (db:swissprot) YBEQ_ECOLI P77234 ESCHERICHIA COLI 562 -11534373
7000691043 hypothetical protein b0644 (db:pir2.dat) B64799 B64799
Escherichia coli 562 -11534373 240158 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:116200) (re:117183) (di:complement) ECU82598 U82598 g1778562 Escherichia coli 562 -11534373 7500896675 ybeq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:f327; this 327 aa orf is 31 pct identical (15 gaps)) (le:700) (re:1683) (di:complement) AE000169 AE000169 g1786864 Escherichia coli 562 -11534373 7502852009 sel-1 protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:ol69#12; similar to pir accession number) (le:11818) (re:12801) (di:complement) D90704 D90704 g4062259 Escherichia coli 562 -11534373 6500730515 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0644 b0644 Escherichia coli 562 -11534373

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843790	10007	32163	1398	465

Description

5000691719 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0645 b0645 Escherichia coli 562 -11534374
7500896677 yber (de:hypothetical 27.7 kd protein in leus-glrl intergenic region) (db:swissprot) YBER_ECOLI P77627 ESCHERICHIA COLI 562 -11534374
7000691044 hypothetical protein b0645 (db:pir2.dat) C64799 C64799
Escherichia coli 562 -11534374 240159 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:117341) (re:118048) (di:direct) ECU82598 U82598 g1778563 Escherichia coli 562 -11534374 7500896679 yber orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:o235; this 235 aa orf is 24 pct identical (5 gaps)) (le:1841) (re:2548) (di:direct) AE000169 AE000169 g1786865 Escherichia coli 562 -11534374 7502852010 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:ol69#13) (le:12959) (re:13666) (di:direct) D90704 D90704 g4062260 Escherichia coli 562 -11534374 6500730516 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0645 b0645 Escherichia coli 562 -11534374

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843791	10008	32164	261	87
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843802	10009	32165	222	73
<u>Description</u>				

5000691720 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0646 b0646 Escherichia coli 562 -11534375
7500896681 ybes (de:hypothetical 55.3 kd protein in leus-gl1 intergenic region) (db:swissprot) YBES_ECOLI P77381 ESCHERICHIA COLI 562 -11534375
7000691045 ybes ybes protein (db:pir2.dat) D64799 D64799 Escherichia coli 562 -11534375 240160 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:118045) (re:119472) (di:direct) ECU82598 U82598 g1778564 Escherichia coli 562 -11534375 7500896683 ybes putative enzyme of polynucleotide modification (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:o475) (le:2545) (re:3972) (di:direct) AE000169 AE000169 g1786866 Escherichia coli 562 -11534375 7502852011 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:o169#14) (le:13663) (re:15090) (di:direct) D90704 D90704 g4062261 Escherichia coli 562 -11534375 6500730517 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0646 b0646 Escherichia coli 562 -11534375

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843807	10010	32166	1389	462

Description

5000691721 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0647 b0647 Escherichia coli 562 -11534376
7500896685 ybet (de:hypothetical 20.9 kd protein in leus-gltl intergenic region) (db:swissprot) YBET_ECOLI P77296 ESCHERICHIA COLI 562 -11534376
7000691046 ybet ybet protein (db:pir2.dat) E64799 E64799 Escherichia coli 562 -11534376 240161 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:119482) (re:120036) (di:complement) ECU82598 U82598 g1778565 Escherichia coli 562 -11534376 7500896687 ybet orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:f184; this 184 aa orf is 36 pct identical (4 gaps)) (le:3982) (re:4536) (di:complement) AE000169 AE000169 g1786867 Escherichia coli 562 -11534376 7502852012 hypothetical protein spac24b11.10c (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:o170#1; similar to pir accession number) (le:15100) (re:15654) (di:complement) D90704 D90704 g4062262 Escherichia coli 562 -11534376 7502852013 hypothetical protein spac24b11.10c (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (nt:orf_id:o170#1; similar to pir accession number) (le:1336) (re:1890) (di:complement) D90705 D90705 g4062267 Escherichia coli 562 -11534376 6500730518 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0647 b0647 Escherichia coli 562 -11534376

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843809	10011	32167	1038	345
<u>Description</u>				
5000691722 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0648 b0648 Escherichia coli 562 -11534377				
7500896689 ybeu (de:hypothetical 27.0 kd protein in leus-gltl intergenic region) (db:swissprot) YBEU_ECOLI P77427 ESCHERICHIA COLI 562 -11534377				
7000691047 hypothetical protein b0648 (db:pir2.dat) F64799 F64799				
Escherichia coli 562 -11534377 240162 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:120138) (re:120845) (di:direct) ECU82598 U82598 gl778566 Escherichia coli 562 -11534377				
7500896691 ybeu putative trna ligase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:o235; this 235 aa orf is 23 pct identical (6 gaps)) (le:4638) (re:5345) (di:direct) AE000169 AE000169				
g1786868 Escherichia coli 562 -11534377 7502852014 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:o170#2) (le:15756) (re:16463) (di:direct) D90704 D90704 g4062263 Escherichia coli 562 -11534377				
7502852015 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (nt:orf_id:o170#2) (le:1992) (re:2699) (di:direct) D90705 D90705 g4062268				
Escherichia coli 562 -11534377 6500730519 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0648 b0648				
Escherichia coli 562 -11534377				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843817	10012	32168	729	243

Description

5000691723 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0649 b0649 Escherichia coli 562 -11534378
7500896693 ybev (de:hypothetical 55.7 kd protein in leus-gl1 intergenic region) (db:swissprot) YBEV_ECOLI P77359 ESCHERICHIA COLI 562 -11534378
7000691048 ybev ybev protein (db:pir2.dat) G64799 G64799 Escherichia coli 562 -11534378 240163 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:120842) (re:122293) (di:direct) ECU82598 U82598 g1778567 Escherichia coli 562 -11534378 7500896695 ybev orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the complete genome.) (nt:o483) (le:5342) (re:6793) (di:direct) AE000169 AE000169 g1786869 Escherichia coli 562 -11534378 7502852016 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:o170#3) (le:16460) (re:17911) (di:direct) D90704 D90704 g4062264 Escherichia coli 562 -11534378 7502852017 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (nt:orf_id:o170#3) (le:2696) (re:4147) (di:direct) D90705 D90705 g4062269 Escherichia coli 562 -11534378 6500730520 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0649 b0649 Escherichia coli 562 -11534378

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843820	10013	32169	789	262

Description

5000691724 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0650 b0650 Escherichia coli 562 -11534379
 7500896697 hsc62 (de:chapeone protein hsc62 (hsc62)) (db:swissprot) HSCC_ECOLI P77319 ESCHERICHIA COLI 562 -11534379 7000691049 ybew probable dnaK-type molecular chaperone ybew:dnaK homolog hsc62 (cl:heat shock protein 70) (db:pir2.dat) H64799 H64799 Escherichia coli 562 -11534379 240164 dnaK homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to m. tuberculosis dnaK) (le:122353) (re:124023) (di:complement) ECU82598 U82598 g1778568 Escherichia coli 562 -11534379
 7500896699 ybew putative dnaK protein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:f556; this 556 aa orf is 40 pct identical (24 gaps)) (le:6853) (re:8523) (di:complement) AE000169 AE000169 g1786870 Escherichia coli 562 -11534379 7502852018 ig heavy chain-binding protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (nt:orf_id:o170#4; similar to pir accession number) (le:4207) (re:5877) (di:complement) D90705 D90705 g4062270 Escherichia coli 562 -11534379 6500730521 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0650 b0650 Escherichia coli 562 -11534379

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843837	10014	32170	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843840	10015	32171	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843841	10016	32172	1176	391

Description

5000691730 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0658 b0658 Escherichia coli 562 -11534380
 7500896701 ybex (de:hypothetical 33.3 kd protein in cute-asnb intergenic region) (db:swissprot) YBEX_ECOLI P77392 ESCHERICHIA COLI 562 -11534380
 7000689491 ybex ybex protein (cl:hypothetical protein b0658) (db:pir2.dat) H64800 H64800 Escherichia coli 562 -11534380 240173 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to h. influenzae) (le:131536) (re:132414) (di:complement) ECU82598 U82598 g1778577 Escherichia coli 562 -11534380 7500896703 ybex putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 60 of 400 of the completegenome.) (nt:f292; this 292 aa orf is 23 pct identical (9 gaps)) (le:4182) (re:5060) (di:complement) AE000170 AE000170 g1786879 Escherichia coli 562 -11534380 6500730522 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0658 b0658 Escherichia coli 562 -11534380

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843842	10017	32173	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843859	10018	32174	831	276

Description

6500730523 ybey:b0659 hypothetical protein:hypothetical 17.5 kd protein in cute-asnb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0659 b0659 Escherichia coli 562 -11534381
 4000708182 ybey (de:hypothetical 17.5 kd protein in cute-asnb intergenic region) (db:swissprot) YBEY_ECOLI P77385 ESCHERICHIA COLI 562 -11534381
 7000687330 ybey ybey protein (db:pir2.dat) A64801 A64801 Escherichia coli 562 -11534381 7500896708 hi0004 homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to h. influenzae hi0004) (le:132504) (re:132971) (di:complement) ECU82598 U82598 g1778578 Escherichia coli 562 -11534381 240174 ybey orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 60 of 400 of the completegenome.) (nt:f155; this 155 aa orf is 24 pct identical (7 gaps)) (le:5150) (re:5617) (di:complement) AE000170 AE000170 g1786880 Escherichia coli 562 -11534381 5000691731 yqfg hypothetical protein hi0004 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (nt:orf_id:o171#3; similar to pir accession number) (le:4669) (re:5136) (di:complement) D90706 D90706 g4062278 Escherichia coli 562 -11534381

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843887	10019	32175	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843888	10020	32176	561	186

Description

5000691732 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0660 b0660 Escherichia coli 562 -11534382
 7500888044 ybez (de:phoh-like protein) (db:swissprot) PHOL_ECOLI P77349
 ESCHERICHIA COLI 562 -11534382 7000691050 ybez ybez protein (cl:phosphate starvation-induced protein) (db:pir2.dat) B64801 B64801 Escherichia coli 562 -11534382 240175 b1937_f1_20 homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to m. leprae b1937_f1_20) (le:132968) (re:134047) (di:complement) ECU82598 U82598 g1778579 Escherichia coli 562 -11534382 7500888046 ybez putative atp-binding protein in pho regulon (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 60 of 400 of the complete genome.) (nt:f359; this 359 aa orf is 43 pct identical (7 gaps)) (le:5614) (re:6693) (di:complement) AE000170 AE000170 g1786881 Escherichia coli 562 -11534382
 7502852019 phoh phoh protein homolog. (sr:escherichia coli (strain:k12) dna, clone:kohara clone #171) (db:genpept) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (nt:orf_id:o171#4; similar to swissprot accession) (le:5133) (re:6212) (di:complement) D90706 D90706 g4062279 Escherichia coli 562 -11534382 6500730524 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0660 b0660 Escherichia coli 562 -11534382

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843913	10021	32177	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843914	10022	32178	831	277

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843919	10023	32179	645	215

Description

GTC ORF with score 227 to: (db:genpept-bct2) (de:acinetobacter sp. adp1 vanillate demethylase region, vanillatedemethylase (vanb) and vanillate demethylase (vana) genes, completedcds.) (nt:similar to salicylate hydroxylase; orf7) (le:10288) (re:11433) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843931	10024	32180	420	139

Description

6500730525 ylea:b0661 hypothetical protein:hypothetical 53.7 kd protein in cute-glnx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0661 b0661 Escherichia coli 562 -11534383 121748 ylea (de:hypothetical 53.7 kd protein in cute-glnx intergenic region) (db:swissprot) YLEA_ECOLI P77645 ESCHERICHIA COLI 562 -11534383 7000688131 ylea ylea protein (cl:conserved hypothetical protein hi0019) (db:pir2.dat) C64801 C64801 Escherichia coli 562 -11534383 7500950958 hi0019 homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to h. influenzae hi0019) (le:134161) (re:135585) (di:complement) ECU82598 U82598 g1778580 Escherichia coli 562 -11534383 240176 ylea orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 60 of 400 of the completegenome.) (nt:f474; similar to bche_rhoa sw: p26168; similar) (le:6807) (re:8231) (di:complement) AE000170 AE000170 g1786882 Escherichia coli 562 -11534383 5000691733 (de:(ecoli_642) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_642 ECOLI_642 Escherichia coli 562 10065216

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843937	10025	32181	363	120

Description

GTC ORF with score 172 to: (sr:human) (db:genpept-pri2) (de:homo sapiens dna sequence from pac 422h11 on chromosome6p21.1-22.2. contains the gene coding for two isoforms of a knownserine kinase. contains ests, stss and a gss, complete sequence.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843938	10026	32182	381	126

Description

GTC ORF with score 105 to: (sr:african clawed frog oocyte) (db:genpept-vrt) (de:xkl-1=kit receptor tyrosine kinase homolog (xenopus laevis, oocyte,mrna partial, 1983 nt).) (nt:kit receptor tyrosine kinase homolog; this sequence) (le:1) (re:1053) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843957	10027	32183	417	138

Description

GTC ORF with score 107 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid r04e5.) (nt:proline rich; coded for by c. elegans cdna) (le:8839:9150:9494) (re:8875:9435:10157) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843963	10028	32184	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843975	10029	32185	1014	337

Description

GTC ORF with score 193 to: (sr:saccharomyces cerevisiae (strain fl100) dna) (db:genpept-pln1) (de:yeast rna i and iii supressor (srp40) gene, complete cds.) (nt:selected as a weak suppressor of a mutant of the) (le:929) (re:2149) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501843976	10030	32186	1080	360

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501843998	10031	32187	426	141

Description

5000691734 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0662 b0662 Escherichia coli 562 -11534384
 7500950960 yleb (de:hypothetical 43.0 kd protein in cute-glnx intergenic region) (db:swissprot) YLEB_ECOLI P75728 ESCHERICHIA COLI 562 -11534384
 7000689008 yleb yleb protein (cl:ubih protein) (db:pir2.dat) D64801 D64801 Escherichia coli 562 -11534384 7500950962 yleb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 60 of 400 of the completegenome.) (nt:o391; this 391 aa orf is 38 pct identical (5 gaps)) (le:8377) (re:9552) (di:direct) AE000170 AE000170 g1786883 Escherichia coli 562 -11534384 7502852020 visc visc protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #171) (db:genpept) (de:escherichia coli genomic dna. (14.8 - 15.2 min).) (nt:orf_id:o171#6; similar to pir accession number) (le:7895) (re:9070) (di:direct) D90706 D90706 g4062280 Escherichia coli 562 -11534384 6500730526 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0662 b0662 Escherichia coli 562 -11534384

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844001	10032	32188	537	179

Description

5000691735 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0663 b0663 Escherichia coli 562 -11534385
 7000691051 hypothetical protein b0663 (db:pir2.dat) E64801 E64801 Escherichia coli 562 -11534385 7500959892 b0663 putative rna (fn:putative rna; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 60 of 400 of the completegenome.) (nt:o111; this 111 aa orf is 28 pct identical (4 gaps)) (le:9634) (re:9969) (di:direct) AE000170 AE000170 g1786884 Escherichia coli 562 -11534385 6500730527 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0663 b0663 Escherichia coli 562 -11534385

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844010	10033	32189	1134	377

Description

5000691736 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0667 b0667 Escherichia coli 562 -11534386
 7000691052 hypothetical protein b0667 (db:pir2.dat) F64801 F64801
 Escherichia coli 562 -11534386 7500959893 b0667 putative rna (fn:putative rna; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 60 of 400 of the completegenome.) (nt:o45; this 45 aa orf is 42 pct identical (0 gaps)) (le:9984) (re:10121) (di:direct) AE000170 AE000170
 g1786885 Escherichia coli 562 -11534386 6500730528 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0667 b0667 Escherichia coli 562 -11534386

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844011	10034	32190	636	211

Description

5000691737 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0669 b0669 Escherichia coli 562 -11534387
 7000691053 hypothetical protein b0669 (db:pir2.dat) G64801 G64801
 Escherichia coli 562 -11534387 7500959894 b0669 putative rna (fn:putative rna; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 60 of 400 of the completegenome.) (nt:o39; this 39 aa orf is 28 pct identical (1 gap)) (le:10118) (re:10237) (di:direct) AE000170 AE000170
 g1786886 Escherichia coli 562 -11534387 6500730529 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0669 b0669 Escherichia coli 562 -11534387

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844012	10035	32191	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844041	10036	32192	564	187

Description

5000691738 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0671 b0671 Escherichia coli 562 -11534388
 7000691054 hypothetical protein b0671 (db:pir2.dat) H64801 H64801
 Escherichia coli 562 -11534388 7500959895 b0671 putative rna (fn:putative rna; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 60 of 400 of the completegenome.) (nt:o50; this 50 aa orf is 34 pct identical (2 gaps)) (le:10238) (re:10390) (di:direct) AE000170 AE000170
 g1786887 Escherichia coli 562 -11534388 6500730530 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0671 b0671 Escherichia coli 562 -11534388

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844044	10037	32193	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844051	10038	32194	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844064	10039	32195	690	229

Description

5000691739 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0681 b0681 Escherichia coli 562 -11534389
 7500896720 ybfm (de:hypothetical 52.8 kd protein in glns-fur intergenic region) (db:swissprot) YBFM_ECOLI P75733 ESCHERICHIA COLI 562 -11534389
 7000691055 ybfm ybfm protein (db:pir2.dat) H64802 H64802 Escherichia coli 562 -11534389 7500896722 ybfm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:o468; this 468 aa orf is 23 pct identical (32 gaps)) (le:319) (re:1725) (di:direct) AE000172 AE000172 g1786897 Escherichia coli 562 -11534389 6500730531 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0681 b0681 Escherichia coli 562 -11534389

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844065	10040	32196	198	65

Description

6500730532 ybfn:b0682 hypothetical protein:hypothetical 12.0 kd lipoprotein in glns-fur intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0682 b0682 Escherichia coli 562 -11534390 1500686810 ybfn (de:precursor) (db:swissprot) YBFN_ECOLI P75734 ESCHERICHIA COLI 562 -11534390 7000687341 ybfn ybfn protein (db:pir2.dat) A64803 A64803 Escherichia coli 562 -11534390 7500896723 ybfn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:o108; this 108 aa orf is 22 pct identical (3 gaps)) (le:1775) (re:2101) (di:direct) AE000172 AE000172 g1786898 Escherichia coli 562 -11534390 5000691740 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf_id:o172#7) (le:9617) (re:9943) (di:direct) D90707 D90707 g4062283 Escherichia coli 562 -11534390

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844066	10041	32197	267	88

Description

5000691741 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0685 b0685 Escherichia coli 562 -11534391 7000687335 ybfe (de:hypothetical 13.9 kd protein in flda-seqa intergenic region) (db:swissprot) YBFE_ECOLI P75735 ESCHERICHIA COLI 562 -11534391 7000687336 ybfe ybfe protein (db:pir2.dat) D64803 D64803 Escherichia coli 562 -11534391 7500896715 ybfe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:f120) (le:3590) (re:3952) (di:complement) AE000172 AE000172 g1786901 Escherichia coli 562 -11534391 7502852021 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf_id:o173#3) (le:11432) (re:11794) (di:complement) D90707 D90707 g4062285 Escherichia coli 562 -11534391 7502852022 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept) (de:escherichia coli genomic dna. (15.3 - 15.7 min).) (nt:orf_id:o173#3) (le:1227) (re:1589) (di:complement) D90708 D90708 g4062289 Escherichia coli 562 -11534391 6500730533 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0685 b0685 Escherichia coli 562 -11534391

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844067	10042	32198	195	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844071	10043	32199	213	70

Description

5000691742 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0686 b0686 Escherichia coli 562 -11534392
7000687337 ybff (ec:3.1.-.-) (de:putative esterase/lipase ybff,) (db:swissprot) YBFF_ECOLI P75736 ESCHERICHIA COLI 562 -11534392 7000687338 ybff ybff protein (cl:tropinesterase) (db:pir2.dat) E64803 E64803 Escherichia coli 562 -11534392 7500896716 ybff orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:f254; this 254 aa orf is 23 pct identical (9 gaps)) (le:4023) (re:4787) (di:complement) AE000172 AE000172 g1786902 Escherichia coli 562 -11534392 7502852023 dihydrolipoamide acetyltransferase acoc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf_id:o173#4; similar to pir accession number) (le:11865) (re:12629) (di:complement) D90707 D90707 g4062286 Escherichia coli 562 -11534392 7502852024 dihydrolipoamide acetyltransferase acoc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept) (de:escherichia coli genomic dna. (15.3 - 15.7 min).) (nt:orf_id:o173#4; similar to pir accession number) (le:1660) (re:2424) (di:complement) D90708 D90708 g4062290 Escherichia coli 562 -11534392 6500730534 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0686 b0686 Escherichia coli 562 -11534392

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844077	10044	32200	516	171

Description

5000691743 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0689 b0689 Escherichia coli 562 -11534393
7000687342 ybfp (de:precursor) (db:swissprot) YBFP_ECOLI P75737 ESCHERICHIA COLI 562 -11534393 7000687343 ybfp ybfp protein:protein b0689 (db:pir2.dat) H64803 H64803 Escherichia coli 562 -11534393 7500896724 ybfp putative pectinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:o164; this 164 aa orf is 29 pct identical (9 gaps)) (le:7397) (re:7891) (di:direct) AE000172 AE000172 g1786905 Escherichia coli 562 -11534393 6500730535 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0689 b0689 Escherichia coli 562 -11534393

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844092	10045	32201	525	174

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844100	10046	32202	504	167

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844101	10047	32203	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844112	10048	32204	501	166

Description

GTC ORF with score 180 to: (sr:baker's yeast strain=s288c (ab972))
(db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmid 9819.)
(nt:small region of similarity to nadh-ubiquinone) (le:3007) (re:3876)
(di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844113	10049	32205	432	143

Description

GTC ORF with score 222 to: (sr:baker's yeast strain=s288c (ab972))
(db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmid 9819.)
(nt:small region of similarity to nadh-ubiquinone) (le:3007) (re:3876)
(di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844118	10050	32206	357	118

Description

6500730536 ybfg:b0690 hypothetical protein in pgm-pote intergenic region:hypothetical 14.0 kd protein in pgm-pote intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0690 b0690 Escherichia coli 562 -11534394 110270 ybfg (de:hypothetical 14.0 kd protein in pgm-pote intergenic region) (db:swissprot) YBFG_ECOLI P37003 ESCHERICHIA COLI 562 -11534394 7000687339 ybfg ybfg protein (db:pir2.dat) A64804 A64804 Escherichia coli 562 -11534394 7500896717 ybfg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:f120; 100 pct identical to ybfg_ecoli sw: p37003) (le:7932) (re:8294) (di:complement) AE000172 AE000172 g1786906 Escherichia coli 562 -11534394 5000691744 ybfg hypothetical 13.2 kd protein in pgm-pote (sr:escherichia coli(strain:k12) dna, clone:kohara clone #172) (db:genpept) (de:escherichia coli genomic dna. (15.1 - 15.5 min).) (nt:orf_id:o173#7; similar to swissprot accession) (le:15774) (re:16136) (di:complement) D90707 D90707 g4062287 Escherichia coli562 -11534394 7502852025 ybfg hypothetical 13.2 kd protein in pgm-pote (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept) (de:escherichia coli genomic dna. (15.3 - 15.7 min).) (nt:orf_id:o173#7; similar to swissprot accession) (le:5569) (re:5931) (di:complement) D90708 D90708 g4062291 Escherichia coli 562 -11534394

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844121	10051	32207	348	115

Description

6500730537 ybfh:b0691 hypothetical protein in pgm-pote intergenic region:hypothetical 11.9 kd protein in pgm-pote intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0691 b0691 Escherichia coli 562 -11534395 110273 ybfh (de:hypothetical 11.9 kd protein in pgm-pote intergenic region) (db:swissprot) YBFH_ECOLI P37004 ESCHERICHIA COLI 562 -11534395 7000687340 ybfh ybfh protein (db:pir2.dat) B64804 B64804 Escherichia coli 562 -11534395 7500896719 ybfh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 62 of 400 of the completegenome.) (nt:f105; 100 pct identical to ybfh_ecoli sw: p37004) (le:8373) (re:8690) (di:complement) AE000172 AE000172 g1786907 Escherichia coli 562 -11534395 5000691745 ybfh hypothetical 11.9 kd protein in pgm-pote (sr:escherichia coli(strain:k12) dna, clone:kohara clone #173) (db:genpept) (de:escherichia coli genomic dna. (15.3 - 15.7 min).) (nt:orf_id:o173#8; similar to swissprot accession) (le:6010) (re:6327) (di:complement) D90708 D90708 g4062292 Escherichia coli 562 -11534395

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844122	10052	32208	222	73

Description

6500730538 ybfa:b0699 hypothetical 8.3 kd protein in rhsc
5region:hypothetical 8.3 kd protein in kdpa-rhsc intergenic region precursor
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0699
b0699 Escherichia coli 562 -11534396 110266 ybfa (de:hypothetical 8.3 kd
protein in kdpa-rhsc intergenic region precursor) (db:swissprot) YBFA_ECOLI
P28913 ESCHERICHIA COLI 562 -11534396 7000687331 ybfa ybfa protein
(db:pir2.dat) B64805 B64805 Escherichia coli 562 -11534396 235814 ybfa
orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 63 of 400 of the completegenome.) (nt:o68; 100 pct
identical to ybfa_ecoli sw: p28913) (le:8406) (re:8612) (di:direct) AE000173
AE000173 g1786916 Escherichia coli 562 -11534396 300031 unknown
(db:genpept-bct2) (de:escherichia coli rhs core protein and rhsc
accessoryelement-encoded genes, complete cds.) (nt:orf) (le:273) (re:479)
(di:direct) ECORHSCA L02373 g147637 Escherichia coli 562 -11534396
5000691746 ybfa hypothetical 8.3 kd protein in rhsc 5region (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #174) (db:genpept) (de:escherichia
coli genomic dna. (15.7 - 16.0 min).) (nt:orf_id:ol74#3; similar to
swissprot accession) (le:2320) (re:2526) (di:direct) D90709 D90709 g4062294
Escherichia coli 562 -11534396

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844125	10053	32209	213	70

Description

5000691748 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0701 b0701 Escherichia coli 562 -11534397
7000691056 hypothetical protein b0701 (db:pir2.dat) D64805 D64805
Escherichia coli 562 -11534397 7500959896 b0701 protein in rhs element
(fn:orf; transposon-related functions) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 63 of 400 of the completegenome.) (nt:o73; this 73
aa orf is 33 pct identical (2 gaps)) (le:12642) (re:12863) (di:direct)
AE000173 AE000173 g1786918 Escherichia coli 562 -11534397 6500730539
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0701 b0701 Escherichia coli 562 -11534397

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844147	10054	32210	1881	626

Description

6500730540 ybfb:b0702 hypothetical 12.6 kd protein in rhsc
3region:hypothetical 12.6 kd protein in rhsc-phrb intergenic region:orf-c2
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0702
b0702 Escherichia coli 562 -11534398 110267 ybfb (de:hypothetical 12.6 kd
protein in rhsc-phrb intergenic region (orf-c2)) (db:swissprot) YBFB_ECOLI
P28914 ESCHERICHIA COLI 562 -11534398 7000687332 ybfb ybfb protein
(db:pir2.dat) E64805 E64805 Escherichia coli 562 -11534398 235816 ybfb
orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 63 of 400 of the completegenome.) (nt:o108; 100 pct
identical to ybfb_ecoli sw: p28914) (le:13048) (re:13374) (di:direct)
AE000173 AE000173 g1786919 Escherichia coli 562 -11534398 300033 rhsc
-c2::orf unknown (db:genpept-bct2) (de:escherichia coli rhs core protein and
rhsc accessoryelement-encoded genes, complete cds.) (le:4915) (re:5241)
(di:direct) ECORHSCA L02373 g147639 Escherichia coli 562 -11534398
5000691749 ybfb hypothetical 12.6 kd protein in rhsc 3region
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #174) (db:genpept)
(de:escherichia coli genomic dna. (15.7 - 16.0 min).) (nt:orf_id:o174#5;
similar to swissprot accession) (le:6962) (re:7288) (di:direct) D90709
D90709 g4062295 Escherichia coli 562 -11534398

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844148	10055	32211	1446	482

Description

5000691750 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0703 b0703 Escherichia coli 562 -11534399
7000691057 hypothetical protein b0703 (db:pir2.dat) F64805 F64805
Escherichia coli 562 -11534399 223164 rhsa rhsa protein precursor
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #174)
(db:genpept-bct1) (de:escherichia coli genomic dna. (15.6 - 15.9 min).)
(le:7406) (re:8839) (di:direct) D90709 D90709 g1651310 Escherichia coli 562
-11534399 7500959897 b0703 orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 64 of 400 of the
completegenome.) (nt:o477; 96 pct identical to 327 aa of 1397) (le:89)
(re:1522) (di:direct) AE000174 AE000174 g1786921 Escherichia coli 562
-11534399 7502852026 rhsa rhsa protein (sr:escherichia coli(strain:k12)
dna, clone:kohara clone #174) (db:genpept) (de:escherichia coli genomic dna.
(15.7 - 16.0 min).) (nt:orf_id:o174#6; similar to pir accession number)
(le:7406) (re:8839) (di:direct) D90709 D90709 g1651310 Escherichia coli 562
-11534399 6500730541 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b0703 b0703 Escherichia coli 562
-11534399

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844171	10056	32212	843	280

Description

6500730542 ybfc:b0704 hypothetical 22 kd protein in rhsc 3 region
precursor:hypothetical 22.0 kd protein in rhsc-phrb intergenic region
precursor:orf-c3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0704 b0704 Escherichia coli 562 -11534400 110268
ybfc (de:(orf-c3)) (db:swissprot) YBFC_ECOLI P28915 ESCHERICHIA COLI 562
-11534400 7000687333 ybfc ybfc protein precursor (db:pir2.dat) G64805
G64805 Escherichia coli 562 -11534400 235817 ybfc orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
64 of 400 of the completegenome.) (nt:o189; 100 pct identical to ybfc_ecoli
sw: 28915) (le:1519) (re:2088) (di:direct) AE000174 AE000174 g1786922
Escherichia coli 562 -11534400 300034 rhsc -c3::orf unknown
(db:genpept-bct2) (de:escherichia coli rhs core protein and rhsc
accessoryelement-encoded genes, complete cds.) (le:6789) (re:7358)
(di:direct) ECORHSCA L02373 g147640 Escherichia coli 562 -11534400
5000691751 ybfc hypothetical 22.0 kd protein in rhsc 3region
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #174) (db:genpept)
(de:escherichia coli genomic dna. (15.7 - 16.0 min).) (nt:orf_id:o174#7;
similar to swissprot accession) (le:8836) (re:9405) (di:direct) D90709
D90709 g4062296 Escherichia coli 562 -11534400

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844190	10057	32213	756	251

Description

GTC ORF with score 766 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe
chromosome i cosmid c3lg5.) (nt:spac3lg5.15, anomaly: splicing may be
incorrectly) (le:24696:24950:25237:25745) (re:24893:25177:25702:26790)
(di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844200	10058	32214	606	201

Description

5000691752 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0705 b0705 Escherichia coli 562 -11534401
7000691058 h repeat-associated protein-like protein b0705 (db:pir2.dat)
H64805 H64805 Escherichia coli 562 -11534401 7500959898 ybfl putative
receptor protein (fn:putative factor; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 64 of 400 of the completegenome.)
(nt:o285; this 285 aa orf is 98 pct identical to) (le:2973) (re:3830)
(di:direct) AE000174 AE000174 g1786923 Escherichia coli 562 -11534401
6500730543 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0705 b0705 Escherichia coli 562 -11534401

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844214	10059	32215	645	214

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844218	10060	32216	534	178

Description

6500730544 ybga:b0707 hypothetical 20.2 kd protein in phrb
5region:hypothetical 20.2 kd protein in rhsc-phrb intergenic
region:tkp:orf169 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0707 b0707 Escherichia coli 562 -11534402 110283
ybga (de:(orf169)) (db:swissprot) YBGA_ECOLI P24252 ESCHERICHIA COLI 562
-11534402 7000687344 ybga ybga protein (db:pir2.dat) B64806 B64806
Escherichia coli 562 -11534402 7500896737 (sr:e.coli k12 genomic dna,
plasmid pms2) (db:genpept-bct1) (de:e.coli phr gene coding for
deoxyribopyrimidine photolyase.) (nt:unidentified protein orf169) (le:38)
(re:547) (di:direct) ECOPHRORF K01299 g147267 Escherichia coli 562 -11534402
235490 ybga orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 64 of 400 of the completegenome.)
(nt:ol69; 100 pct identical to ybga_ecoli sw: p24252) (le:4870) (re:5379)
(di:direct) AE000174 AE000174 g1786925 Escherichia coli 562 -11534402
5000691754 ybga hypothetical 20.2 kd protein in phrb 5region
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #174) (db:genpept)
(de:escherichia coli genomic dna. (15.7 - 16.0 min).) (nt:orf_id:ol75#2;
similar to swissprot accession) (le:12187) (re:12696) (di:direct) D90709
D90709 g4062300 Escherichia coli 562 -11534402 7502852027 ybga hypothetical
20.2 kd protein in phrb 5region (sr:escherichia coli(strain:k12) dna,
clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna.
(15.9 - 16.3 min).) (nt:orf_id:ol75#2; similar to swissprot accession)
(le:1725) (re:2234) (di:direct) D90710 D90710 g4062304 Escherichia coli 562
-11534402

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844234	10061	32217	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844238	10062	32218	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844266	10063	32219	288	95

Description

GTC ORF with score 184 to: (fn:catalyzes conversion of 4-sulfobenzyl alcohol) (db:genpept-bct2) (de:comamonas testosteroni tsar (tsar), toluenesulfonatemethyl-monooxygenase oxygenase component (tsam), toluenesulfonatemethyl-monooxygenase reductase ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844267	10064	32220	243	80

Description

GTC ORF with score 167 to: (fn:catalyzes conversion of 4-sulfobenzyl alcohol) (db:genpept-bct2) (de:comamonas testosteroni tsar (tsar), toluenesulfonatemethyl-monooxygenase oxygenase component (tsam), toluenesulfonatemethyl-monooxygenase reductase ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844269	10065	32221	267	88

Description

GTC ORF with score 235 to: (fn:catalyzes conversion of 4-sulfobenzyl alcohol) (db:genpept-bct2) (de:comamonas testosteroni tsar (tsar), toluenesulfonatemethyl-monooxygenase oxygenase component (tsam), toluenesulfonatemethyl-monooxygenase reductase ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844276	10066	32222	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844282	10067	32223	939	312

Description

5000691755 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0709 b0709 Escherichia coli 562 -11534403
 7000687349 ybgh (de:hypothetical 54.2 kd protein in phrb-nei intergenic region) (db:swissprot) YBGH_ECOLI P75742 ESCHERICHIA COLI 562 -11534403
 7000687350 ybgh probable proton/oligopeptide symporter ybgh (cl:peptide transporter protein) (db:pir2.dat) D64806 D64806 Escherichia coli 562 -11534403 7500896744 ybgh putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 64 of 400 of the completegenome.) (nt:f493; this 493 aa orf is 58 pct identical (10 gaps)) (le:6944) (re:8425) (di:complement) AE000174 AE000174 g1786927 Escherichia coli 562 -11534403 7502852028 hypothetical protein f485 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).) (nt:orf_id:o175#4; similar to pir accession number) (le:3799) (re:5280) (di:complement) D90710 D90710 g4062305 Escherichia coli 562 -11534403
 6500730545 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0709 b0709 Escherichia coli 562 -11534403

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844310	10068	32224	1050	350

Description

6500730546 ybgi:b0710 hypothetical protein:hypothetical 26.9 kd protein in phrb-nei intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0710 b0710 Escherichia coli 562 -11534404
 5500686478 ybgi (de:hypothetical 26.9 kd protein in phrb-nei intergenic region) (db:swissprot) YBGI_ECOLI P75743 ESCHERICHIA COLI 562 -11534404
 7000687351 ybgi ybgi protein (db:pir2.dat) E64806 E64806 Escherichia coli 562 -11534404 7500896745 ybgi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 64 of 400 of the completegenome.) (nt:o247; this 247 aa orf is 51 pct identical (0 gaps)) (le:8696) (re:9439) (di:direct) AE000174 AE000174 g1786928 Escherichia coli 562 -11534404 5000691756 hypothetical protein hi0105 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).) (nt:orf_id:o175#5; similar to pir accession number) (le:5551) (re:6294) (di:direct) D90710 D90710 g4062306 Escherichia coli 562 -11534404

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844313	10069	32225	918	305

Description

6500730547 ybgj:b0711 hypothetical protein:hypothetical 23.9 kd protein in phrb-nei intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0711 b0711 Escherichia coli 562 -11534405 4000708184 ybgj (de:hypothetical 23.9 kd protein in phrb-nei intergenic region) (db:swissprot) YBGJ_ECOLI P75744 ESCHERICHIA COLI 562 -11534405 7000687352 ybgj ybgj protein (cl:hypothetical protein hi1731) (db:pir2.dat) F64806 F64806 Escherichia coli 562 -11534405 7500896747 ybgj putative carboxylase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 64 of 400 of the completegenome.) (nt:o218; this 218 aa orf is 47 pct identical (1 gap)) (le:9462) (re:10118) (di:direct) AE000174 AE000174 g1786929 Escherichia coli 562 -11534405 5000691757 hypothetical protein hi1731 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).) (nt:orf_id:o175#6; similar to pir accession number) (le:6317) (re:6973) (di:direct) D90710 D90710 g4062307 Escherichia coli 562 -11534405

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844317	10070	32226	528	175

Description

6500730548 ybgk:b0712 hypothetical protein:hypothetical 34.4 kd protein in phrb-nei intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0712 b0712 Escherichia coli 562 -11534406 4000708185 ybgk (de:hypothetical 34.4 kd protein in phrb-nei intergenic region) (db:swissprot) YBGK_ECOLI P75745 ESCHERICHIA COLI 562 -11534406 7000687353 ybgk ybgk protein (cl:hypothetical protein hi1730) (db:pir2.dat) G64806 G64806 Escherichia coli 562 -11534406 7500896749 ybgk putative carboxylase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 64 of 400 of the completegenome.) (nt:o310; this 310 aa orf is 48 pct identical (1 gap)) (le:10112) (re:11044) (di:direct) AE000174 AE000174 g1786930 Escherichia coli 562 -11534406 5000691758 hypothetical protein hi1730 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).) (nt:orf_id:o175#7; similar to pir accession number) (le:6967) (re:7899) (di:direct) D90710 D90710 g4062308 Escherichia coli 562 -11534406

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844336	10071	32227	312	103

Description

6500730549 ybgl:b0713 hypothetical protein:hypothetical 25.8 kd protein in phrb-nei intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0713 b0713 Escherichia coli 562 -11534407
 4000708186 ybgl (de:hypothetical 25.8 kd protein in phrb-nei intergenic region) (db:swissprot) YBGL_ECOLI P75746 ESCHERICHIA COLI 562 -11534407
 7000687354 ybgl ybgl protein (cl:bacillus subtilis lactam utilization protein ycsf) (db:pir2.dat) H64806 H64806 Escherichia coli 562 -11534407
 7500896751 ybgl putative lactam utilization protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 64 of 400 of the completegenome.) (nt:o244; this 244 aa orf is 52 pct identical (0 gaps)) (le:11034) (re:11768) (di:direct) AE000174 AE000174 g1786931 Escherichia coli 562 -11534407 5000691759 lactam utilization protein lamb homolog (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).) (nt:orf_id:o175#8; similar to pir accession number) (le:7889) (re:8623) (di:direct) D90710 D90710 g4062309 Escherichia coli 562 -11534407

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844340	10072	32228	378	125

Description

5000691761 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0715 b0715 Escherichia coli 562 -11534408
 7000687355 abrb (de:abrb protein) (db:swissprot) ABRB_ECOLI P75747 ESCHERICHIA COLI 562 -11534408 7000687356 abrb abrb protein (db:pir2.dat) B64807 B64807 Escherichia coli 562 -11534408 7500876269 abrb putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 64 of 400 of the completegenome.) (nt:f363; this 363 aa orf is 20 pct identical (11 gaps)) (le:12592) (re:13683) (di:complement) AE000174 AE000174 g1786933 Escherichia coli 562 -11534408 7502852029 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).) (nt:orf_id:o175#10) (le:9447) (re:10538) (di:complement) D90710 D90710 g4062311 Escherichia coli 562 -11534408 6500730550 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0715 b0715 Escherichia coli 562 -11534408

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844342	10073	32229	204	67

Description

7000687357 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0716 b0716 Escherichia coli 562 -11534409
 7000687358 ybgo ybgo protein (cl:ybgo protein) (db:pir2.dat) C64807 C64807 Escherichia coli 562 -11534409 7500959900 ybgo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 65 of 400 of the completegenome.) (nt:f362; this 362 aa orf is 23 pct identical (6 gaps)) (le:84) (re:1172) (di:complement) AE000175 AE000175 g1786935 Escherichia coli 562 -11534409 7502852030 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).) (nt:orf_id:ol75#11) (le:10645) (re:11733) (di:complement) D90710 D90710 g4062312 Escherichia coli 562 -11534409 6500730551 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0716 b0716 Escherichia coli 562 -11534409 5000691762 (de:(ecoli_690) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_690 ECOLI_690 Escherichia coli 562 -11534409

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844345	10074	32230	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844368	10075	32231	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844376	10076	32232	2034	677

Description

5000691763 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0717 b0717 Escherichia coli 562 -11534410
7000687359 ybgp (de:precursor) (db:swissprot) YBGP_ECOLI P75749 ESCHERICHIA COLI 562 -11534410 7000687360 ybgp probable molecular chaperone ybgp:probable fimbrial chaperone ybgp (cl:chaperone protein papd) (db:pir2.dat) D64807 D64807 Escherichia coli 562 -11534410 7500896754 ybgp putative chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 65 of 400 of the completegenome.) (nt:f242; this 242 aa orf is 40 pct identical (11 gaps)) (le:1142) (re:1870) (di:complement) AE000175 AE000175 g1786936 Escherichia coli 562 -11534410 7502852031 papd chaperone protein papd precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).) (nt:orf_id:o175#12; similar to pir accession number) (le:11703) (re:12431) (di:complement) D90710 D90710 g4062313 Escherichia coli 562 -11534410 6500730552 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0717 b0717 Escherichia coli 562 -11534410

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844381	10077	32233	486	161

Description

5000691764 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0718 b0718 Escherichia coli 562 -11534411
7000687361 ybgq (de:region precursor) (db:swissprot) YBGQ_ECOLI P75750 ESCHERICHIA COLI 562 -11534411 7000687362 ybgq outer membrane usher protein ybgq precursor (cl:outer membrane usher protein fimd) (db:pir2.dat) E64807 E64807 Escherichia coli 562 -11534411 7500896755 ybgq putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 65 of 400 of the completegenome.) (nt:f818; this 818 aa orf is 38 pct identical (31 gaps)) (le:1885) (re:4341) (di:complement) AE000175 AE000175 g1786937 Escherichia coli 562 -11534411 6500730553 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0718 b0718 Escherichia coli 562 -11534411

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844393	10078	32234	639	212

Description

6500730554 ybgd:b0719 hypothetical fimbrial-like protein in glta
3region:hypothetical fimbrial-like protein in nei-glta intergenic region
precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtd-escherichia
coli) b0719 b0719 Escherichia coli 562 -11534412 110288 ybgd (de:precursor)
(db:swissprot) YBGD_ECOLI P37909 ESCHERICHIA COLI 562 -11534412 7000687345
ybgd ybgd protein precursor (cl:f7-2 fimbrial protein) (db:pir2.dat) F64807
F64807 Escherichia coli 562 -11534412 7500896740 ybgd putative
fimbrial-like protein (fn:putative structure; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 65 of 400 of the
completegenome.) (nt:f188; 98 pct identical to ybgd_ecoli sw: p37909)
(le:4392) (re:4958) (di:complement) AE000175 AE000175 g1786938 Escherichia
coli 562 -11534412 5000691765 ybgd hypothetical fimbrial-like protein in
glta (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175)
(db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).)
(nt:orf_id:o176#1; similar to swissprot accession) (le:14953) (re:15519)
(di:complement) D90710 D90710 g4062315 Escherichia coli 562 -11534412
7502852032 ybgd hypothetical fimbrial-like protein in glta (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #176) (db:genpept) (de:escherichia
coli genomic dna. (16.2 - 16.5 min).) (nt:orf_id:o176#1; similar to
swissprot accession) (le:1453) (re:2019) (di:complement) D90711 D90711
g4062317 Escherichia coli 562 -11534412

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844402	10079	32235	1800	599

Description

GTC ORF with score 522 to: (db:genpept-bct2) (de:myxococcus xanthus
saframycin mx1 synthetase b (safb), saframycinmx1 synthetase a (safa), and
safc genes, complete cds.) (nt:contains two putative amino acid activating)
(le:5491) (re:13308) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844424	10080	32236	1401	466

Description

5000691766 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0725 b0725 Escherichia coli 562 -11534413
7000691059 hypothetical protein b0725 (db:pir2.dat) D64808 D64808
Escherichia coli 562 -11534413 7500959901 b0725 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 65 of 400 of the completegenome.) (nt:o86; this 86 aa orf is 33 pct identical (4 gaps)) (le:10627) (re:10887) (di:direct) AE000175 AE000175
g1786944 Escherichia coli 562 -11534413 6500730555 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0725 b0725 Escherichia coli 562 -11534413

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844449	10081	32237	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844459	10082	32238	1806	601

Description

6500730556 ybgf:b0742 hypothetical 28.2 kd protein in pal-lyst intergenic region:hypothetical 28.2 kd protein in pal-lyst intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0742 b0742 Escherichia coli 562 -11534414 110290 ybgf (de:hypothetical 28.2 kd protein in pal-lyst intergenic region precursor) (db:swissprot) YBGF_ECOLI P45955 ESCHERICHIA COLI 562 -11534414 7000687347 ybgf ybgf protein precursor (db:pir2.dat) E64810 E64810 Escherichia coli 562 -11534414
7500896742 ybgf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 67 of 400 of the completegenome.) (nt:o263; this 263 aa orf is 84 pct identical to the) (le:5383) (re:6174) (di:direct) AE000177 AE000177 g1786963 Escherichia coli 562 -11534414 5000691771 ybgf hypothetical 28.2 kd protein in pal-lyst (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept) (de:escherichia coli genomic dna. (16.5 - 16.9 min).) (nt:orf_id:o178#11; similar to swissprot accession) (le:12788) (re:13579) (di:direct) D90713 D90713 g4062322 Escherichia coli 562 -11534414

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844476	10083	32239	1794	597

Description

6500730557 ybgr:b0752 hypothetical protein:hypothetical 34.7 kd protein in pnuc-arog intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0752 b0752 Escherichia coli 562 -11534415
 4000708187 ybgr (de:hypothetical 34.7 kd protein in pnuc-arog intergenic region) (db:swissprot) YBGR_ECOLI P75757 ESCHERICHIA COLI 562 -11534415
 7000687363 ybgr ybgr protein (cl:zinc transporter znt-2) (db:pir2.dat) H64810 H64810 Escherichia coli 562 -11534415 7500896756 ybgr putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 67 of 400 of the completegenome.) (nt:f313; this 313 aa orf is 40 pct identical (4 gaps)) (le:9667) (re:10608) (di:complement) AE000177 AE000177 g1786966 Escherichia coli 562 -11534415 5000691772 czcd cation efflux system protein czcd. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept) (de:escherichia coli genomic dna. (16.8 - 17.1 min).) (nt:orf_id:ol79#3; similar to pir accession number) (le:3946) (re:4887) (di:complement) D90714 D90714 g4062324 Escherichia coli 562 -11534415

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844481	10084	32240	537	178

Description

6500730558 ybgs:b0753 hypothetical protein:hypothetical 12.9 kd protein in pnuc-arog intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0753 b0753 Escherichia coli 562 -11534416 4000708188 ybgs (de:hypothetical 12.9 kd protein in pnuc-arog intergenic region precursor) (db:swissprot) YBGS_ECOLI P75758 ESCHERICHIA COLI 562 -11534416 7000687364 ybgs ybgs protein precursor (db:pir2.dat) A64811 A64811 Escherichia coli 562 -11534416 7500896757 b0753 putative homeobox protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 68 of 400 of the completegenome.) (nt:f126) (le:87) (re:467) (di:complement) AE000178 AE000178 g1786968 Escherichia coli 562 -11534416 5000691773 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #179) (db:genpept) (de:escherichia coli genomic dna. (16.8 - 17.1 min).) (nt:orf_id:ol79#4) (le:5001) (re:5381) (di:complement) D90714 D90714 g4062325 Escherichia coli 562 -11534416

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844482	10085	32241	252	83

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501844485	10086	32242	342	113

Description

5000691776 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0762 b0762 Escherichia coli 562 -11534417
7000691060 hypothetical protein b0762 (db:pir2.dat) B64812 B64812
Escherichia coli 562 -11534417 7500959902 b0762 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 68 of 400 of the completegenome.) (nt:o49; this 49 aa orf is 50 pct identical to) (le:9923) (re:10072) (di:direct) AE000178 AE000178 g1786977
Escherichia coli 562 -11534417 6500730559 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0762 b0762
Escherichia coli 562 -11534417

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501844490	10087	32243	399	132

Description

5000691780 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0769 b0769 Escherichia coli 562 -11534418
7000687370 ybhh (de:hypothetical 37.1 kd protein in modc-bioa intergenic region) (db:swissprot) YBHH_ECOLI P75762 ESCHERICHIA COLI 562 -11534418
7000687371 ybhh ybhh protein (db:pir2.dat) A64813 A64813 Escherichia coli 562 -11534418 7500896771 ybhh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 69 of 400 of the completegenome.) (nt:o350; this 350 aa orf is 36 pct identical (4 gaps)) (le:5784) (re:6836) (di:direct) AE000179 AE000179 g1786985 Escherichia coli 562 -11534418 7502852033 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept) (de:escherichia coli genomic dna. (17.1 - 17.4 min).) (nt:orf_id:o201#2) (le:7565) (re:8617) (di:direct) D90715 D90715 g4062336 Escherichia coli 562 -11534418 6500730560 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0769 b0769 Escherichia coli 562 -11534418

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844526	10088	32244	1065	354

Description

6500730561 ybhi:b0770 hypothetical protein:hypothetical 51.4 kd protein in modc-bioa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0770 b0770 Escherichia coli 562 -11534419
 5500686481 ybhi (de:hypothetical 51.4 kd protein in modc-bioa intergenic region) (db:swissprot) YBHI_ECOLI P75763 ESCHERICHIA COLI 562 -11534419
 7000687372 ybhi ybhi protein (cl:2-oxoglutarate/malate translocator) (db:pir2.dat) B64813 B64813 Escherichia coli 562 -11534419 7500896772 ybhi putative membrane pump protein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 69 of 400 of the completegenome.) (nt:o477; this 477 aa orf is 27 pct identical (27 gaps)) (le:6912) (re:8345) (di:direct) AE000179 AE000179 g1786986 Escherichia coli 562 -11534419
 5000691781 2-oxoglutarate/malate translocator sodit1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept) (de:escherichia coli genomic dna. (17.1 - 17.4 min).) (nt:orf_id:o201#3; similar to pir accession number) (le:8693) (re:10126) (di:direct) D90715 D90715 g4062337 Escherichia coli 562 -11534419

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844538	10089	32245	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844547	10090	32246	261	86

Description

5000691782 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0771 b0771 Escherichia coli 562 -11534420
 7000687374 ybhj ybhj protein (db:pir2.dat) C64813 C64813 Escherichia coli 562 -11534420 7500896774 ybhj putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 69 of 400 of the completegenome.) (nt:o761; this 761 aa orf is 26 pct identical (82 gaps)) (le:8504) (re:10789) (di:direct) AE000179 AE000179 g1786987 Escherichia coli 562 -11534420 7000687373 ybhj (de:hypothetical 82.6 kd protein in modc-bioa intergenic region) (db:swissprot) YBHJ_ECOLI P75764 ESCHERICHIA COLI 562 -11534420 6500730562 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0771 b0771 Escherichia coli 562 -11534420

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844548	10091	32247	537	178

Description

6500730563 ybhc:b0772 hypothetical protein in bioa 5region:hypothetical 46.1 kd protein in modc-bioa intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0772 b0772 Escherichia coli 562 -11534421 110299 ybhc (de:hypothetical 46.1 kd protein in modc-bioa intergenic region precursor) (db:swissprot) YBHC_ECOLI P46130 ESCHERICHIA COLI 562 -11534421 7000687367 ybhc ybhc protein precursor (cl:pectinesterase pemb) (db:pir2.dat) D64813 D64813 Escherichia coli 562 -11534421 7500896767 ybhc putative pectinesterase (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 70 of 400 of the completegenome.) (nt:f427; 98 pct identical to fragment ybhc_ecoli) (le:147) (re:1430) (di:complement) AE000180 AE000180 g1786989 Escherichia coli 562 -11534421 5000691783 (de:(ecoli_739) (pn:hypothetical protein in bioa 5"region:fragment) (gn:ybhc) (gtcfc:13.7:14.1) (ec:) (ybhc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_739 ECOLI_739 Escherichia coli 562 10122987

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844554	10092	32248	1179	393

Description

6500730564 ybhb:b0773 hypothetical 17.1 kd protein in bioa 5region:hypothetical 17.1 kd protein in modc-bioa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0773 b0773 Escherichia coli 562 -11534422 110298 ybhb (de:hypothetical 17.1 kd protein in modc-bioa intergenic region) (db:swissprot) YBHB_ECOLI P12994 ESCHERICHIA COLI 562 -11534422 7000687366 ybhb conserved hypothetical protein ybhb (cl:conserved hypothetical protein ybhb) (db:pir1.dat) (mp:17 min) Q3ECBA E64813 Escherichia coli 562 -11534422 4000714806 ybhb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 70 of 400 of the completegenome.) (nt:f158; 99 pct identical to ybhb_ecoli sw: p12994) (le:1582) (re:2058) (di:complement) AE000180 AE000180 g1786990 Escherichia coli 562 -11534422 5000691784 orfi protein (fn:unknown, involved in biotin synthesis) (db:genpept-pat) (de:sequence 1 from patent wo9408023.) (le:5098) (re:5574) (di:direct) A38246 A38246 g2294848 Escherichia coli 562 -11534422

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844562	10093	32249	348	115

Description

5000691785 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0780 b0780 Escherichia coli 562 -11534423
7500896775 ybhk (de:hypothetical 32.8 kd protein in uvrB-moaa intergenic region) (db:swissprot) YBHK_ECOLI P75767 ESCHERICHIA COLI 562 -11534423
7000691061 ybhk ybhk protein (cl:escherichia coli ybhk protein) (db:pir2.dat) D64814 D64814 Escherichia coli 562 -11534423 7500896777 ybhk putative structural protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 70 of 400 of the completegenome.) (nt:f302; this 302 aa orf is 34 pct identical (12 gaps)) (le:9888) (re:10796) (di:complement) AE000180 AE000180 g1786997 Escherichia coli 562 -11534423 7502852034 hypothetical protein 1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o203#1; similar to pir accession number) (le:1713) (re:2621) (di:complement) D90716 D90716 g4062340 Escherichia coli 562 -11534423 6500730565 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0780 b0780 Escherichia coli 562 -11534423

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844568	10094	32250	1419	472

Description

5000691786 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0786 b0786 Escherichia coli 562 -11534424
7500896778 ybhl (de:hypothetical 25.9 kd protein in moae-rhle intergenic region) (db:swissprot) YBHL_ECOLI P75768 ESCHERICHIA COLI 562 -11534424
7000691062 ybhl ybhl protein (cl:escherichia coli ybhl protein) (db:pir2.dat) B64815 B64815 Escherichia coli 562 -11534424 7500896780 ybhl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:o234; this 234 aa orf is 26 pct identical (15 gaps)) (le:3069) (re:3773) (di:direct) AE000181 AE000181 g1787004 Escherichia coli 562 -11534424 7502852035 hypothetical protein:23.5k (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o203#7; similar to pir accession number) (le:5858) (re:6562) (di:direct) D90716 D90716 g4062342 Escherichia coli 562 -11534424 6500730566 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0786 b0786 Escherichia coli 562 -11534424

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844581	10095	32251	336	111

Description

5000691787 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0787 b0787 Escherichia coli 562 -11534425
 7500896781 ybhm (de:hypothetical 26.1 kd protein in moae-rhle intergenic region) (db:swissprot) YBHM_ECOLI P75769 ESCHERICHIA COLI 562 -11534425
 7000691063 ybhm ybhm protein (db:pir2.dat) C64815 C64815 Escherichia coli 562 -11534425 7500896783 ybhm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completgenome.) (nt:o237; this 237 aa orf is 24 pct identical (2 gaps)) (le:3978) (re:4691) (di:direct) AE000181 AE000181 g1787005 Escherichia coli 562 -11534425 7502852036 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o203#9) (le:6767) (re:7480) (di:direct) D90716 D90716 g4062344 Escherichia coli 562 -11534425 6500730567 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0787 b0787 Escherichia coli 562 -11534425

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844582	10096	32252	1335	445

Description

5000691788 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0788 b0788 Escherichia coli 562 -11534426
 7500896784 ybhn (de:hypothetical 35.9 kd protein in moae-rhle intergenic region) (db:swissprot) YBHN_ECOLI P75770 ESCHERICHIA COLI 562 -11534426
 7000691064 ybhn ybhn protein (db:pir2.dat) D64815 D64815 Escherichia coli 562 -11534426 7500896786 ybhn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completgenome.) (nt:f318; this 318 aa orf is 28 pct identical (12 gaps)) (le:4727) (re:5683) (di:complement) AE000181 AE000181 g1787006 Escherichia coli 562 -11534426 7502852037 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o203#10) (le:7516) (re:8472) (di:complement) D90716 D90716 g4062345 Escherichia coli 562 -11534426 6500730568 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0788 b0788 Escherichia coli 562 -11534426

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844609	10097	32253	546	181

Description

5000691789 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0789 b0789 Escherichia coli 562 -11534427
 7500896787 ybho (de:hypothetical 47.6 kd protein in moae-rhle intergenic region) (db:swissprot) YBHO_ECOLI P75771 ESCHERICHIA COLI 562 -11534427
 7000691065 ybho ybho protein:protein b0789 (db:pir2.dat) E64815 E64815 Escherichia coli 562 -11534427 7500896789 ybho putative synthetase (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completgenome.) (nt:f413; this 413 aa orf is 28 pct identical (11 gaps)) (le:5683) (re:6924) (di:complement) AE000181 AE000181 g1787007 Escherichia coli 562 -11534427 7502852038 hypothetical 54.3 kd protein in lpd-3 5region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o203#11; similar to swissprot accession) (le:8472) (re:9713) (di:complement) D90716 D90716 g4062346 Escherichia coli 562 -11534427 6500730569 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0789 b0789 Escherichia coli 562 -11534427

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844615	10098	32254	849	282

Description

5000691790 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0790 b0790 Escherichia coli 562 -11534428
 7500896790 ybhp (de:hypothetical 28.8 kd protein in moae-rhle intergenic region) (db:swissprot) YBHP_ECOLI P75772 ESCHERICHIA COLI 562 -11534428
 7000691066 ybhp ybhp protein (db:pir2.dat) F64815 F64815 Escherichia coli 562 -11534428 7500896792 ybhp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completgenome.) (nt:f253; this 253 aa orf is 35 pct identical (5 gaps)) (le:6921) (re:7682) (di:complement) AE000181 AE000181 g1787008 Escherichia coli 562 -11534428 7502852039 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o203#12) (le:9710) (re:10471) (di:complement) D90716 D90716 g4062347 Escherichia coli 562 -11534428 6500730570 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0790 b0790 Escherichia coli 562 -11534428

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844618	10099	32255	336	111

Description

GTC ORF with score 117 to: (sr:herpes simplex virus type 1 (strain kos(m)) dna derived fro) (db:genpept-vr1) (de:herpes simplex virus type one (hsv-1) latency associated transcript(lat).) (nt:latency associated transcript (lat) orf-2) (le:1160) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844620	10100	32256	1572	523

Description

5000691791 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0791 b0791 Escherichia coli 562 -11534429
 7500896793 ybhq (de:hypothetical 15.5 kd protein in moae-rhle intergenic region) (db:swissprot) YBHQ_ECOLI P75773 ESCHERICHIA COLI 562 -11534429
 7000691067 ybhq ybhq protein (db:pir2.dat) G64815 G64815 Escherichia coli 562 -11534429 7500896795 ybhq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:o136; this 136 aa orf is 24 pct identical (0 gaps)) (le:7815) (re:8225) (di:direct) AE000181 AE000181 g1787009 Escherichia coli 562 -11534429 7502852040 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o203#13) (le:10604) (re:11014) (di:direct) D90716 D90716 g4062348 Escherichia coli 562 -11534429 6500730571 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0791 b0791 Escherichia coli 562 -11534429

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844637	10101	32257	579	193

Description

5000691792 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0792 b0792 Escherichia coli 562 -11534430
 7500896796 ybhr (de:hypothetical 41.6 kd protein in moae-rhle intergenic region) (db:swissprot) YBHR_ECOLI P75774 ESCHERICHIA COLI 562 -11534430
 7000691068 ybhr ybhr protein (db:pir2.dat) H64815 H64815 Escherichia coli 562 -11534430 7500896798 ybhr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:f368; this 368 aa orf is 22 pct identical (5 gaps)) (le:8187) (re:9293) (di:complement) AE000181 AE000181 g1787010 Escherichia coli 562 -11534430 6500730572 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0792 b0792 Escherichia coli 562 -11534430

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844650	10102	32258	1269	422

Description

5000691793 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0793 b0793 Escherichia coli 562 -11534431
7500896799 ybhs (de:hypothetical 42.1 kd protein in moae-rhle intergenic region) (db:swissprot) YBHS_ECOLI P75775 ESCHERICHIA COLI 562 -11534431
7000691069 ybhs ybhs protein (db:pir2.dat) A64816 A64816 Escherichia coli 562 -11534431 7500896801 ybhs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:f377; this 377 aa orf is 31 pct identical (8 gaps)) (le:9304) (re:10437) (di:complement) AE000181 AE000181 g1787011 Escherichia coli 562 -11534431 7502852041 hypothetical protein f648 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o203#16; similar to pir accession number) (le:12092) (re:13225) (di:complement) D90716 D90716 g4062351 Escherichia coli 562 -11534431 6500730573 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0793 b0793 Escherichia coli 562 -11534431

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844679	10103	32259	1503	501

Description

5000691794 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0794 b0794 Escherichia coli 562 -11534432
7000691070 ybhf abc-type transport protein ybhf (cl:atp-binding cassette homology) (db:pir2.dat) B64816 B64816 Escherichia coli 562 -11534432
7500959903 ybhf putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:f583; this 583 aa orf is 44 pct identical (7 gaps)) (le:10430) (re:12181) (di:complement) AE000181 AE000181 g1787012 Escherichia coli 562 -11534432 7502852042 atp binding cassette transporter abc2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o203#17; similar to pir accession number) (le:13218) (re:14969) (di:complement) D90716 D90716 g4062352 Escherichia coli 562 -11534432 6500730574 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0794 b0794 Escherichia coli 562 -11534432

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844691	10104	32260	2250	750

Description

5000691795 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0795 b0795 Escherichia coli 562 -11534433
7000691071 hypothetical protein b0795 precursor (db:pir2.dat) C64816 C64816 Escherichia coli 562 -11534433 7500959904 b0795 putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:f332; this 332 aa orf is 30 pct identical (7 gaps)) (le:12159) (re:13157) (di:complement) AE000181 AE000181 g1787013 Escherichia coli 562 -11534433
7502852043 hypothetical protein f355 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o204#1; similar to pir accession number) (le:14947) (re:15945) (di:complement) D90716 D90716 g4062353 Escherichia coli 562 -11534433 7502852044 hypothetical protein f355 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #204) (db:genpept) (de:escherichia coli genomic dna. (17.9 - 18.2 min).) (nt:orf_id:o204#1; similar to pir accession number) (le:276) (re:1274) (di:complement) D90717 D90717 g4062358 Escherichia coli 562 -11534433 6500730575 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0795 b0795 Escherichia coli 562 -11534433

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844703	10105	32261	822	273

Description

6500730576 ybih:b0796 hypothetical transcriptional regulator in moae-rhle intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0796 b0796 Escherichia coli 562 -11534434
7000691850 ybih probable transcription regulator ybih (db:pir2.dat) D64816 D64816 Escherichia coli 562 -11534434 7500960367 ybih putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 71 of 400 of the completegenome.) (nt:f227; 100 pct identical to 103 residues of) (le:13157) (re:13840) (di:complement) AE000181 AE000181 g1787014 Escherichia coli 562 -11534434 5000691796 (de:(ecoli_763) (pn:hypothetical transcriptional regulator in moae-rhle intergenic region:fragment) (gn:ybih) (gtcfc:13.7:14.1) (ec:) (ybih_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) ECOLI_763 ECOLI_763 Escherichia coli 562 10123002

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844704	10106	32262	639	212

Description

6500730577 ybia:b0798 hypothetical 18.7 kd protein in rhle-ding/rarb intergenic region:hypothetical 18.7 kd protein in rhle-ding intergenic region:f160 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0798 b0798 Escherichia coli 562 -11534435 110306 ybia (de:hypothetical 18.7 kd protein in rhle-ding intergenic region (f160)) (db:swissprot) YBIA_ECOLI P30176 ESCHERICHIA COLI 562 -11534435 7000687375 ybia ybia protein (db:pir2.dat) F64816 F64816 Escherichia coli 562 -11534435 7500896808 ybia (fn:unknown) (db:genpept-bct1) (de:escherichia coli putative atp-dependent rna helicase (rhle),putative dna helicase (ding), ybia, ybib, and ybic genes, completedcs.) (nt:swissprot accession number p30176) (le:2135) (re:2617) (di:complement) ECORHLEA L02123 g147599 Escherichia coli 562 -11534435 235788 ybia orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 72 of 400 of the completegenome.) (nt:f160; 100 pct identical to ybia_ecoli sw: p30176) (le:1735) (re:2217) (di:complement) AE000182 AE000182 g1787017 Escherichia coli 562 -11534435 5000691797 ybia hypothetical 18.7 kd protein in rhle-ding/rarb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #203) (db:genpept) (de:escherichia coli genomic dna. (17.6 - 18.0 min).) (nt:orf_id:o204#4; similar to swissprot accession) (le:18441) (re:18923) (di:complement) D90716 D90716 g4062356 Escherichia coli 562 -11534435 7502852045 ybia hypothetical 18.7 kd protein in rhle-ding/rarb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #204) (db:genpept) (de:escherichia coli genomic dna. (17.9 - 18.2 min).) (nt:orf_id:o204#4; similar to swissprot accession) (le:3770) (re:4252) (di:complement) D90717 D90717 g4062360 Escherichia coli 562 -11534435

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844705	10107	32263	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844711	10108	32264	582	193

Description

6500730578 ybib:b0800 hypothetical 35.0 kd protein in ding/rarb
3region:hypothetical 35.0 kd protein in ding-glnq intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0800
b0800 Escherichia coli 562 -11534436 110307 ybib (de:hypothetical 35.0 kd
protein in ding-glnq intergenic region) (db:swissprot) YBIB_ECOLI P30177
ESCHERICHIA COLI 562 -11534436 7000687376 ybib ybib protein (db:pir2.dat)
H64816 H64816 Escherichia coli 562 -11534436 7500896809 ybib (fn:unknown)
(db:genpept-bct1) (de:escherichia coli putative atp-dependent rna helicase
(rhle),putative dna helicase (ding), ybia, ybib, and ybic genes,
completedcds.) (nt:some similarity to anthranilate) (le:4915) (re:5877)
(di:direct) ECORHLEA L02123 g147602 Escherichia coli 562 -11534436 235790
ybib putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 72 of 400 of the completegenome.)
(nt:o320; 99 pct identical to ybib_ecoli sw: p30177) (le:4515) (re:5477)
(di:direct) AE000182 AE000182 g1787019 Escherichia coli 562 -11534436
5000691798 ybib hypothetical 35.0 kd protein in ding/rarb (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #204) (db:genpept) (de:escherichia
coli genomic dna. (17.9 - 18.2 min).) (nt:orf_id:o204#6; similar to
swissprot accession) (le:6550) (re:7512) (di:direct) D90717 D90717 g4062361
Escherichia coli 562 -11534436

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844715	10109	32265	2082	693

Description

GTC ORF with score 104 to: (sr:caenorhabditis elegans strain=bristol n2)
(db:genpept-inv) (de:caenorhabditis elegans cosmid c34d4.) (nt:coded for by
c. elegans cdna yk34b1.5; coded for by) (le:18124:18287:18407)
(re:18231:18360:18674) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844735	10110	32266	345	114

Description

6500730579 ybic:b0801 hypothetical 38.9 kd protein in ding/rarb
3region:hypothetical 38.9 kd protein in ding-glnq intergenic region:o361
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0801
b0801 Escherichia coli 562 -11534437 110308 ybic (de:hypothetical 38.9 kd
protein in ding-glnq intergenic region (o361)) (db:swissprot) YBIC_ECOLI
P30178 ESCHERICHIA COLI 562 -11534437 7000687377 ybic malate dehydrogenase
homolog ybic (cl:ybic protein) (db:pir2.dat) A64817 A64817 Escherichia coli
562 -11534437 7500896810 ybic putative dehydrogenase (fn:putative enzyme;
not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
72 of 400 of the completegenome.) (nt:o361; 99 pct identical to ybic_ecoli
sw: p30178) (le:5618) (re:6703) (di:direct) AE000182 AE000182 g1787020
Escherichia coli 562 -11534437 5000691799 ybic hypothetical 38.9 kd protein
in ding/rarb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #204)
(db:genpept) (de:escherichia coli genomic dna. (17.9 - 18.2 min).)
(nt:orf_id:o204#7; similar to swissprot accession) (le:7653) (re:8738)
(di:direct) D90717 D90717 g4062362 Escherichia coli 562 -11534437

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844741	10111	32267	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844761	10112	32268	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844771	10113	32269	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844784	10114	32270	1125	374

Description

6500730580 ybij:b0802 hypothetical 8.6 kd protein in ding/rarb
3region:hypothetical 8.6 kd protein in ding-glnq intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0802
b0802 Escherichia coli 562 -11534438 110312 ybij (de:hypothetical 8.6 kd
protein in ding-glnq intergenic region precursor) (db:swissprot) YBIJ_ECOLI
P41038 ESCHERICHIA COLI 562 -11534438 7000687379 ybij ybij protein
precursor (cl:conserved hypothetical protein b3238) (db:pir2.dat) B64817
B64817 Escherichia coli 562 -11534438 7500896813 ybij orf:hypothetical
protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
section 72 of 400 of the completegenome.) (nt:f86; 100 pct identical to
ybij_ecoli sw: p41038) (le:6932) (re:7192) (di:complement) AE000182 AE000182
g1787021 Escherichia coli 562 -11534438 5000691800 ybij hypothetical 8.6 kd
protein in ding/rarb (sr:escherichia coli(strain:k12) dna, clone:kohara
clone #204) (db:genpept) (de:escherichia coli genomic dna. (17.9 - 18.2
min).) (nt:orf_id:o204#8; similar to swissprot accession) (le:8967)
(re:9227) (di:complement) D90717 D90717 g4062363 Escherichia coli 562
-11534438

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844797	10115	32271	189	62

Description

GTC ORF with score 144 to: (db:genpept-pln1) (ec:3.2.1.28) (de:emericella
nidulans neutral trehalase (treb) gene, complete cds.)
(nt:alpha,alpha-trehalase; treb) (le:513:743:873:1063:2847)
(re:677:815:998:2791:3000) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844809	10116	32272	282	93

Description

6500730581 ybii:b0803 hypothetical 9.8 kd protein in ding/rarb
3region:hypothetical 9.8 kd protein in ding-glnq intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0803
b0803 Escherichia coli 562 -11534439 110311 ybii (de:hypothetical 9.8 kd
protein in ding-glnq intergenic region) (db:swissprot) YBII_ECOLI P41039
ESCHERICHIA COLI 562 -11534439 7000687378 ybii ybii protein (cl:trar
protein) (db:pir2.dat) C64817 Escherichia coli 562 -11534439
7500896812 ybii orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 72 of 400 of the
completegenome.) (nt:f88; 100 pct identical to ybii_ecoli sw: p41039)
(le:7457) (re:7723) (di:complement) AE000182 AE000182 g1787022 Escherichia
coli 562 -11534439 5000691801 ybii hypothetical 9.8 kd protein in ding/rarb
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #204) (db:genpept)
(de:escherichia coli genomic dna. (17.9 - 18.2 min).) (nt:orf_id:o204#9;
similar to swissprot accession) (le:9492) (re:9758) (di:complement) D90717
D90717 g4062364 Escherichia coli 562 -11534439

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844810	10117	32273	1839	612

Description

GTC ORF with score 2670 to: (db:genpept-pln1) (ec:3.2.1.28) (de:emericeella
nidulans neutral trehalase (treb) gene, complete cds.)
(nt:alpha,alpha-trehalase; treb) (le:513:743:873:1063:2847)
(re:677:815:998:2791:3000) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844824	10118	32274	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844826	10119	32275	717	238

Description

5000691802 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0804 b0804 Escherichia coli 562 -11534440
7500896835 ybix (de:hypothetical 26.9 kd protein in ding-glnq intergenic
region) (db:swissprot) YBIX_ECOLI P75779 ESCHERICHIA COLI 562 -11534440
7000691072 ybix ybix protein (db:pir2.dat) D64817 D64817 Escherichia coli
562 -11534440 7500896837 ybix putative enzyme (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 72 of
400 of the completegenome.) (nt:f237; this 237 aa orf is 26 pct identical (4
gaps)) (le:7797) (re:8510) (di:complement) AE000182 AE000182 g1787023
Escherichia coli 562 -11534440 7502852046 (sr:escherichia coli(strain:k12)
dna, clone:kohara clone #204) (db:genpept) (de:escherichia coli genomic dna.
(17.9 - 18.2 min).) (nt:orf_id:o204#10) (le:9832) (re:10545) (di:complement)
D90717 D90717 g4062365 Escherichia coli 562 -11534440 6500730582
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b0804 b0804 Escherichia coli 562 -11534440

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844828	10120	32276	303	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844832	10121	32277	1155	384

Description

5000691803 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0805 b0805 Escherichia coli 562 -11534441
 7502852047 ybil (de:precursor) (db:swissprot) YBIL_ECOLI P75780 ESCHERICHIA COLI 562 -11534441 7000691073 probable membrane protein b0805 (db:pir2.dat) E64817 E64817 Escherichia coli 562 -11534441 7500959905 b0805 putative outer membrane receptor for iron (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 72 of 400 of the completegenome.) (nt:f760; this 760 aa orf is 25 pct identical (75 gaps)) (le:8516) (re:10798) (di:complement) AE000182 AE000182 g1787024 Escherichia coli 562 -11534441 7502852048 fpta fe iii -pyochelin receptor fpta precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #204) (db:genpept) (de:escherichia coli genomic dna. (17.9 - 18.2 min).) (nt:orf_id:o205#1; similar to pir accession number) (le:10551) (re:12833) (di:complement) D90717 D90717 g4062366 Escherichia coli 562 -11534441 7502852049 fpta fe iii -pyochelin receptor fpta precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna. (18.1 - 18.4 min).) (nt:orf_id:o205#1; similar to pir accession number) (le:567) (re:2849) (di:complement) D90718 D90718 g4062371 Escherichia coli 562 -11534441 6500730583 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0805 b0805 Escherichia coli 562 -11534441

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844834	10122	32278	441	147

Description

GTC ORF with score 140 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid r148.) (nt:contains similarity to drosophila dna-binding) (le:95:939:2277:3336:4475) (re:435:1303:2489:4014:4559) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844851	10123	32279	492	164

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844863	10124	32280	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844864	10125	32281	276	91

Description

5000691804 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0806 b0806 Escherichia coli 562 -11534442

7500896815 ybim (de:hypothetical 14.6 kd protein in ding-glnq intergenic region) (db:swissprot) YBIM_ECOLI P75781 ESCHERICHIA COLI 562 -11534442

7000691074 ybim probable membrane protein ybim (db:pir2.dat) F64817 F64817 Escherichia coli 562 -11534442 7500896817 ybim orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl1655 section 73 of 400 of the completegenome.) (nt:fl34; 46 pct identical to 86 amino acids of) (le:163) (re:567) (di:complement) AE000183 AE000183 g1787026 Escherichia coli 562 -11534442 7502852050 hypothetical 8.6 kd protein in ding/rarb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #204) (db:genpept) (de:escherichia coli genomic dna. (17.9 - 18.2 min).) (nt:orf_id:o205#2; similar to swissprot accession) (le:13098) (re:13502) (di:complement) D90717 D90717 g4062367 Escherichia coli 562 -11534442

7502852051 hypothetical 8.6 kd protein in ding/rarb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna. (18.1 - 18.4 min).) (nt:orf_id:o205#2; similar to swissprot accession) (le:3114) (re:3518) (di:complement) D90718 D90718 g4062372 Escherichia coli 562 -11534442 6500730584 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0806 b0806 Escherichia coli 562 -11534442

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844867	10126	32282	615	204

Description

5000691805 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0807 b0807 Escherichia coli 562 -11534443
7000691075 ybin probable membrane protein ybin (db:pir2.dat) G64817 G64817 Escherichia coli 562 -11534443 7500896820 ybin orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 73 of 400 of the completegenome.) (nt:o335; this 335 aa orf is 24 pct identical (2 gaps)) (le:618) (re:1625) (di:direct) AE000183 AE000183 g1787027 Escherichia coli 562 -11534443 7502852052 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #204) (db:genpept) (de:escherichia coli genomic dna. (17.9 - 18.2 min).) (nt:orf_id:o205#3) (le:13553) (re:14560) (di:direct) D90717 D90717 g4062368 Escherichia coli 562 -11534443 7502852053 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna. (18.1 - 18.4 min).) (nt:orf_id:o205#3) (le:3569) (re:4576) (di:direct) D90718 D90718 g4062373 Escherichia coli 562 -11534443 7500896818 ybin (de:hypothetical 37.3 kd protein in ding-glnq intergenic region) (db:swissprot) YBIN_ECOLI P75782 ESCHERICHIA COLI 562 -11534443 6500730585 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0807 b0807 Escherichia coli 562 -11534443

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844869	10127	32283	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844885	10128	32284	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844896	10129	32285	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844898	10130	32286	663	220

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844928	10131	32287	1575	524

Description

5000691806 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0808 b0808 Escherichia coli 562 -11534444
 7000691076 ybio probable membrane protein ybio (db:pir2.dat) H64817 H64817 Escherichia coli 562 -11534444 7500896823 ybio putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 73 of 400 of the completegenome.) (nt:f786; this 786 aa orf is 26 pct identical (13 gaps)) (le:1622) (re:3982) (di:complement) AE000183 AE000183 g1787028 Escherichia coli 562 -11534444 7500896821 ybio (de:hypothetical 86.8 kd protein in ding-glnq intergenic region) (db:swissprot) YBIO_ECOLI P75783 ESCHERICHIA COLI 562 -11534444 6500730586 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0808 b0808 Escherichia coli 562 -11534444

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844929	10132	32288	564	187

Description

6500730587 ybif:b0813 hypothetical 31.3 kd protein in dps/pexb 5region:hypothetical 31.3 kd protein in dps-ompx intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0813 b0813 Escherichia coli 562 -11534445 7000690935 ybif probable membrane protein ybif (db:pir2.dat) E64818 E64818 Escherichia coli 562 -11534445 7500959804 ybif putative transmembrane subunit (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 73 of 400 of the completegenome.) (nt:f295; 99 pct identical to ybif_ecoli sw: p36545) (le:7577) (re:8464) (di:complement) AE000183 AE000183 g1787033 Escherichia coli 562 -11534445 5000691807 ybif hypothetical protein 1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna. (18.1 - 18.4 min).) (nt:orf_id:o206#5; similar to pir accession number) (le:10527) (re:11414) (di:complement) D90718 D90718 g4062377 Escherichia coli 562 -11534445 7502852054 ybif hypothetical protein 1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf_id:o206#5; similar to pir accession number) (le:3742) (re:4629) (di:complement) D90719 D90719 g4062382 Escherichia coli 562 -11534445

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844931	10133	32289	555	184

Description

6500730588 ybip:b0815 hypothetical protein:hypothetical 59.7 kd protein in ompx-moeb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0815 b0815 Escherichia coli 562 -11534446
5500686482 ybip (de:hypothetical 59.7 kd protein in ompx-moeb intergenic region) (db:swissprot) YBIP_ECOLI P75785 ESCHERICHIA COLI 562 -11534446
7000687381 ybip probable membrane protein ybip (db:pir2.dat) G64818 G64818 Escherichia coli 562 -11534446 7500896824 ybip putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 73 of 400 of the completegenome.) (nt:f527; this 527 aa orf is 32 pct identical (21 gaps)) (le:9381) (re:10964) (di:complement) AE000183 AE000183 g1787035 Escherichia coli 562 -11534446 5000691809 hypothetical protein hi1005 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna. (18.1 - 18.4 min).) (nt:orf_id:o206#7; similar to pir accession number) (le:12331) (re:13914) (di:complement) D90718 D90718 g4062378 Escherichia coli 562 -11534446
7502852055 hypothetical protein hi1005 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf_id:o206#7; similar to pir accession number) (le:5546) (re:7129) (di:complement) D90719 D90719 g4062383 Escherichia coli 562 -11534446

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844937	10134	32290	414	137

Description

5000691810 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0816 b0816 Escherichia coli 562 -11534447
7000691077 probable membrane protein b0816 (db:pir2.dat) H64818 H64818 Escherichia coli 562 -11534447 7500959906 b0816 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 74 of 400 of the completegenome.) (nt:o89; this 89 aa orf is 26 pct identical (0 gaps)) (le:67) (re:336) (di:direct) AE000184 AE000184 g1787037 Escherichia coli 562 -11534447 6500730589 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0816 b0816 Escherichia coli 562 -11534447

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844940	10135	32291	609	202

Description

5000691811 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0817 b0817 Escherichia coli 562 -11534448
7000691078 hypothetical protein b0817 (db:pir2.dat) A64819 A64819
Escherichia coli 562 -11534448 7500959907 b0817 putative toxin (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 74 of 400 of the completegenome.) (nt:o155; residues 40-136 are 38 pct identical to) (le:579) (re:1046) (di:direct) AE000184 AE000184 g1787038 Escherichia coli 562 -11534448 7502852056 hypothetical 16.7 kd protein in gcvt-spoiiiaa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna. (18.1 - 18.4 min).) (nt:orf_id:o206#8; similar to swissprot accession) (le:14500) (re:14967) (di:direct) D90718 D90718 g4062379 Escherichia coli 562 -11534448 7502852057 hypothetical 16.7 kd protein in gcvt-spoiiiaa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf_id:o206#8; similar to swissprot accession) (le:7715) (re:8182) (di:direct) D90719 D90719 g4062384 Escherichia coli 562 -11534448 6500730590 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0817 b0817 Escherichia coli 562 -11534448

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844941	10136	32292	1608	535

Description

6500730591 ybir:b0818 hypothetical protein:hypothetical 41.2 kd protein im ompx-moeb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0818 b0818 Escherichia coli 562 -11534449
4000708189 ybir (de:hypothetical 41.2 kd protein im ompx-moeb intergenic region) (db:swissprot) YBIR_ECOLI P75788 ESCHERICHIA COLI 562 -11534449
7000687382 ybir probable membrane protein ybir (db:pir2.dat) B64819 B64819 Escherichia coli 562 -11534449 7500896825 ybir orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 74 of 400 of the completegenome.) (nt:o372; this 372 aa orf is 26 pct identical (21 gaps)) (le:1043) (re:2161) (di:direct) AE000184 AE000184 g1787039 Escherichia coli 562 -11534449 5000691812 hypothetical protein mj0456 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf_id:o207#1; similar to pir accession number) (le:8179) (re:9297) (di:direct) D90719 D90719 g4062385 Escherichia coli 562 -11534449 7502852058 hypothetical protein mj0456 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #207) (db:genpept) (de:escherichia coli genomic dna. (18.4 - 18.8 min).) (nt:orf_id:o207#1; similar to pir accession number) (le:208) (re:1326) (di:direct) D90720 D90720 g4062392 Escherichia coli 562 -11534449

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844946	10137	32293	1128	375

Description

5000691813 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0819 b0819 Escherichia coli 562 -11534450
7500896826 ybis (de:30.9 kd protein in ompx-moeb intergenic region precursor) (db:swissprot) YBIS_ECOLI P75789 ESCHERICHIA COLI 562 -11534450
7000691079 ybis ybis protein precursor (cl:conserved hypothetical protein b0819) (db:pir2.dat) C64819 C64819 Escherichia coli 562 -11534450
7500896828 ybis orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 74 of 400 of the completegenome.) (nt:f306; this 306 aa orf is 66 pct identical (0 gaps)) (le:2220) (re:3140) (di:complement) AE000184 AE000184 g1787040 Escherichia coli 562 -11534450 7502852059 erfk protein erfk/srfk precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf_id:o207#2; similar to swissprot accession) (le:9356) (re:10276) (di:complement) D90719 D90719 g4062386 Escherichia coli 562 -11534450 7502852060 erfk protein erfk/srfk precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #207) (db:genpept) (de:escherichia coli genomic dna. (18.4 - 18.8 min).) (nt:orf_id:o207#2; similar to swissprot accession) (le:1385) (re:2305) (di:complement) D90720 D90720 g4062393 Escherichia coli 562 -11534450 6500730592 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0819 b0819 Escherichia coli 562 -11534450

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501844961	10138	32294	249	82

Description

5000691814 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0820 b0820 Escherichia coli 562 -11534451
7500896829 ybit (de:hypothetical abc transporter atp-binding protein ybit) (db:swissprot) YBIT_ECOLI P75790 ESCHERICHIA COLI 562 -11534451 7000691080 ybit probable abc-type transport protein ybit (cl:atp-binding cassette homology) (db:pir2.dat) D64819 D64819 Escherichia coli 562 -11534451
7500896831 ybit putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 74 of 400 of the completegenome.) (nt:o530; this 530 aa orf is 33 pct identical (14 gaps)) (le:3359) (re:4951) (di:direct) AE000184 AE000184 g1787041 Escherichia coli 562 -11534451 7502852061 hypothetical protein hi0658 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf_id:o207#3; similar to pir accession number) (le:10495) (re:12087) (di:direct) D90719 D90719 g4062387 Escherichia coli 562 -11534451
7502852062 hypothetical protein hi0658 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #207) (db:genpept) (de:escherichia coli genomic dna. (18.4 - 18.8 min).) (nt:orf_id:o207#3; similar to pir accession number) (le:2524) (re:4116) (di:direct) D90720 D90720 g4062394 Escherichia coli 562 -11534451 6500730593 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0820 b0820 Escherichia coli 562 -11534451

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844964	10139	32295	477	159

Description

5000691815 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0821 b0821 Escherichia coli 562 -11534452
7500896832 ybiu (de:hypothetical 47.3 kd protein in ompx-moeb intergenic region) (db:swissprot) YBIU_ECOLI P75791 ESCHERICHIA COLI 562 -11534452
7000691081 ybiu ybiu protein (db:pir2.dat) E64819 E64819 Escherichia coli 562 -11534452 7500896834 ybiu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 74 of 400 of the completegenome.) (nt:f421; this 421 aa orf is 31 pct identical (3 gaps)) (le:5192) (re:6457) (di:complement) AE000184 AE000184 g1787042 Escherichia coli 562 -11534452 7502852063 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf_id:o207#4) (le:12328) (re:13593) (di:complement) D90719 D90719 g4062388 Escherichia coli 562 -11534452 7502852064 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #207) (db:genpept) (de:escherichia coli genomic dna. (18.4 - 18.8 min).) (nt:orf_id:o207#4) (le:4357) (re:5622) (di:complement) D90720 D90720 g4062395 Escherichia coli 562 -11534452 6500730594 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0821 b0821 Escherichia coli 562 -11534452

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844965	10140	32296	498	165

Description

5000691816 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0822 b0822 Escherichia coli 562 -11534453
7000691082 hypothetical protein b0822 (db:pir2.dat) F64819 F64819 Escherichia coli 562 -11534453 7500959908 b0822 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 74 of 400 of the completegenome.) (nt:f271; this 271 aa orf is 24 pct identical (16 gaps)) (le:6609) (re:7424) (di:complement) AE000184 AE000184 g1787043 Escherichia coli 562 -11534453 7502852065 hypothetical protein 1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf_id:o207#5; similar to pir accession number) (le:13745) (re:14560) (di:complement) D90719 D90719 g4062389 Escherichia coli 562 -11534453 7502852066 hypothetical protein 1 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #207) (db:genpept) (de:escherichia coli genomic dna. (18.4 - 18.8 min).) (nt:orf_id:o207#5; similar to pir accession number) (le:5774) (re:6589) (di:complement) D90720 D90720 g4062396 Escherichia coli 562 -11534453 6500730595 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0822 b0822 Escherichia coli 562 -11534453

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844969	10141	32297	1287	428

Description

5000691817 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0823 b0823 Escherichia coli 562 -11534454
7500887898 ybiw (ec:2.3.1.54) (de:lyase 3)) (db:swissprot) PFLF_ECOLI
P75793 ESCHERICHIA COLI 562 -11534454 7000691083 ybiw probable formate
c-acetyltransferase::pyruvate formate-lyase 3 (cl:formate
c-acetyltransferase 2:glycyl radical homology) (ec:2.3.1.54) (db:pir2.dat)
G64819 G64819 Escherichia coli 562 -11534454 7500887900 ybiw putative
formate acetyltransferase (fn:putative enzyme; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 74 of 400 of the
completegenome.) (nt:f810; this 810 aa orf is 38 pct identical (43 gaps))
(le:7570) (re:10002) (di:complement) AE000184 AE000184 g1787044 Escherichia
coli 562 -11534454 7502852067 pflD formate acetyltransferase 2 ec 2.3.1.54
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #207) (db:genpept)
(de:escherichia coli genomic dna. (18.4 - 18.8 min).) (nt:orf_id:o207#6;
similar to swissprot accession) (le:6735) (re:9167) (di:complement) D90720
D90720 g4062397 Escherichia coli 562 -11534454 6500730596 hypothetical
protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)
b0823 b0823 Escherichia coli 562 -11534454

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844986	10142	32298	858	286

Description

5000691818 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0824 b0824 Escherichia coli 562 -11534455
7500887895 ybiy (ec:1.97.1.4) (de:putative pyruvate formate-lyase 3
activating enzyme,) (db:swissprot) PFLE_ECOLI P75794 ESCHERICHIA COLI 562
-11534455 7000691084 ybiy probable pyruvate formate-lyase activating
enzyme:3 (cl:conserved hypothetical protein b0824) (ec:1.97.1.4)
(db:pir2.dat) H64819 H64819 Escherichia coli 562 -11534455 7500887897 ybiy
putative pyruvate formate-lyase 2 activating (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 74 of
400 of the completegenome.) (nt:f308; this 308 aa orf is 35 pct identical
(35 gaps)) (le:10008) (re:10934) (di:complement) AE000184 AE000184 g1787045
Escherichia coli 562 -11534455 7502852068 pflC iron-dependent pyruvate
formate-lyase-activating (sr:escherichia coli(strain:k12) dna, clone:kohara
clone #207) (db:genpept) (de:escherichia coli genomic dna. (18.4 - 18.8
min).) (nt:orf_id:o207#7; similar to pir accession number) (le:9173)
(re:10099) (di:complement) D90720 D90720 g4062398 Escherichia coli 562
-11534455 6500730597 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b0824 b0824 Escherichia coli 562
-11534455

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844987	10143	32299	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501844989	10144	32300	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845004	10145	32301	672	223

Description

5000691819 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0825 b0825 Escherichia coli 562 -11534456
7000691085 transaldolase-like protein (cl:bacillus subtilis 23k phosphoprotein orfu) (ec:2.2.1.-) (db:pir2.dat) A64820 A64820 Escherichia coli 562 -11534456 7500959909 mipb putative transaldolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 74 of 400 of the completegenome.) (nt:o244; 70 pct identical to 220 amino acids) (le:10966) (re:11700) (di:direct) AE000184 AE000184 g1787046 Escherichia coli 562 -11534456 7502852069 talc transaldolase-like protein ec 2.2.1.-. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #207) (db:genpept) (de:escherichia coli genomic dna. (18.4 - 18.8 min).) (nt:orf_id:o208#1; similar to swissprot accession) (le:10131) (re:10865) (di:direct) D90720 D90720 g4062399 Escherichia coli 562 -11534456 7502852070 talc transaldolase-like protein ec 2.2.1.-. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept) (de:escherichia coli genomic dna. (18.6 - 19.0 min).) (nt:orf_id:o208#1; similar to swissprot accession) (le:588) (re:1322) (di:direct) D90721 D90721 g4062404 Escherichia coli 562 -11534456 6500730598 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0825 b0825 Escherichia coli 562 -11534456

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845011	10146	32302	405	134

Description

6500730599 ybik:b0828 hypothetical protein in moea-grxa intergenic region:hypothetical 33.4 kd protein in moea-grxa intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0828 b0828 Escherichia coli 562 -11534457 110313 ybik (de:hypothetical 33.4 kd protein in moea-grxa intergenic region precursor) (db:swissprot) YBIK_ECOLI P37595 ESCHERICHIA COLI 562 -11534457 7000687380 ybik probable asparaginase:ybik (cl:ybik protein) (ec:3.5.1.1) (db:pir2.dat) D64820 D64820 Escherichia coli 562 -11534457 7500896814 ybik putative asparaginase (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 75 of 400 of the completegenome.) (nt:o321; 100 pct identical to fragment ybik_ecoli) (le:2256) (re:3221) (di:direct) AE000185 AE000185 g1787050 Escherichia coli 562 -11534457 5000691820 ybik hypothetical protein in moea-grxa intergenic (sr:escherichia coli(strain:k12) dna, clone:kohara clone #207) (db:genpept) (de:escherichia coli genomic dna. (18.4 - 18.8 min).) (nt:orf_id:o208#4; similar to swissprot accession) (le:13129) (re:14094) (di:direct) D90720 D90720 g4062400 Escherichia coli 562 -11534457 7502852071 ybik hypothetical protein in moea-grxa intergenic (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept) (de:escherichia coli genomic dna. (18.6 - 19.0 min).) (nt:orf_id:o208#4; similar to swissprot accession) (le:3586) (re:4551) (di:direct) D90721 D90721 g4062405 Escherichia coli 562 -11534457

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845014	10147	32303	192	63

Description

GTC ORF with score 100 to: (sr:human) (db:genpept) (de:human dna sequence from clone 1042k10 on chromosome 22q13.1-13.2.contains the adsl gene for adenylosuccinate lyase (ec 4.3.2.2,adenylosuccinase, asl) and 4 novel genes (one with probable ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845027	10148	32304	561	186

Description

5000691821 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0829 b0829 Escherichia coli 562 -11534458
 7500950967 ylia (de:hypothetical abc transporter atp-binding protein ylia) (db:swissprot) YLIA_ECOLI P75796 ESCHERICHIA COLI 562 -11534458 7000691086 probable oligopeptide transport protein (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) E64820 E64820 Escherichia coli 562 -11534458 7500950969 b0829 putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 75 of 400 of the completegenome.) (nt:o612; 48 pct identical (33 gaps) to 525 residues) (le:3241) (re:5079) (di:direct) AE000185 AE000185 g1787051 Escherichia coli 562 -11534458 6500730600 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0829 b0829 Escherichia coli 562 -11534458

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845030	10149	32305	615	204

Description

5000691822 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0830 b0830 Escherichia coli 562 -11534459
 7500950970 ylib (de:putative binding protein ylib precursor) (db:swissprot) YLIB_ECOLI P75797 ESCHERICHIA COLI 562 -11534459 7000691087 probable oligopeptide-binding periplasmic protein precursor (cl:dipeptide transport protein) (db:pir2.dat) F64820 F64820 Escherichia coli 562 -11534459
 7500950972 b0830 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 75 of 400 of the completegenome.) (nt:o512; this 512 aa orf is 29 pct identical (39 gaps)) (le:5099) (re:6637) (di:direct) AE000185 AE000185 g1787052 Escherichia coli 562 -11534459 6500730601 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0830 b0830 Escherichia coli 562 -11534459

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845037	10150	32306	1098	365

Description

5000691823 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0831 b0831 Escherichia coli 562 -11534460
7500950973 ylic (de:hypothetical abc transporter permease protein ylic) (db:swissprot) YLIC_ECOLI P75798 ESCHERICHIA COLI 562 -11534460 7000691088 probable oligopeptide transport protein b0831:probable oligopeptide permease b0831 (cl:oligopeptide permease protein oppb) (db:pir2.dat) G64820 G64820 Escherichia coli 562 -11534460 7500950975 b0831 putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 75 of 400 of the completegenome.) (nt:o306; this 306 aa orf is 46 pct identical (32 gaps)) (le:6655) (re:7575) (di:direct) AE000185 AE000185 g1787053 Escherichia coli 562 -11534460
7502852072 nikb hypothetical protein o314 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept) (de:escherichia coli genomic dna. (18.6 - 19.0 min).) (nt:orf_id:o209#1; similar to pir accession number) (le:7985) (re:8905) (di:direct) D90721 D90721 g4062408 Escherichia coli 562 -11534460 7502852073 nikb hypothetical protein o314 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o209#1; similar to pir accession number) (le:67) (re:987) (di:direct) D90722 D90722 g4062416 Escherichia coli 562 -11534460 6500730602 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0831 b0831 Escherichia coli 562 -11534460

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845039	10151	32307	876	292

Description

5000691824 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0832 b0832 Escherichia coli 562 -11534461
 7500950976 ylid (de:hypothetical abc transporter permease protein ylid) (db:swissprot) YLID_ECOLI P75799 ESCHERICHIA COLI 562 -11534461 7000691089 probable oligopeptide transport protein b0832:probable oligopeptide permease b0832 (cl:oligopeptide permease protein oppb) (db:pir2.dat) H64820 H64820 Escherichia coli 562 -11534461 7500950978 b0832 putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 75 of 400 of the completegenome.) (nt:o303; this 303 aa orf is 42 pct identical (5 gaps)) (le:7578) (re:8489) (di:direct) AE000185 AE000185 g1787054 Escherichia coli 562 -11534461
 7502852074 dppc transmembrane protein dppc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept) (de:escherichia coli genomic dna. (18.6 - 19.0 min).) (nt:orf_id:o209#2; similar to pir accession number) (le:8908) (re:9819) (di:direct) D90721 D90721 g4062409 Escherichia coli 562 -11534461 7502852075 dppc transmembrane protein dppc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o209#2; similar to pir accession number) (le:990) (re:1901) (di:direct) D90722 D90722 g4062417 Escherichia coli 562 -11534461 6500730603 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0832 b0832 Escherichia coli 562 -11534461

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845047	10152	32308	609	202

Description

GTC ORF with score 439 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmid 9781, 8198, 9115,9981, and lambda clones 3955 and 6052.) (le:39281) (re:40066) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845048	10153	32309	300	99

Description

GTC ORF with score 310 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmid 9781, 8198, 9115,9981, and lambda clones 3955 and 6052.) (le:39281) (re:40066) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845057	10154	32310	201	66

Description

5000691825 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0833 b0833 Escherichia coli 562 -11534462
7000691090 probable membrane protein b0833 (db:pir2.dat) A64821 A64821 Escherichia coli 562 -11534462 7500959910 b0833 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 75 of 400 of the completegenome.) (nt:o782; this 782 aa orf is 35 pct identical (4 gaps)) (le:8667) (re:11015) (di:direct) AE000185 AE000185 g1787055 Escherichia coli 562 -11534462 7502852076 hypothetical 67.7 kd protein cy02b10.18c. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept) (de:escherichia coli genomic dna. (18.6 - 19.0 min).) (nt:orf_id:o209#3; similar to swissprot accession) (le:9997) (re:12345) (di:direct) D90721 D90721 g4062410 Escherichia coli 562 -11534462 7502852077 hypothetical 67.7 kd protein cy02b10.18c. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o209#3; similar to swissprot accession) (le:2079) (re:4427) (di:direct) D90722 D90722 g4062418 Escherichia coli 562 -11534462 6500730604 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0833 b0833 Escherichia coli 562 -11534462

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845058	10155	32311	222	73

Description

5000691826 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0834 b0834 Escherichia coli 562 -11534463
7000691091 probable membrane protein b0834 precursor (db:pir2.dat) B64821 B64821 Escherichia coli 562 -11534463 7500959911 b0834 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 75 of 400 of the completegenome.) (nt:o442; this 442 aa orf is 32 pct identical (6 gaps)) (le:11023) (re:12351) (di:direct) AE000185 AE000185 g1787056 Escherichia coli 562 -11534463 7502852078 hypothetical 24.0k protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept) (de:escherichia coli genomic dna. (18.6 - 19.0 min).) (nt:orf_id:o209#4; similar to pir accession number) (le:12353) (re:13681) (di:direct) D90721 D90721 g4062411 Escherichia coli 562 -11534463 7502852079 hypothetical 24.0k protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o209#4; similar to pir accession number) (le:4435) (re:5763) (di:direct) D90722 D90722 g4062419 Escherichia coli 562 -11534463 6500730605 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0834 b0834 Escherichia coli 562 -11534463

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845062	10156	32312	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845063	10157	32313	438	145

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845067	10158	32314	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845071	10159	32315	408	135

Description

6500730606 ylig:b0835 hypothetical protein:hypothetical 49.6 kd protein in moea-dacc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0835 b0835 Escherichia coli 562 -11534464
5500686620 ylig (de:hypothetical 49.6 kd protein in moea-dacc intergenic region) (db:swissprot) YLIG_ECOLI P75802 ESCHERICHIA COLI 562 -11534464
7000688132 conserved hypothetical protein b0835 (cl:conserved hypothetical protein hi0019) (db:pir2.dat) C64821 C64821 Escherichia coli 562 -11534464
7500950979 ylig orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 75 of 400 of the completegenome.) (nt:f441; this 441 aa orf is 23 pct identical (8 gaps)) (le:12398) (re:13723) (di:complement) AE000185 AE000185 g1787057 Escherichia coli 562 -11534464 5000691827 yqev hypothetical 51.7 kd protein in dna-j-rpsu (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept) (de:escherichia coli genomic dna. (18.6 - 19.0 min).) (nt:orf_id:o209#5; similar to swissprot accession) (le:13728) (re:15053) (di:complement) D90721 D90721 g4062412 Escherichia coli 562 -11534464
7502852080 yqev hypothetical 51.7 kd protein in dna-j-rpsu (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o209#5; similar to swissprot accession) (le:5810) (re:7135) (di:complement) D90722 D90722 g4062420 Escherichia coli 562 -11534464

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845091	10160	32316	231	76

Description

5000691828 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0836 b0836 Escherichia coli 562 -11534465
7500950980 ylih (de:hypothetical 14.5 kd protein in moea-dacc intergenic region) (db:swissprot) YLIH_ECOLI P75803 ESCHERICHIA COLI 562 -11534465
7000691092 ylig ylig protein (db:pir2.dat) D64821 D64821 Escherichia coli 562 -11534465 7500950982 b0836 putative receptor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 76 of 400 of the completegenome.) (nt:o127; this 127 aa orf is 29 pct identical (5 gaps)) (le:137) (re:520) (di:direct) AE000186 AE000186 g1787059 Escherichia coli 562 -11534465 7502852081 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #208) (db:genpept) (de:escherichia coli genomic dna. (18.6 - 19.0 min).) (nt:orf_id:o209#6) (le:15266) (re:15649) (di:direct) D90721 D90721 g4062413 Escherichia coli 562 -11534465 7502852082 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o209#6) (le:7348) (re:7731) (di:direct) D90722 D90722 g4062421 Escherichia coli 562 -11534465 6500730607 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0836 b0836 Escherichia coli 562 -11534465

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845097	10161	32317	288	95

Description

5000691829 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0837 b0837 Escherichia coli 562 -11534466
7500950983 ylii (de:hypothetical 41.1 kd protein in moea-dacc intergenic region precursor) (db:swissprot) YLII_ECOLI P75804 ESCHERICHIA COLI 562 -11534466 7000689509 ylii ylii protein precursor (cl:hypothetical protein b0837) (db:pir2.dat) E64821 E64821 Escherichia coli 562 -11534466
7500950985 ylii putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 76 of 400 of the completegenome.) (nt:o371; this 371 aa orf is 34 pct identical (28 gaps)) (le:631) (re:1746) (di:direct) AE000186 AE000186 g1787060 Escherichia coli 562 -11534466 7502852083 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o209#7) (le:7842) (re:8957) (di:direct) D90722 D90722 g4062422 Escherichia coli 562 -11534466 6500730608 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0837 b0837 Escherichia coli 562 -11534466

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845098	10162	32318	1014	338

Description

5000691830 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0838 b0838 Escherichia coli 562 -11534467
7500950986 ylij (de:hypothetical 23.9 kd protein in moea-dacc intergenic region) (db:swissprot) YLIJ_ECOLI P75805 ESCHERICHIA COLI 562 -11534467
7000691093 ylij probable glutathione transferase:ylij (cl:hypothetical protein b0838) (ec:2.5.1.18) (db:pir2.dat) F64821 F64821 Escherichia coli 562 -11534467 7500950988 ylij putative transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 76 of 400 of the completegenome.) (nt:f210; residues 68-151 are 40 pct identical to) (le:1743) (re:2375) (di:complement) AE000186 AE000186 g1787061 Escherichia coli 562 -11534467 6500730609 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0838 b0838 Escherichia coli 562 -11534467

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845099	10163	32319	828	275

Description

5000691831 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0841 b0841 Escherichia coli 562 -11534468
7500896859 ybjg (de:hypothetical 22.4 kd protein in deor-cmr intergenic region) (db:swissprot) YBJG_ECOLI P75806 ESCHERICHIA COLI 562 -11534468
7000691094 ybjg probable membrane protein ybjg (db:pir2.dat) A64822 A64822 Escherichia coli 562 -11534468 7500896861 ybjg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 76 of 400 of the completegenome.) (nt:f198; this 198 aa orf is 31 pct identical (4 gaps)) (le:4681) (re:5277) (di:complement) AE000186 AE000186 g1787064 Escherichia coli 562 -11534468 6500730610 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0841 b0841 Escherichia coli 562 -11534468

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845126	10164	32320	966	322

Description

6500730611 cmr:mdfa:b0842 hypothetical protein:multidrug translocase
mdfa:chloramphenicol resistance pump cmr (gtcfc:12.6:13.3) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b0842 b0842 Escherichia coli 562
-11534469 1500687417 cmr:mdfa (de:multidrug translocase mdfa
(chloramphenicol resistance pump cmr)) (db:swissprot) MDFA_ECOLI Q46966
ESCHERICHIA COLI 562 -11534469 7000685805 cmr:mdfa multidrug translocase
protein mdfa:chloramphenicol resistance pump cmr (cl:escherichia coli
hypothetical protein (iada-mcrd intergenic region)) (db:pir2.dat) B64822
B64822 Escherichia coli 562 -11534469 7500885415 cmr proton motive force
efflux pump (fn:transport; transport of small molecules: other)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 76 of 400 of the
completegenome.) (nt:o410; this 410 aa orf is 41 pct identical (2 gaps))
(le:5562) (re:6794) (di:direct) AE000186 AE000186 g1787065 Escherichia coli
562 -11534469 5000691832 hypothetical protein f410 (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia
coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o210#1; similar to pir
accession number) (le:12772) (re:14004) (di:direct) D90722 D90722 g4062426
Escherichia coli 562 -11534469 7502852084 hypothetical protein f410
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept)
(de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf_id:o210#1;
similar to pir accession number) (le:357) (re:1589) (di:direct) D90723
D90723 g4062433 Escherichia coli 562 -11534469

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845127	10165	32321	276	91

Description

5000691833 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0843 b0843 Escherichia coli 562 -11534470
7500896862 ybjh (de:hypothetical 10.0 kd protein in cmr-grxa intergenic region precursor) (db:swissprot) YBJH_ECOLI P75808 ESCHERICHIA COLI 562 -11534470 7000691095 ybjh ybjh protein precursor (db:pir2.dat) C64822 C64822 Escherichia coli 562 -11534470 7500896864 ybjh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 76 of 400 of the completegenome.) (nt:f94; this 94 aa orf is 52 pct identical (1 gap)) (le:6835) (re:7119) (di:complement) AE000186 AE000186 g1787066 Escherichia coli 562 -11534470 7502852085 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o210#2) (le:14045) (re:14329) (di:complement) D90722 D90722 g4062427 Escherichia coli 562 -11534470 7502852086 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf_id:o210#2) (le:1630) (re:1914) (di:complement) D90723 D90723 g4062434 Escherichia coli 562 -11534470 6500730612 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0843 b0843 Escherichia coli 562 -11534470

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845133	10166	32322	201	66

Description

5000691834 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0844 b0844 Escherichia coli 562 -11534471
7000691096 hypothetical protein b0844 (db:pir2.dat) D64822 D64822 Escherichia coli 562 -11534471 7500959912 b0844 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 76 of 400 of the completegenome.) (nt:f262; this 262 aa orf is 20 pct identical (7 gaps)) (le:7205) (re:7993) (di:complement) AE000186 AE000186 g1787067 Escherichia coli 562 -11534471 6500730613 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0844 b0844 Escherichia coli 562 -11534471

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845134	10167	32323	882	293

Description

5000691835 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0845 b0845 Escherichia coli 562 -11534472
7000691097 probable membrane protein b0845 (cl:cynx protein) (db:pir2.dat) E64822 E64822 Escherichia coli 562 -11534472 7500955453 b0845 putative deor-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 76 of 400 of the completegenome.) (nt:f402; this 402 aa orf is 26 pct identical (13 gaps)) (le:8020) (re:9228) (di:complement) AE000186 AE000186 g1787068 Escherichia coli 562 -11534472 7502852087 mosc membrane protein mosc. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o210#4; similar to pir accession number) (le:15230) (re:16438) (di:complement) D90722 D90722 g4062429 Escherichia coli 562 -11534472 7502852088 mosc membrane protein mosc. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf_id:o210#4; similar to pir accession number) (le:2815) (re:4023) (di:complement) D90723 D90723 g4062436 Escherichia coli 562 -11534472
6500730614 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0845 b0845 Escherichia coli 562 -11534472

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845137	10168	32324	909	302

Description

5000691836 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0846 b0846 Escherichia coli 562 -11534473
7000691098 hypothetical protein b0846 (db:pir2.dat) F64822 F64822 Escherichia coli 562 -11534473 7500959913 b0846 putative deor-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 76 of 400 of the completegenome.) (nt:o178; this 178 aa orf is 28 pct identical (16 gaps)) (le:9312) (re:9848) (di:direct) AE000186 AE000186 g1787069 Escherichia coli 562 -11534473 6500730615 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0846 b0846 Escherichia coli 562 -11534473

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845138	10169	32325	948	315

Description

GTC ORF with score 1355 to: (or:Neurospora crassa) (sr:neurospora crassa) (db:genpept-pln1) (de:neurospora crassa mrna for mitochondrial f(1)-atpase beta-subunitprecursor.) (nt:f(1)-atpase beta-subunit precursor (519 aa)) (le:31) (re:1590) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845148	10170	32326	708	235

Description

5000691837 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0847 b0847 Escherichia coli 562 -11534474
7000691099 probable membrane protein b0847 (db:pir2.dat) G64822 G64822 Escherichia coli 562 -11534474 7500959914 b0847 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:f561; this 561 aa orf is 26 pct identical (41 gaps)) (le:118) (re:1803) (di:complement) AE000187 AE000187 g1787071 Escherichia coli 562 -11534474 7502852089 hypothetical protein hi0035 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #209) (db:genpept) (de:escherichia coli genomic dna. (18.8 - 19.2 min).) (nt:orf_id:o210#6; similar to pir accession number) (le:17233) (re:18918) (di:complement) D90722 D90722 g4062431 Escherichia coli 562 -11534474 7502852090 hypothetical protein hi0035 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf_id:o210#6; similar to pir accession number) (le:4818) (re:6503) (di:complement) D90723 D90723 g4062438 Escherichia coli 562 -11534474 6500730616 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0847 b0847 Escherichia coli 562 -11534474

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845149	10171	32327	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845156	10172	32328	861	286

Description

GTC ORF with score 178 to: (db:genpept-bct2) (de:myxococcus xanthus response regulator frzz (frzz) gene, partialcds; alanine dehydrogenase (alda), putative ecf sigma factor rpoel(rpoel), and response regulator homolog genes, complete cds; andunknown ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845159	10173	32329	975	324

Description

5000691838 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0848 b0848 Escherichia coli 562 -11534475
7500896865 ybjm (de:hypothetical 14.2 kd protein in cmr-grxa intergenic region) (db:swissprot) YBJM_ECOLI P75813 ESCHERICHIA COLI 562 -11534475
7000691100 ybjm probable membrane protein ybjm (db:pir2.dat) H64822 H64822 Escherichia coli 562 -11534475 7500896867 ybjm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:o125; this 125 aa orf is 34 pct identical (5 gaps)) (le:2073) (re:2450) (di:direct) AE000187 AE000187 g1787072 Escherichia coli 562 -11534475 6500730617 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0848 b0848 Escherichia coli 562 -11534475

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845185	10174	32330	1434	477

Description

6500730618 ybjc:b0850 hypothetical 10.5 kd protein in grxa-mdaa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0850 b0850 Escherichia coli 562 -11534476 110321 ybjc (de:hypothetical 10.5 kd protein in grxa-mdaa intergenic region) (db:swissprot) YBJC_ECOLI P46119 ESCHERICHIA COLI 562 -11534476 7000687383 ybjc probable membrane protein ybjc (db:pir2.dat) B64823 B64823 Escherichia coli 562 -11534476 7500896849 ybjc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:o95; 100 pct identical to ybjc_ecoli sw: p46119) (le:2897) (re:3184) (di:direct) AE000187 AE000187 g1787074 Escherichia coli 562 -11534476 5000691839 ybjc hypothetical 10.5 kd protein in grxa-mdaa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf_id:o210#8; similar to swissprot accession) (le:7597) (re:7884) (di:direct) D90723 D90723 g4062439 Escherichia coli 562 -11534476

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845188	10175	32331	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845190	10176	32332	750	249

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845201	10177	32333	864	287

Description

5000691841 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0853 b0853 Escherichia coli 562 -11534477
 7500896868 ybjn (de:hypothetical 17.7 kd protein in rimk-potf intergenic region) (db:swissprot) YBJN_ECOLI P75815 ESCHERICHIA COLI 562 -11534477
 7000691101 ybjn ybjn protein (db:pir2.dat) E64823 E64823 Escherichia coli 562 -11534477 7500896870 ybjn putative sensory transduction regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:o158; this 158 aa orf is 27 pct identical (7 gaps)) (le:4941) (re:5417) (di:direct) AE000187 AE000187 g1787077 Escherichia coli 562 -11534477 7502852091 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf_id:o210#11) (le:9641) (re:10117) (di:direct) D90723 D90723 g4062440 Escherichia coli 562 -11534477 6500730619 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0853 b0853 Escherichia coli 562 -11534477

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845219	10178	32334	720	239

Description

6500730620 ybjo:b0858 hypothetical protein:hypothetical 18.5 kd protein in poti-artj intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0858 b0858 Escherichia coli 562 -11534478
 4000709319 ybjo (de:hypothetical 18.5 kd protein in poti-artj intergenic region) (db:swissprot) YBJO_ECOLI P75816 ESCHERICHIA COLI 562 -11534478
 7000687385 ybjo probable membrane protein ybjo (db:pir2.dat) B64824 B64824 Escherichia coli 562 -11534478 7500896871 ybjo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:o162) (le:9973) (re:10461) (di:direct) AE000187 AE000187 g1787082 Escherichia coli 562 -11534478 5000691842 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf_id:o211#1) (le:14673) (re:15161) (di:direct) D90723 D90723 g4062441 Escherichia coli 562 -11534478 7502852092 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf_id:o211#1) (le:268) (re:756) (di:direct) D90724 D90724 g4062443 Escherichia coli 562 -11534478

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845222	10179	32335	816	271

Description

GTC ORF with score 221 to: (fn:involved in poly-3-hydroxybutyrate degradation) (db:genpept-bct2) (ec:6.2.1.16) (de:sinorhizobium meliloti acetoacetyl-coa synthetase (acsa) gene,complete cds.) (nt:acetoacetyl-coa ligase; acyl-activating enzyme) (le:548)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845232	10180	32336	963	320

Description

5000691844 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0865 b0865 Escherichia coli 562 -11534479
7500896872 ybjp (de:precursor) (db:swissprot) YBJP_ECOLI P75818 ESCHERICHIA COLI 562 -11534479 7000691102 ybjp ybjp protein precursor (db:pir2.dat) A64825 A64825 Escherichia coli 562 -11534479 7500896874 ybjp putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.) (nt:f171; this 171 aa orf is 30 pct identical (3 gaps)) (le:4238) (re:4753) (di:complement) AE000188 AE000188 g1787090 Escherichia coli 562 -11534479 7502852093 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf_id:o211#8) (le:6231) (re:6746) (di:complement) D90724 D90724 g4062445 Escherichia coli 562 -11534479 6500730621 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0865 b0865 Escherichia coli 562 -11534479

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845240	10181	32337	1287	428

Description

5000691845 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0866 b0866 Escherichia coli 562 -11534480
7000691103 hypothetical protein b0866 (cl:hypothetical protein mj1413) (db:pir2.dat) B64825 B64825 Escherichia coli 562 -11534480 7500959915 b0866 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.) (nt:o107; this 107 aa orf is 50 pct identical (0 gaps)) (le:4879) (re:5202) (di:direct) AE000188 AE000188 g1787091 Escherichia coli 562 -11534480 7502852094 orfb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf_id:o211#9; similar to pir accession number) (le:6872) (re:7195) (di:direct) D90724 D90724 g4062446 Escherichia coli 562 -11534480 6500730622 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0866 b0866 Escherichia coli 562 -11534480

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845251	10182	32338	498	165

Description

5000691846 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0867 b0867 Escherichia coli 562 -11534481
7000691104 hypothetical protein b0867 precursor (db:pir2.dat) C64825 C64825 Escherichia coli 562 -11534481 7500959916 b0867 putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.) (nt:o276; this 276 aa orf is 41 pct identical (11 gaps)) (le:5199) (re:6029) (di:direct) AE000188 AE000188 g1787092 Escherichia coli 562 -11534481 7502852095 ampd ampd protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf_id:o211#10; similar to pir accession number) (le:7192) (re:8022) (di:direct) D90724 D90724 g4062447 Escherichia coli 562 -11534481
6500730623 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0867 b0867 Escherichia coli 562 -11534481

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845257	10183	32339	768	255

Description

5000691847 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0868 b0868 Escherichia coli 562 -11534482
7000691105 hypothetical protein b0868 (db:pir2.dat) D64825 D64825 Escherichia coli 562 -11534482 7500959917 b0868 putative nucleotide di-p-sugar epimerase or (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.) (nt:f349; this 349 aa orf is 27 pct identical (35 gaps)) (le:6026) (re:7075) (di:complement) AE000188 AE000188 g1787093 Escherichia coli 562 -11534482 7502852096 3b-hydroxysteroid dehydrogenase v (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf_id:o211#11; similar to pir accession number) (le:8019) (re:9068) (di:complement) D90724 D90724 g4062448 Escherichia coli 562 -11534482 6500730624 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0868 b0868 Escherichia coli 562 -11534482

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845260	10184	32340	504	168

Description

5000691848 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0869 b0869 Escherichia coli 562 -11534483
7000691106 ybjt ybjt protein (db:pir2.dat) E64825 E64825 Escherichia coli 562 -11534483 7500896877 ybjt putative dtdp-glucose enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 78 of 400 of the completegenome.) (nt:f486; this 486 aa orf is 21 pct identical (13 gaps)) (le:7138) (re:8598) (di:complement) AE000188 AE000188 g1787094 Escherichia coli 562 -11534483 7500896875 ybjt (de:hypothetical 55.0 kd protein in artp-poxb intergenic region) (db:swissprot) YBJT_ECOLI P75822 ESCHERICHIA COLI 562 -11534483 6500730625 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0869 b0869 Escherichia coli 562 -11534483

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845261	10185	32341	972	323

Description

5000691850 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0872 b0872 Escherichia coli 562 -11534484
7000691107 hypothetical protein b0872 (db:pir2.dat) H64825 H64825 Escherichia coli 562 -11534484 7500959918 b0872 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 79 of 400 of the completegenome.) (nt:f322; this 322 aa orf is 25 pct identical (14 gaps)) (le:97) (re:1065) (di:complement) AE000189 AE000189 g1787098 Escherichia coli 562 -11534484 6500730626 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0872 b0872 Escherichia coli 562 -11534484

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845267	10186	32342	921	306

Description

5000691851 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0873 b0873 Escherichia coli 562 -11534485
5500685756 ybjw (de:prismene protein homolog) (db:swissprot) PRIS_ECOLI P75825 ESCHERICHIA COLI 562 -11534485 7000686178 ybjw 6fe-6s prismene-containing protein) (cl:prismene (6fe-6s) protein) (db:pir2.dat) A64826 A64826 Escherichia coli 562 -11534485 7500888493 ybjw putative prismene (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 79 of 400 of the completegenome.) (nt:f552; this 552 aa orf is 41 pct identical (22 gaps)) (le:1077) (re:2735) (di:complement) AE000189 AE000189 g1787099 Escherichia coli 562 -11534485 6500730627 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0873 b0873 Escherichia coli 562 -11534485

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845269	10187	32343	807	268

Description

5000691852 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0874 b0874 Escherichia coli 562 -11534486
7500896853 ybje (de:hypothetical 34.4 kd protein in poxb-aqpz intergenic region) (db:swissprot) YBJE_ECOLI P75826 ESCHERICHIA COLI 562 -11534486
7000691108 ybje probable membrane protein ybje (db:pir2.dat) B64826 B64826 Escherichia coli 562 -11534486 7500896855 ybje putative surface protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 79 of 400 of the completegenome.) (nt:f315; this 315 aa orf is 47 pct identical (0 gaps)) (le:2873) (re:3820) (di:complement) AE000189 AE000189 g1787100 Escherichia coli 562 -11534486 6500730628 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0874 b0874 Escherichia coli 562 -11534486

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845273	10188	32344	285	94

Description

5000691854 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0876 b0876 Escherichia coli 562 -11534487
7500896850 ybjd (de:hypothetical 63.6 kd protein in aqpz-cspd intergenic region) (db:swissprot) YBJD_ECOLI P75828 ESCHERICHIA COLI 562 -11534487
7000691109 ybjd ybjd protein (db:pir2.dat) D64826 D64826 Escherichia coli 562 -11534487 7500896852 ybjd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 79 of 400 of the completegenome.) (nt:o552; this 552 aa orf is 28 pct identical (9 gaps)) (le:5388) (re:7046) (di:direct) AE000189 AE000189 g1787102 Escherichia coli 562 -11534487 7502852097 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #212) (db:genpept) (de:escherichia coli genomic dna. (19.7 - 20.0 min).) (nt:orf_id:o212#3) (le:3410) (re:5068) (di:direct) D90725 D90725 g4062459 Escherichia coli 562 -11534487 6500730629 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0876 b0876 Escherichia coli 562 -11534487

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845297	10189	32345	555	184

Description

5000691855 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0877 b0877 Escherichia coli 562 -11534488
5500686483 ybjx (de:hypothetical 38.4 kd protein in agpz-cspd intergenic region) (db:swissprot) YBJX_ECOLI P75829 ESCHERICHIA COLI 562 -11534488
7000687386 ybjx ybjx protein (db:pir2.dat) E64826 E64826 Escherichia coli 562 -11534488 7500896878 ybjx putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 79 of 400 of the completegenome.) (nt:f330; this 330 aa orf is 21 pct identical (10 gaps)) (le:7043) (re:8035) (di:complement) AE000189 AE000189 g1787103 Escherichia coli 562 -11534488 7502852098 virk virk protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #212) (db:genpept) (de:escherichia coli genomic dna. (19.7 - 20.0 min).) (nt:orf_id:o213#1; similar to pir accession number) (le:5065) (re:6057) (di:complement) D90725 D90725 g4062460 Escherichia coli 562 -11534488 6500730630 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0877 b0877 Escherichia coli 562 -11534488

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845299	10190	32346	183	60

Description

5000691856 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0878 b0878 Escherichia coli 562 -11534489
7000691110 probable membrane protein b0878 (db:pir2.dat) F64826 F64826 Escherichia coli 562 -11534489 7500959919 b0878 putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 79 of 400 of the completegenome.) (nt:o380; 27 pct identical (27 gaps) to 332 residues) (le:8123) (re:9265) (di:direct) AE000189 AE000189 g1787104 Escherichia coli 562 -11534489 6500730631 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0878 b0878 Escherichia coli 562 -11534489

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845301	10191	32347	315	104

Description

5000691857 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0879 b0879 Escherichia coli 562 -11534490
5500686484 ybjz (de:hypothetical abc transporter atp-binding protein ybjz) (db:swissprot) YBJZ_ECOLI P75831 ESCHERICHIA COLI 562 -11534490 7000687387 ybjz probable abc-type transport protein ybjz (cl:atp-binding cassette homology) (db:pir2.dat) G64826 G64826 Escherichia coli 562 -11534490
7500896879 ybjz putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 79 of 400 of the completegenome.) (nt:o648; similar to ybba_haein sw: p45247) (le:9262) (re:11208) (di:direct) AE000189 AE000189 g1787105 Escherichia coli 562 -11534490 7502852099 abc transporter probable atp-binding subunit (sr:escherichia coli(strain:k12) dna, clone:kohara clone #212) (db:genpept) (de:escherichia coli genomic dna. (19.7 - 20.0 min).) (nt:orf_id:o213#4; similar to pir accession number) (le:7284) (re:9230) (di:direct) D90725 D90725 g4062463 Escherichia coli 562 -11534490
6500730632 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0879 b0879 Escherichia coli 562 -11534490

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845302	10192	32348	555	184

Description

6500730633 ylja:b0881 hypothetical protein:hypothetical 12.2 kd protein in cspd-clpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0881 b0881 Escherichia coli 562 -11534491
5500686621 ylja (de:12.2 kd protein in cspd-clpa intergenic region) (db:swissprot) YLJA_ECOLI P75832 ESCHERICHIA COLI 562 -11534491 7000688133 ylja ylja protein (cl:hypothetical protein hp0032) (db:pir2.dat) A64827 A64827 Escherichia coli 562 -11534491 7500950989 ylja orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 80 of 400 of the completegenome.) (nt:o106; this 106 aa orf is 25 pct identical (2 gaps)) (le:614) (re:934) (di:direct) AE000190 AE000190 g1787108 Escherichia coli 562 -11534491 5000691859 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #212) (db:genpept) (de:escherichia coli genomic dna. (19.7 - 20.0 min).) (nt:orf_id:o213#6) (le:9850) (re:10170) (di:direct) D90725 D90725 g4062464 Escherichia coli 562 -11534491

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845304	10193	32349	297	99

Description

6500730634 ycaj:b0892 hypothetical protein in sers 5region:hypothetical 49.6 kd protein in lola-sers intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0892 b0892 Escherichia coli 562 -11534492 110570 ycaj (de:hypothetical 49.6 kd protein in lola-sers intergenic region) (db:swissprot) YCAJ_ECOLI P45526 ESCHERICHIA COLI 562 -11534492 7000687395 ycaj ycaj protein (cl:haemophilus influenzae conserved hypothetical protein hi1590) (db:pir2.dat) C64828 C64828 Escherichia coli 562 -11534492 7500921546 ycaj putative polynucleotide enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 81 of 400 of the completegenome.) (nt:o447; 98 pct identical to fragment ycaj_ecoli) (le:5702) (re:7045) (di:direct) AE000191 AE000191 g1787119 Escherichia coli 562 -11534492 5000691862 hypothetical protein hi1590 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept) (de:escherichia coli genomic dna. (19.9 - 20.3 min).) (nt:orf_id:o215#5; similar to pir accession number) (le:13874) (re:15217) (di:direct) D90726 D90726 g4062469 Escherichia coli 562 -11534492 7502852100 hypothetical protein hi1590 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept) (de:escherichia coli genomic dna. (20.1 - 20.4 min).) (nt:orf_id:o215#5; similar to pir accession number) (le:7177) (re:8520) (di:direct) D90727 D90727 g4062470 Escherichia coli 562 -11534492

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845305	10194	32350	201	66

Description

6500730635 ycac:b0897 hypothetical 23.1 kd protein in dmcs
3region:hypothetical 23.1 kd protein in dmcs-pfla intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0897
b0897 Escherichia coli 562 -11534493 110564 ycac (de:hypothetical 23.1 kd
protein in dmcs-pfla intergenic region) (db:swissprot) YCAC_ECOLI P21367
ESCHERICHIA COLI 562 -11534493 163897 ycac probable membrane protein ycac
(db:pir2.dat) (mp:20 min) S09671 S09671 Escherichia coli 562 -11534493
7500921543 (sr:escherichia coli (strain c600) dna) (db:genpept-bct1)
(de:e.coli dmsa, dmsb and dmcs genes encoding anaerobic dimethylsulfoxide
reductase, complete cds.) (nt:orf z; putative) (le:4760) (re:5386)
(di:complement) ECODMS J03412 g1128948 Escherichia coli 562 -11534493
234176 ycac orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 81 of 400 of the completegenome.)
(nt:f208; 100 pct identical to ycac_ecoli sw: p21367) (le:12639) (re:13265)
(di:complement) AE000191 AE000191 g1787124 Escherichia coli 562 -11534493
5000691864 ycac hypothetical protein z dmcs 3 region (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #215) (db:genpept) (de:escherichia
coli genomic dna. (20.1 - 20.4 min).) (nt:orf_id:o216#1; similar to pir
accession number) (le:14114) (re:14740) (di:complement) D90727 D90727
g4062471 Escherichia coli 562 -11534493 7502852101 ycac hypothetical
protein z dmcs 3 region (sr:escherichia coli(strain:k12) dna, clone:kohara
clone #216) (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8
min).) (nt:orf_id:o216#1; similar to pir accession number) (le:624)
(re:1250) (di:complement) D90728 D90728 g4062473 Escherichia coli 562
-11534493

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845306	10195	32351	522	173

Description

6500730636 ycad:b0898 hypothetical protein in dm5c 3 region:hypothetical 41.4 kd protein in dm5c-pfla intergenic region:orf y (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0898 b0898 Escherichia coli 562 -11534494 110565 ycad (de:hypothetical 41.4 kd protein in dm5c-pfla intergenic region (orf y)) (db:swissprot) YCAD_ECOLI P21503 ESCHERICHIA COLI 562 -11534494 7000687393 ycad membrane protein ycad (db:pir2.dat) (mp:20 min) A64829 A64829 Escherichia coli 562 -11534494 7500921544 ycad putative transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 82 of 400 of the completegenome.) (nt:o382; 100 pct identical to fragment ycad_ecoli) (le:187) (re:1335) (di:direct) AE000192 AE000192 g1787126 Escherichia coli 562 -11534494 5000691865 ycad hypothetical protein y (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept) (de:escherichia coli genomic dna. (20.1 - 20.4 min).) (nt:orf_id:o216#2; similar to pir accession number) (le:15054) (re:16202) (di:direct) D90727 D90727 g4062472 Escherichia coli 562 -11534494 7502852102 ycad hypothetical protein y (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (nt:orf_id:o216#2; similar to pir accession number) (le:1564) (re:2712) (di:direct) D90728 D90728 g4062474 Escherichia coli 562 -11534494

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845307	10196	32352	186	61

Description

GTC ORF with score 107 to: (cl:nad(p)+ transhydrogenase (b-specific):alanine dehydrogenase homology:nad(p)+ transhydrogenase (b-specific) alpha chain homology:nad(p)+ transhydrogenase (b-specific) beta chain homology) (sr:, man) (ec:1.6.1.1) (db:pir2.dat)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845308	10197	32353	267	88

Description

5000691866 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0899 b0899 Escherichia coli 562 -11534495 7000691111 membrane protein b0899 (db:pir2.dat) B64829 B64829 Escherichia coli 562 -11534495 7500959920 b0899 putative transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 82 of 400 of the completegenome.) (nt:o540; this 540 aa orf is 22 pct identical (10 gaps)) (le:1353) (re:2975) (di:direct) AE000192 AE000192 g1787127 Escherichia coli 562 -11534495 6500730637 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0899 b0899 Escherichia coli 562 -11534495

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845312	10198	32354	267	88

Description

GTC ORF with score 321 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c15h9.) (nt:similar to nad(p) transhydrogenase, mitochondrial;) (le:33405:33566:34288:34689) (re:33522:33744:34635:34934) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845314	10199	32355	222	73

Description

6500730638 ycan:b0900 hypothetical protein:hypothetical transcriptional regulator in dm5c-pfla intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0900 b0900 Escherichia coli 562 -11534496 5500686491 ycan (de:hypothetical transcriptional regulator in dm5c-pfla intergenic region) (db:swissprot) YCAN_ECOLI P75836 ESCHERICHIA COLI 562 -11534496 7000687397 ycan transcription regulator ycan (cl:hypothetical protein b1328) (db:pir2.dat) C64829 C64829 Escherichia coli 562 -11534496 7500921550 ycan putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 82 of 400 of the completegenome.) (nt:f302; this 302 aa orf is 43 pct identical (4 gaps)) (le:2976) (re:3884) (di:complement) AE000192 AE000192 g1787128 Escherichia coli 562 -11534496 5000691867 hypothetical protein 3 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (nt:orf_id:o216#4; similar to pir accession number) (le:4353) (re:5261) (di:complement) D90728 D90728 g4062476 Escherichia coli 562 -11534496

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845316	10200	32356	186	61

Description

6500730639 ycak:b0901 hypothetical protein in pfla 3region:hypothetical nadph oxidoreductase in dsmc-pfla intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0901 b0901 Escherichia coli 562 -11534497 110572 ycak (ec:1.6.99.-) (de:putative nad(p)h oxidoreductase ycak,) (db:swissprot) YCAK_ECOLI P43340 ESCHERICHIA COLI 562 -11534497 7000687396 ycak probable nad p h dehydrogenase quinone:ycak (ec:1.6.99.2) (db:pir2.dat) D64829 D64829 Escherichia coli 562 -11534497 7500921548 ycak orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 82 of 400 of the completegenome.) (nt:o196; 100 pct identical to fragment ycak_ecoli) (le:3984) (re:4574) (di:direct) AE000192 AE000192 g1787129 Escherichia coli 562 -11534497 5000691868 ycak hypothetical protein in pfla 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (nt:orf_id:o216#5; similar to swissprot accession) (le:5361) (re:5951) (di:direct) D90728 D90728 g4062477 Escherichia coli 562 -11534497

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845317	10201	32357	465	154

Description

6500730640 ycao:b0905 hypothetical protein:hypothetical 66.0 kd protein in foca-serc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0905 b0905 Escherichia coli 562 -11534498 7000687398 ycao ycao protein (db:pir2.dat) H64829 H64829 Escherichia coli 562 -11534498 7500921551 ycao orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 82 of 400 of the completegenome.) (nt:f589; this 589 aa orf is 66 pct identical (1 gap)) (le:9188) (re:10957) (di:complement) AE000192 AE000192 g1787133 Escherichia coli 562 -11534498 5000691870 hypothetical protein hil265 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (nt:orf_id:o217#2; similar to pir accession number) (le:10565) (re:12334) (di:complement) D90728 D90728 g4062479 Escherichia coli 562 -11534498 7502852103 hypothetical protein hil265 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept) (de:escherichia coli genomic dna. (20.5 - 20.9 min).) (nt:orf_id:o217#2; similar to pir accession number) (le:3032) (re:4801) (di:complement) D90729 D90729 g4062482 Escherichia coli 562 -11534498 4000708190 ycao (de:hypothetical 66.0 kd protein in foca-serc intergenic region) (db:swissprot) YCAO_ECOLI P75838 ESCHERICHIA COLI 562 -11534498

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845319	10202	32358	312	103

Description

6500730641 ycap:b0906 hypothetical protein:hypothetical 26.3 kd protein in foca-serc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0906 b0906 Escherichia coli 562 -11534499
 4000708191 ycap (de:hypothetical 26.3 kd protein in foca-serc intergenic region) (db:swissprot) YCAP_ECOLI P75839 ESCHERICHIA COLI 562 -11534499
 7000687399 ycap probable membrane protein ycap (cl:probable membrane protein ycap) (db:pir2.dat) A64830 A64830 Escherichia coli 562 -11534499
 7500921553 ycap orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 83 of 400 of the completegenome.) (nt:o230; this 230 aa orf is 30 pct identical (8 gaps)) (le:91) (re:783) (di:direct) AE000193 AE000193 g1787135 Escherichia coli 562 -11534499 5000691871 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (nt:orf_id:o217#3) (le:12455) (re:13147) (di:direct) D90728 D90728 g4062480 Escherichia coli 562 -11534499 7502852104 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept) (de:escherichia coli genomic dna. (20.5 - 20.9 min).) (nt:orf_id:o217#3) (le:4922) (re:5614) (di:direct) D90729 D90729 g4062483 Escherichia coli 562 -11534499

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845325	10203	32359	429	142

Description

5000691872 hypothetical protein 3 to aroa (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0909 b0909 Escherichia coli 562 -11534500 7000690862 cmk cmk protein precursor (db:pir2.dat) D64830 D64830 Escherichia coli 562 -11534500 7500959709 ycal putative heat shock protein (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 83 of 400 of the completegenome.) (nt:o262; 100 pct identical to gb: ecu3153_2 accession) (le:3569) (re:4357) (di:direct) AE000193 AE000193 g1787138 Escherichia coli 562 -11534500 6500730642 hypothetical protein 3 to aroa (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0909 b0909 Escherichia coli 562 -11534500

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845328	10204	32360	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845341	10205	32361	1743	580

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845346	10206	32362	723	240

Description

6500730643 ycai:b0913 hypothetical protein in msba 5 region:hypothetical 87.3 kd protein in himd-msba intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0913 b0913 Escherichia coli 562 -11534501 110568 ycai (de:hypothetical 87.3 kd protein in himd-msba intergenic region) (db:swissprot) YCAI_ECOLI P37443 ESCHERICHIA COLI 562 -11534501 7000687394 ycai probable membrane protein ycai (db:pir2.dat) H64830 H64830 Escherichia coli 562 -11534501 7500921545 ycai orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 83 of 400 of the completegenome.) (nt:o780; 100 pct identical to 159 residues of a 174) (le:7571) (re:9913) (di:direct) AE000193 AE000193 g1787142 Escherichia coli 562 -11534501 5000691873 ycai hypothetical protein msba 5 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept) (de:escherichia coli genomic dna. (20.5 - 20.9 min).) (nt:orf_id:o217#10; similar to pir accession number) (le:12402) (re:14744) (di:direct) D90729 D90729 g4062485 Escherichia coli 562 -11534501

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845353	10207	32363	603	200

Description

6500730644 ycah:b0915 hypothetical 35.6 kd protein in msba-kdsb intergenic region:orfe (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0915 b0915 Escherichia coli 562 -11534502 7500885148 lpxk (ec:2.7.1.130) (de:tetraacyldisaccharide 4'-kinase, (lipid a 4'-kinase)) (db:swissprot) LPXK_ECOLI P27300 ESCHERICHIA COLI 562 -11534502 7000690938 ycah ycah protein (db:pir2.dat) B64831 B64831 Escherichia coli 562 -11534502 7500885150 ycah putative ec 1.2 enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 83 of 400 of the completegenome.) (nt:o328; 99 pct identical to ycah_ecoli sw: p27300) (le:11695) (re:12681) (di:direct) AE000193 AE000193 g1787144 Escherichia coli 562 -11534502 5000691874 ycah hypothetical protein e msba 3 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf_id:o218#1; similar to pir accession number) (le:720) (re:1706) (di:direct) D90730 D90730 g4062487 Escherichia coli 562 -11534502

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845363	10208	32364	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845368	10209	32365	273	90

Description

5000691875 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0916 b0916 Escherichia coli 562 -11534503
7500921554 ycaq (de:hypothetical 47.7 kd protein in msba-kdsb intergenic region) (db:swissprot) YCAQ_ECOLI P75843 ESCHERICHIA COLI 562 -11534503
7000691112 ycaq ycaq protein (db:pir2.dat) C64831 C64831 Escherichia coli 562 -11534503 7500921556 ycaq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 83 of 400 of the completegenome.) (nt:o410; this 410 aa orf is 26 pct identical (1 gap)) (le:12718) (re:13950) (di:direct) AE000193 AE000193 g1787145 Escherichia coli 562 -11534503 7502852105 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf_id:o218#2) (le:1743) (re:2975) (di:direct) D90730 D90730 g4062488 Escherichia coli 562 -11534503 6500730645 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0916 b0916 Escherichia coli 562 -11534503

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845369	10210	32366	1173	391

Description

5000691876 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0917 b0917 Escherichia coli 562 -11534504
7500921557 ycar (de:hypothetical 6.9 kd protein in msba-kdsb intergenic region) (db:swissprot) YCAR_ECOLI P75844 ESCHERICHIA COLI 562 -11534504
7000691113 ycar ycar protein (db:pir2.dat) D64831 D64831 Escherichia coli 562 -11534504 7500921559 ycar orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 83 of 400 of the completegenome.) (nt:o60; this 60 aa orf is 37 pct identical (0 gaps)) (le:14002) (re:14184) (di:direct) AE000193 AE000193 g1787146 Escherichia coli 562 -11534504 7502852106 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf_id:o218#3) (le:3027) (re:3209) (di:direct) D90730 D90730 g4062489 Escherichia coli 562 -11534504 6500730646 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0917 b0917 Escherichia coli 562 -11534504

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845379	10211	32367	1824	607
<u>Description</u>				
5000691877 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0919 b0919 Escherichia coli 562 -11534505				
7000691114 hypothetical protein b0919 (db:pir2.dat) F64831 F64831 Escherichia coli 562 -11534505 7500959921 b0919 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 84 of 400 of the completegenome.) (nt:o297; this 297 aa orf is 23 pct identical (8 gaps)) (le:107) (re:1000) (di:direct) AE000194 AE000194 g1787149 Escherichia coli 562 -11534505 7502852107 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf_id:o218#5) (le:4106) (re:4999) (di:direct) D90730 D90730 g4062490 Escherichia coli 562 -11534505				
6500730647 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0919 b0919 Escherichia coli 562 -11534505				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845406	10212	32368	1128	375
<u>Description</u>				
6500730648 ycbc:b0920 hypothetical protein in kdsb-kicb intergenic region:hypothetical 28.7 kd protein in kdsb-mukf intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0920 b0920 Escherichia coli 562 -11534506 110590 ycbc (de:hypothetical 28.7 kd protein in kdsb-mukf intergenic region) (db:swissprot) YCBC_ECOLI P36565 ESCHERICHIA COLI 562 -11534506 7000687402 ycbc probable membrane protein ycbc (db:pir2.dat) G64831 G64831 Escherichia coli 562 -11534506 7500921568 ycbc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 84 of 400 of the completegenome.) (nt:f259; 99 pct identical to fragment ycbc_ecoli) (le:977) (re:1756) (di:complement) AE000194 AE000194 g1787150 Escherichia coli 562 -11534506				
5000691878 ycbc hypothetical protein in kdsb-mukf intergenic (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf_id:o218#6; similar to swissprot accession) (le:4976) (re:5755) (di:complement) D90730 D90730 g4062491 Escherichia coli 562 -11534506				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845407	10213	32369	942	313

Description

6500730649 smta:b0921 hypothetical 29.8 kd protein in kdsb-kicb intergenic region:smta protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0921 b0921 Escherichia coli 562 -11534507 98722 smta (de:smta protein) (db:swissprot) SMTA_ECOLI P36566 ESCHERICHIA COLI 562 -11534507 7000686614 smta probable s-adenosylmethionine-dependent methyltransferase (db:pir2.dat) H64831 H64831 Escherichia coli 562 -11534507 223280 stma hypothetical 29.8 kd protein in kdsb-kicb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.8 - 21.2 min).) (le:5891) (re:6676) (di:direct) D90730 D90730 g1651445 Escherichia coli 562 -11534507 7500891776 smta s-adenosylmethionine-dependent (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 84 of 400 of the completegenome.) (nt:o261; 99 pct identical to ycbd_ecoli sw: p36566) (le:1892) (re:2677) (di:direct) AE000194 AE000194 g1787151 Escherichia coli 562 -11534507 5000691879 smta smta protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf_id:o218#7; similar to swissprot accession) (le:5891) (re:6676) (di:direct) D90730 D90730 g1651445 Escherichia coli 562 -11534507

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845418	10214	32370	240	79

Description

6500730650 yccb:b0925 hypothetical protein in mukb 3 region:hypothetical 67.8 kd protein in mukb-aspc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0925 b0925 Escherichia coli 562 -11534508 110589 yccb (de:hypothetical 67.8 kd protein in mukb-aspc intergenic region) (db:swissprot) YCBB_ECOLI P22525 ESCHERICHIA COLI 562 -11534508 7000687401 yccb yccb protein precursor (db:pir2.dat) D64832 D64832 Escherichia coli 562 -11534508 7500921566 yccb putative amidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 84 of 400 of the completegenome.) (nt:o615; 96 pct identical to fragment yccb_ecoli) (le:9402) (re:11249) (di:direct) AE000194 AE000194 g1787155 Escherichia coli 562 -11534508 5000691882 yccb hypothetical protein 63 mukb 3 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf_id:o218#11; similar to pir accession number) (le:13401) (re:15248) (di:direct) D90730 D90730 g4062492 Escherichia coli 562 -11534508

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845419	10215	32371	477	158

Description

6500730651 ycbk:b0926 hypothetical protein:hypothetical 20.4 kd protein in mukb-aspc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0926 b0926 Escherichia coli 562 -11534509
5500686492 ycbk (de:hypothetical 20.4 kd protein in mukb-aspc intergenic region) (db:swissprot) YCBK_ECOLI P75848 ESCHERICHIA COLI 562 -11534509
7000687408 ycbk ycbk protein precursor (db:pir2.dat) E64832 E64832
Escherichia coli 562 -11534509 7500921575 ycbk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 85 of 400 of the completegenome.) (nt:ol82; residues 9-100 are 46 pct identical to) (le:121) (re:669) (di:direct) AE000195 AE000195 g1787157
Escherichia coli 562 -11534509 5000691883 hypothetical protein hil666 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf_id:o219#1; similar to pir accession number) (le:15429) (re:15977) (di:direct) D90730 D90730 g4062493 Escherichia coli 562 -11534509 7502852108 hypothetical protein hil666 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #219) (db:genpept) (de:escherichia coli genomic dna. (21.2 - 21.5 min).) (nt:orf_id:o219#1; similar to pir accession number) (le:228) (re:776) (di:direct) D90731 D90731 g4062496 Escherichia coli 562 -11534509

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845421	10216	32372	264	87

Description

GTC ORF with score 101 to: (sr:pseudomonas putida (strain:icr3460) dna) (db:genpept-bct1) (ec:4.4.1.11) (de:pseudomonas putida genes for mder,mdea and mdeb,complete cds.) (nt:mdea is a pyridoxal-5'phosphate enzyme that) (le:644) (re:1840) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845425	10217	32373	1461	486

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845442	10218	32374	657	218

Description

6500730652 ycb1:b0927 hypothetical protein:hypothetical 23.8 kd protein in mukb-aspc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0927 b0927 Escherichia coli 562 -11534510
500684914 ycb1 (de:hypothetical 23.8 kd protein in mukb-aspc intergenic region) (db:swissprot) YCBL_ECOLI P75849 ESCHERICHIA COLI 562 -11534510
7000687410 ycb1 probable hydrolase:ycb1 (cl:glyoxalase) (ec:3.-.-.-)
(db:pir2.dat) F64832 Escherichia coli 562 -11534510 7500921578 ycb1 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 85 of 400 of the completegenome.) (nt:o215; this 215 aa orf is 32 pct identical (24 gaps)) (le:696) (re:1343) (di:direct) AE000195 AE000195 g1787158 Escherichia coli 562 -11534510 5000691884 hypothetical 23.2 kd protein in soda-comga (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf_id:o219#2; similar to swissprot accession) (le:16004) (re:16651) (di:direct) D90730 D90730 g4062494 Escherichia coli 562 -11534510 7502852109 hypothetical 23.2 kd protein in soda-comga (sr:escherichia coli(strain:k12) dna, clone:kohara clone #219) (db:genpept) (de:escherichia coli genomic dna. (21.2 - 21.5 min).) (nt:orf_id:o219#2; similar to swissprot accession) (le:803) (re:1450) (di:direct) D90731 D90731 g4062497 Escherichia coli 562 -11534510

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845443	10219	32375	1944	647

Description

6500730653 ycbm:b0934 hypothetical protein:hypothetical abc transporter permease protein ycbm (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0934 b0934 Escherichia coli 562 -11534511
7000687412 ycbm nitrate transport protein nrtb homolog ycbm (cl:synechococcus nitrate transport protein nrtb) (db:pir2.dat) E64833 E64833 Escherichia coli 562 -11534511 7500921581 ycbm putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 85 of 400 of the completegenome.) (nt:f278; this 253 aa orf is 47 pct identical (0 gaps)) (le:11087) (re:11923) (di:complement) AE000195 AE000195 g1787165 Escherichia coli 562 -11534511 5000691886 yzeb prow protein homolog (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#2; similar to pir accession number) (le:1779) (re:2615) (di:complement) D90732 D90732 g4062502 Escherichia coli 562 -11534511 5500686493 ycbm (de:hypothetical abc transporter permease protein ycbm) (db:swissprot) YCBM_ECOLI P75851 ESCHERICHIA COLI 562 -11534511

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845453	10220	32376	624	207

Description

GTC ORF with score 123 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0143.) (nt:unnamed protein product) (le:<1) (re:951) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845462	10221	32377	1407	469

Description

6500730654 ycbn:b0935 hypothetical protein:sulfate starvation-induced protein 6:ssi6 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0935 b0935 Escherichia coli 562 -11534512
7000691115 ycbn sulfate starvation-induced protein ssi6 (db:pir2.dat) F64833 F64833 Escherichia coli 562 -11534512 7500959922 ycbn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 85 of 400 of the completegenome.) (nt:f381; this 381 aa orf is 64 pct identical (2 gaps)) (le:11889) (re:13034) (di:complement) AE000195 AE000195 g1787166 Escherichia coli 562 -11534512
5000691887 yzec hypothetical protein m (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#3; similar to pir accession number) (le:2581) (re:3726) (di:complement) D90732 D90732 g4062503 Escherichia coli 562 -11534512

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845476	10222	32378	321	106

Description

5000691888 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0936 b0936 Escherichia coli 562 -11534513
7000691116 probable nitrate transport protein b0936 precursor (db:pir2.dat) G64833 G64833 Escherichia coli 562 -11534513 7500921587 ycbo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 85 of 400 of the completegenome.) (nt:f333; this 333 aa orf is 32 pct identical (6 gaps)) (le:13031) (re:14032) (di:complement) AE000195 AE000195 g1787167 Escherichia coli 562 -11534513
7500921585 ycbo (de:hypothetical 36.3 kd protein in pepn-pyrd intergenic region) (db:swissprot) YCBO_ECOLI P75853 ESCHERICHIA COLI 562 -11534513
6500730655 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0936 b0936 Escherichia coli 562 -11534513

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845481	10223	32379	672	223

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845501	10224	32380	384	127

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845508	10225	32381	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845518	10226	32382	444	147

Description

6500730656 ycbp:b0937 hypothetical protein:sulfate starvation-induced protein 4:ssi4 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0937 b0937 Escherichia coli 562 -11534514 99572 ycbp (de:sulfate starvation-induced protein 4 (ssi4)) (db:swissprot) SSI4_ECOLI P80644 ESCHERICHIA COLI 562 -11534514 7000686686 ycbp sulfate starvation-induced protein ssi4 (db:pir2.dat) H64833 H64833 Escherichia coli 562 -11534514 7500892134 ycbp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 85 of 400 of the completegenome.) (nt:f191; this 191 aa orf is 30 pct identical (7 gaps)) (le:13983) (re:14558) (di:complement) AE000195 AE000195 g1787168 Escherichia coli 562 -11534514 5000691889 sulfate starvation protein 4 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#5; similar to swissprot accession) (le:4675) (re:5250) (di:complement) D90732 D90732 g4062505 Escherichia coli 562 -11534514

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845521	10227	32383	189	62

Description

5000691890 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0938 b0938 Escherichia coli 562 -11534515
7500921589 ycbq (de:precursor) (db:swissprot) YCBQ_ECOLI P75855 ESCHERICHIA COLI 562 -11534515 7000691117 ycbq probable fimbrial protein-like protein ycbq precursor (cl:type 1 fimbrial protein) (db:pir2.dat) A64834 A64834 Escherichia coli 562 -11534515 7500921591 ycbq putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 86 of 400 of the completegenome.) (nt:o182; this 182 aa orf is 38 pct identical (5 gaps)) (le:204) (re:752) (di:direct) AE000196 AE000196 g1787170 Escherichia coli 562 -11534515 7502852110 f17 fimbrial protein precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#6; similar to pir accession number) (le:5598) (re:6146) (di:direct) D90732 D90732 g4062506 Escherichia coli 562 -11534515 6500730657 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0938 b0938 Escherichia coli 562 -11534515

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845533	10228	32384	201	66

Description

5000691891 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0939 b0939 Escherichia coli 562 -11534516
7500921593 ycbr (de:region precursor) (db:swissprot) YCBR_ECOLI P75856 ESCHERICHIA COLI 562 -11534516 7000691118 ycbr probable fimbrial chaperone ycbr precursor (cl:chaperone protein papd) (db:pir2.dat) B64834 B64834 Escherichia coli 562 -11534516 7500921595 ycbr putative chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 86 of 400 of the completegenome.) (nt:o233; this 233 aa orf is 45 pct identical (2 gaps)) (le:835) (re:1536) (di:direct) AE000196 AE000196 g1787171 Escherichia coli 562 -11534516 7502852111 focc periplasmic chaperone focc protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#7; similar to pir accession number) (le:6229) (re:6930) (di:direct) D90732 D90732 g4062507 Escherichia coli 562 -11534516 6500730658 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0939 b0939 Escherichia coli 562 -11534516

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845537	10229	32385	243	80

Description

5000691892 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0940 b0940 Escherichia coli 562 -11534517
7000687416 yCBS (de:region precursor) (db:swissprot) YCBS_ECOLI P75857
ESCHERICHIA COLI 562 -11534517 7000687417 yCBS probable outer membrane usher protein yCBS (cl:outer membrane usher protein fimd) (db:pir2.dat) C64834 C64834 Escherichia coli 562 -11534517 7500921596 yCBS putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 86 of 400 of the completegenome.) (nt:o866; this 866 aa orf is 49 pct identical (21 gaps)) (le:1561) (re:4161) (di:direct) AE000196 AE000196 g1787172 Escherichia coli 562 -11534517
7502852112 fimD fimD protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#8; similar to pir accession number) (le:6955) (re:9555) (di:direct) D90732 D90732 g4062508 Escherichia coli 562 -11534517 6500730659 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0940 b0940 Escherichia coli 562 -11534517

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845539	10230	32386	672	224

Description

5000691893 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0941 b0941 Escherichia coli 562 -11534518
7502852113 yCBT (de:hypothetical 37.9 kd protein in pepn-pyrd intergenic region precursor) (db:swissprot) YCBT_ECOLI P75858 ESCHERICHIA COLI 562 -11534518 7000691119 probable membrane protein b0941 precursor (db:pir2.dat) D64834 D64834 Escherichia coli 562 -11534518 7500959923 b0941 homolog of salmonella fimH protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 86 of 400 of the completegenome.) (nt:o356; this 356 aa orf is 27 pct identical (23 gaps)) (le:4152) (re:5222) (di:direct) AE000196 AE000196 g1787173 Escherichia coli 562 -11534518 7502852114 hypothetical 38.5 kd protein in agai-mtr (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#9; similar to swissprot accession) (le:9546) (re:10616) (di:direct) D90732 D90732 g4062509 Escherichia coli 562 -11534518 6500730660 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0941 b0941 Escherichia coli 562 -11534518

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845559	10231	32387	345	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845562	10232	32388	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845563	10233	32389	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845567	10234	32390	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845568	10235	32391	1197	398

Description

5000691894 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0942 b0942 Escherichia coli 562 -11534519
 7000691120 probable type 1 fimbrial protein b0942 precursor (cl:type 1 fimbrial protein) (db:pir2.dat) E64834 E64834 Escherichia coli 562 -11534519
 7500959924 b0942 putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 86 of 400 of the completegenome.) (nt:o180; residues 119-179 are 31 pct identical to) (le:5234) (re:5776) (di:direct) AE000196 AE000196 g1787174 Escherichia coli 562 -11534519 7502852115 sfag type 1 fimbrial protein precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#10; similar to pir accession number) (le:10628) (re:11170) (di:direct) D90732 D90732 g4062510 Escherichia coli 562 -11534519 6500730661 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0942 b0942 Escherichia coli 562 -11534519

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845575	10236	32392	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845586	10237	32393	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845587	10238	32394	195	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845588	10239	32395	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845589	10240	32396	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845595	10241	32397	2118	705

Description

5000691895 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0943 b0943 Escherichia coli 562 -11534520
7000691121 probable fimbrial protein-like protein b0943 (cl:type 1 fimbrial protein) (db:pir2.dat) F64834 F64834 Escherichia coli 562 -11534520
7500959925 b0943 putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 86 of 400 of the completegenome.) (nt:o187; this 187 aa orf is 39 pct identical (5 gaps)) (le:5736) (re:6299) (di:direct) AE000196 AE000196 g1787175
Escherichia coli 562 -11534520 7502852116 fimf fimf protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#11; similar to pir accession number) (le:11130) (re:11693) (di:direct) D90732 D90732 g4062511
Escherichia coli 562 -11534520 6500730662 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0943 b0943
Escherichia coli 562 -11534520

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845620	10242	32398	744	247

Description

6500730663 ycbf:b0944 hypothetical fimbrial chaperone in pepn-pyrd intergenic region:hypothetical fimbrial chaperone in pepn-pyrd intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0944 b0944 Escherichia coli 562 -11534521 110592
ycbf (de:precursor) (db:swissprot) YCBF_ECOLI P40876 ESCHERICHIA COLI 562 -11534521 7000687404 ycbf probable fimbrial chaperone precursor (cl:chaperone protein papd) (db:pir2.dat) G64834 G64834 Escherichia coli 562 -11534521 7500921570 ycbf putative chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 86 of 400 of the completegenome.) (nt:o245; 100 pct identical to fragment ycbf_ecoli) (le:6265) (re:7002) (di:direct) AE000196 AE000196 g1787176
Escherichia coli 562 -11534521 5000691896 ycbf hypothetical fimbrial chaperone in pepn-pyrd (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#12; similar to swissprot accession) (le:11659) (re:12396) (di:direct) D90732 D90732 g4062512 Escherichia coli 562 -11534521

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501845623	10243	32399	399	132

Description

5000691897 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0946 b0946 Escherichia coli 562 -11534522
7500921604 ycbw (de:hypothetical 22.1 kd protein in pyrd-uup intergenic region) (db:swissprot) YCBW_ECOLI P75862 ESCHERICHIA COLI 562 -11534522
7000691122 ycbw probable membrane protein ycbw (db:pir2.dat) A64835 A64835 Escherichia coli 562 -11534522 7500921606 ycbw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 86 of 400 of the completegenome.) (nt:o192; this 192 aa orf is 26 pct identical (4 gaps)) (le:8261) (re:8839) (di:direct) AE000196 AE000196 g1787178 Escherichia coli 562 -11534522 7502852117 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#14) (le:13655) (re:14233) (di:direct) D90732 D90732 g4062513 Escherichia coli 562 -11534522
6500730664 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0946 b0946 Escherichia coli 562 -11534522

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501845645	10244	32400	852	283

Description

5000691898 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0947 b0947 Escherichia coli 562 -11534523
7000691123 probable iron-sulfur-binding protein b0947 (db:pir2.dat) B64835 B64835 Escherichia coli 562 -11534523 7500959926 b0947 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 86 of 400 of the completegenome.) (nt:f369; this 369 aa orf is 36 pct identical (6 gaps)) (le:8836) (re:9945) (di:complement) AE000196 AE000196 g1787179 Escherichia coli 562 -11534523 6500730665 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0947 b0947 Escherichia coli 562 -11534523

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845661	10245	32401	771	256

Description

6500730666 ycbj:b0948 hypothetical protein:hypothetical 78.9 kd protein in pyrd-pgia intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0948 b0948 Escherichia coli 562 -11534524
 1500686256 ycbj (de:hypothetical 78.9 kd protein in pyrd-pgia intergenic region) (db:swissprot) YCBY_ECOLI P75864 ESCHERICHIA COLI 562 -11534524
 7000687418 hypothetical protein b0948 (db:pir2.dat) C64835 C64835 Escherichia coli 562 -11534524 7500921607 ycbj putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 87 of 400 of the completegenome.) (nt:o702; this 702 aa orf is 61 pct identical (11 gaps)) (le:152) (re:2260) (di:direct) AE000197 AE000197 g1787181 Escherichia coli 562 -11534524 5000691899 hypothetical protein hi0115 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o222#1; similar to pir accession number) (le:15583) (re:17691) (di:direct) D90732 D90732 g4062515 Escherichia coli 562 -11534524
 7502852118 hypothetical protein hi0115 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna. (21.7 - 22.1 min).) (nt:orf_id:o222#1; similar to pir accession number) (le:1196) (re:3304) (di:direct) D90733 D90733 g4062518 Escherichia coli 562 -11534524

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845662	10246	32402	1017	339

Description

6500730667 ycbh:b0949 hypothetical protein:hypothetical abc transporter atp-binding protein in pyrd-pgia intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0949 b0949 Escherichia coli 562 -11534525 110597 uup (de:abc transporter atp-binding protein uup) (db:swissprot) UUP_ECOLI P43672 ESCHERICHIA COLI 562 -11534525
 7000686913 uup abc-type transport protein uup (cl:atp-binding cassette homology) (db:pir2.dat) D64835 D64835 Escherichia coli 562 -11534525
 7500893881 uup putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 87 of 400 of the completegenome.) (nt:o635; this 635 aa orf is 68 pct identical (8 gaps)) (le:2272) (re:4179) (di:direct) AE000197 AE000197 g1787182 Escherichia coli 562 -11534525 5000691900 hypothetical protein hi1300 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna. (21.7 - 22.1 min).) (nt:orf_id:o222#2; similar to pir accession number) (le:3316) (re:5223) (di:direct) D90733 D90733 g4062519 Escherichia coli 562 -11534525

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845663	10247	32403	516	171

Description

5000691903 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0952 b0952 Escherichia coli 562 -11534526
 7500951259 ymba (de:hypothetical 20.0 kd protein in pqib-rmf intergenic region) (db:swissprot) YMBA_ECOLI P75866 ESCHERICHIA COLI 562 -11534526
 7000691124 ymba ymba protein (db:pir2.dat) G64835 G64835 Escherichia coli 562 -11534526 7500951261 ymba orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 87 of 400 of the completegenome.) (nt:o182) (le:7219) (re:7767) (di:direct) AE000197 AE000197 g1787185 Escherichia coli 562 -11534526 6500730668 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0952 b0952 Escherichia coli 562 -11534526

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845668	10248	32404	681	226

Description

5000691904 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0955 b0955 Escherichia coli 562 -11534527
 7000691125 probable atp-dependent proteinase b0955 (cl:hypothetical protein b0955) (db:pir2.dat) B64836 B64836 Escherichia coli 562 -11534527
 7500959927 b0955 putative atp-dependent protease (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 87 of 400 of the completegenome.) (nt:f586; this 586 aa orf is 42 pct identical (22 gaps)) (le:8847) (re:10607) (di:complement) AE000197 AE000197 g1787188 Escherichia coli 562 -11534527 6500730669 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0955 b0955 Escherichia coli 562 -11534527

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845671	10249	32405	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845675	10250	32406	456	151

Description

6500730670 ycbg:b0956 hypothetical protein in ompa 3 region:hypothetical 17.7 kd protein in faba-ompa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0956 b0956 Escherichia coli 562 -11534528 110594 ycbg (de:hypothetical 17.7 kd protein in faba-ompa intergenic region) (db:swissprot) YCBG_ECOLI P45569 ESCHERICHIA COLI 562 -11534528 7000687406 ycbg ycbg protein (db:pir2.dat) C64836 C64836 Escherichia coli 562 -11534528 7500921572 ycbg putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 88 of 400 of the completegenome.) (nt:o150; 100 pct identical to fragment ycbg_ecoli) (le:123) (re:575) (di:direct) AE000198 AE000198 g1787190 Escherichia coli 562 -11534528 5000691905 ycbg hypothetical protein in ompa 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna. (21.7 - 22.1 min).) (nt:orf_id:o223#1; similar to swissprot accession) (le:11837) (re:12289) (di:direct) D90733 D90733 g4062522 Escherichia coli 562 -11534528 7502852119 ycbg hypothetical protein in ompa 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223) (db:genpept) (de:escherichia coli genomic dna. (22.0 - 22.3 min).) (nt:orf_id:o223#1; similar to swissprot accession) (le:8) (re:460) (di:direct) D90734 D90734 g4062526 Escherichia coli 562 -11534528

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845683	10251	32407	234	77

Description

5000691906 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0959 b0959 Escherichia coli 562 -11534529 7502852120 yccr (de:hypothetical 24.1 kd protein in sula-held intergenic region) (db:swissprot) YCCR_ECOLI P75869 ESCHERICHIA COLI 562 -11534529 7000691126 probable membrane protein b0959 (db:pir2.dat) F64836 F64836 Escherichia coli 562 -11534529 7500959928 b0959 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 88 of 400 of the completegenome.) (nt:o209; this 209 aa orf is 31 pct identical (8 gaps)) (le:2776) (re:3405) (di:direct) AE000198 AE000198 g1787193 Escherichia coli 562 -11534529 7502852121 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna. (21.7 - 22.1 min).) (nt:orf_id:o223#4) (le:14490) (re:15119) (di:direct) D90733 D90733 g4062523 Escherichia coli 562 -11534529 7502852122 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223) (db:genpept) (de:escherichia coli genomic dna. (22.0 - 22.3 min).) (nt:orf_id:o223#4) (le:2661) (re:3290) (di:direct) D90734 D90734 g4062527 Escherichia coli 562 -11534529 6500730671 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0959 b0959 Escherichia coli 562 -11534529

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845686	10252	32408	522	173

Description

5000691907 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0960 b0960 Escherichia coli 562 -11534530
7500921628 yccs (de:hypothetical 82.0 kd protein in sula-held intergenic region) (db:swissprot) YCCS_ECOLI P75870 ESCHERICHIA COLI 562 -11534530
7000691127 yccs probable membrane protein yccs (cl:hypothetical protein hil680) (db:pir2.dat) G64836 G64836 Escherichia coli 562 -11534530
7500921630 b0960 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 88 of 400 of the completegenome.) (nt:f720; this 720 aa orf is 38 pct identical (20 gaps)) (le:3368) (re:5530) (di:complement) AE000198 AE000198 g1787194 Escherichia coli 562 -11534530 7502852123 hypothetical protein hil680 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna. (21.7 - 22.1 min).) (nt:orf_id:o223#5; similar to pir accession number) (le:15082) (re:17244) (di:complement) D90733 D90733 g4062524 Escherichia coli 562 -11534530 7502852124 hypothetical protein hil680 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223) (db:genpept) (de:escherichia coli genomic dna. (22.0 - 22.3 min).) (nt:orf_id:o223#5; similar to pir accession number) (le:3253) (re:5415) (di:complement) D90734 D90734 g4062528 Escherichia coli 562 -11534530
6500730672 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0960 b0960 Escherichia coli 562 -11534530

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845689	10253	32409	192	63

Description

6500730673 yccf:b0961 hypothetical protein in held 5 region:hypothetical 16.3 kd protein in sula-held intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0961 b0961 Escherichia coli 562 -11534531 110627 yccf (de:hypothetical 16.3 kd protein in sula-held intergenic region) (db:swissprot) YCCF_ECOLI P37065 ESCHERICHIA COLI 562 -11534531 7000687422 yccf probable membrane protein yccf (db:pir2.dat) H64836 H64836 Escherichia coli 562 -11534531 7500921620 yccf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 88 of 400 of the completegenome.) (nt:f148; 100 pct to fragment yccf_ecoli sw: p37065) (le:5540) (re:5986) (di:complement) AE000198 AE000198 g1787195 Escherichia coli 562 -11534531 5000691908 yccf hypothetical protein in held 5region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna. (21.7 - 22.1 min).) (nt:orf_id:o223#6; similar to swissprot accession) (le:17254) (re:17700) (di:complement) D90733 D90733 g4062525 Escherichia coli 562 -11534531 7502852125 yccf hypothetical protein in held 5region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223) (db:genpept) (de:escherichia coli genomic dna. (22.0 - 22.3 min).) (nt:orf_id:o223#6; similar to swissprot accession) (le:5425) (re:5871) (di:complement) D90734 D90734 g4062529 Escherichia coli 562 -11534531

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845690	10254	32410	1305	435

Description

5000691910 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0964 b0964 Escherichia coli 562 -11534532 7502852126 ycct (de:hypothetical 24.6 kd protein in mgsa-hyaa intergenic region precursor) (db:swissprot) YCCT_ECOLI P75873 ESCHERICHIA COLI 562 -11534532 7000691128 hypothetical protein b0964 precursor (db:pir2.dat) C64837 C64837 Escherichia coli 562 -11534532 7500959929 b0964 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 88 of 400 of the completegenome.) (nt:f220; this 220 aa orf is 26 pct identical (6 gaps)) (le:8749) (re:9411) (di:complement) AE000198 AE000198 g1787198 Escherichia coli 562 -11534532 7502852127 hypothetical protein 2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223) (db:genpept) (de:escherichia coli genomic dna. (22.0 - 22.3 min).) (nt:orf_id:o223#9; similar to pir accession number) (le:8634) (re:9296) (di:complement) D90734 D90734 g4062531 Escherichia coli 562 -11534532 6500730674 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0964 b0964 Escherichia coli 562 -11534532

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845731	10255	32411	459	152

Description

5000691911 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0965 b0965 Escherichia coli 562 -11534533
7000691129 hypothetical protein b0965 (cl:hypothetical protein ynet) (db:pir2.dat) D64837 D64837 Escherichia coli 562 -11534533 7500955840 b0965 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 88 of 400 of the completegenome.) (nt:o164; this 164 aa orf is 27 pct identical (5 gaps)) (le:9503) (re:9997) (di:direct) AE000198 AE000198 g1787199 Escherichia coli 562 -11534533 6500730675 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0965 b0965 Escherichia coli 562 -11534533

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845732	10256	32412	297	98

Description

5000691912 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0966 b0966 Escherichia coli 562 -11534534
7500921632 yccv (de:hypothetical 13.8 kd protein in mgsa-hyaa intergenic region) (db:swissprot) YCCV_ECOLI P75875 ESCHERICHIA COLI 562 -11534534
7000691130 yccv yccv protein (db:pir2.dat) E64837 E64837 Escherichia coli 562 -11534534 7500921634 yccv orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 88 of 400 of the completegenome.) (nt:f122; this 122 aa orf is 32 pct identical (1 gap)) (le:10042) (re:10410) (di:complement) AE000198 AE000198 g1787200 Escherichia coli 562 -11534534 7502852128 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223) (db:genpept) (de:escherichia coli genomic dna. (22.0 - 22.3 min).) (nt:orf_id:o223#11) (le:9927) (re:10295) (di:complement) D90734 D90734 g4062533 Escherichia coli 562 -11534534 6500730676 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0966 b0966 Escherichia coli 562 -11534534

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845733	10257	32413	996	331

Description

5000691913 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0967 b0967 Escherichia coli 562 -11534535
 7500921635 yccw (de:hypothetical 41.1 kd protein in mgsa-hyaa intergenic region) (db:swissprot) YCCW_ECOLI P75876 ESCHERICHIA COLI 562 -11534535
 7000691131 probable methyltransferase b0967 (db:pir2.dat) F64837 F64837 Escherichia coli 562 -11534535 7500921637 b0967 putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 88 of 400 of the completegenome.) (nt:f367; this 396 aa orf is 32 pct identical (9 gaps)) (le:10417) (re:11520) (di:complement) AE000198 AE000198 g1787201 Escherichia coli 562 -11534535 6500730677 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0967 b0967 Escherichia coli 562 -11534535

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845741	10258	32414	384	127

Description

5000691914 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0968 b0968 Escherichia coli 562 -11534536
 7500876547 yccx (ec:3.6.1.7) (de:phosphohydrolase) (db:swissprot) ACYP_ECOLI P75877 ESCHERICHIA COLI 562 -11534536 7000691132 yccx probable acylphosphatase (cl:acylphosphatase) (ec:3.6.1.7) (db:pir2.dat) G64837 G64837 Escherichia coli 562 -11534536 7500876549 b0968 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 89 of 400 of the completegenome.) (nt:o93; 44 pct identical (2 gaps) to 85 residues) (le:121) (re:399) (di:direct) AE000199 AE000199 g1787203 Escherichia coli 562 -11534536 6500730678 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0968 b0968 Escherichia coli 562 -11534536

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845764	10259	32415	207	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845766	10260	32416	1491	496

Description

6500730679 ycck:b0969 hypothetical protein in held-sert intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0969 b0969 Escherichia coli 562 -11534537 7000691831 ycck probable sulfite reductase gamma chain (cl:sulfite reductase gamma chain) (db:pir2.dat) H64837 H64837 Escherichia coli 562 -11534537 7500960347 ycck putative sulfite reductase ec 1.8.-.- (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 89 of 400 of the completegenome.) (nt:f128; 100 pct identical to fragment ycck_ecoli) (le:396) (re:782) (di:complement) AE000199 AE000199 g1787204 Escherichia coli 562 -11534537 5000691915 (de:(ecoli_935) (pn:hypothetical protein in held-sert intergenic region:fragment) (gn:ycck) (gtcfc:13.7:14.1) (ec:) (ycck_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_935 ECOLI_935 Escherichia coli 562 10123102

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845768	10261	32417	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845778	10262	32418	1212	403

Description

6500730680 ycca:b0970 hypothetical 23.4 kd protein in sert
5region:hypothetical 23.4 kd protein in held-sert intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0970
b0970 Escherichia coli 562 -11534538 7500921615 ycca (de:hypothetical 23.4
kd protein in held-sert intergenic region) (db:swissprot) YCCA_ECOLI P06967
ESCHERICHIA COLI 562 -11534538 163903 ycca probable glutamate receptor ycca
(db:pir2.dat) (mp:22 min) S07180 S07180 Escherichia coli 562 -11534538
5000691916 (db:genpept-bct1) (de:e.coli trna-ser-1 and put. 23.5kd protein
gene.) (nt:put. 23.5-kd protein) (le:422) (re:1081) (di:direct) ECDIVE
X00547 g41284 Escherichia coli 562 -11534538 232688 ycca putative
carrier/transport protein (fn:putative transport; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 89 of 400 of the
completegenome.) (nt:f219; 100 pct identical to ycca_ecoli sw: p06967)
(le:816) (re:1475) (di:complement) AE000199 AE000199 g1787205 Escherichia
coli 562 -11534538 7502852129 ycca hypothetical protein:23.5k
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #223) (db:genpept)
(de:escherichia coli genomic dna. (22.0 - 22.3 min).) (nt:orf_id:o224#3;
similar to pir accession number) (le:12282) (re:12941) (di:complement)
D90734 D90734 g4062537 Escherichia coli 562 -11534538 110621 ycca
(de:hypothetical 23.4 kd protein in held-sert intergenic region)
(db:swissprot) YCCA_ECOLI P06967 ESCHERICHIA COLI 562 -11534538

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845794	10263	32419	240	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845812	10264	32420	543	180

Description

6500730681 yccc:b0981 hypothetical protein in appa 3region:hypothetical 81.2 kd protein in appa-cspi intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0981 b0981 Escherichia coli 562 -11534539 110624 yccc (de:hypothetical 81.2 kd protein in appa-csph intergenic region) (db:swissprot) YCCC_ECOLI P38134 ESCHERICHIA COLI 562 -11534539 7000687419 yccc probable atpase yccc (db:pir2.dat) C64839 C64839 Escherichia coli 562 -11534539 7500921617 yccc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 90 of 400 of the completegenome.) (nt:f726; 100 pct identical to fragment yccc_ecoli) (le:1536) (re:3716) (di:complement) AE000200 AE000200 g1787216 Escherichia coli 562 -11534539 5000691917 membrane-associated atp-hydrolase amsa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf_id:o225#8; similar to pir accession number) (le:7949) (re:10129) (di:complement) D90735 D90735 g4062541 Escherichia coli 562 -11534539

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845816	10265	32421	477	158

Description

6500730682 yccy:b0982 hypothetical protein:probable low molecular weight protein-tyrosine-phosphatase yccy (gtcfc:14.1) (ec:3.1.3.48) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0982 b0982 Escherichia coli 562 -11534540 4000709417 yccy (ec:3.1.3.48) (de:(ec 3.1.3.48)) (db:swissprot) YCCY_ECOLI P75880 ESCHERICHIA COLI 562 -11534540 7000687425 yccy probable protein-tyrosine-phosphatase:yccy:low molecular weight (cl:protein-tyrosine-phosphatase, low molecular weight) (ec:3.1.3.48) (db:pir2.dat) D64839 D64839 Escherichia coli 562 -11534540 7500921638 yccy putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 90 of 400 of the completegenome.) (nt:f152; this 152 aa orf is 33 pct identical (13 gaps)) (le:3736) (re:4194) (di:complement) AE000200 AE000200 g1787217 Escherichia coli 562 -11534540 5000691918 amsi protein-tyrosine-phosphatase ec 3.1.3.48:low (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf_id:o225#9; similar to pir accession number) (le:10149) (re:10607) (di:complement) D90735 D90735 g4062542 Escherichia coli 562 -11534540

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845818	10266	32422	828	275

Description

6500730683 yccz:b0983 hypothetical protein:putative polysaccharide export protein yccz precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0983 b0983 Escherichia coli 562 -11534541
 4000709440 yccz (de:putative polysaccharide export protein yccz precursor) (db:swissprot) YCCZ_ECOLI P75881 ESCHERICHIA COLI 562 -11534541 7000687426 yccz probable polysaccharide export protein yccz precursor (db:pir2.dat) E64839 E64839 Escherichia coli 562 -11534541 7500921639 yccz putative function in exopolysaccharide (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 90 of 400 of the completegenome.) (nt:f379; this 379 aa orf is 29 pct identical (33 gaps)) (le:4170) (re:5309) (di:complement) AE000200 AE000200 g1787218 Escherichia coli 562 -11534541 5000691919 bexd protein homolog (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf_id:o225#10; similar to pir accession number) (le:10583) (re:11722) (di:complement) D90735 D90735 g4062543 Escherichia coli 562 -11534541

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845832	10267	32423	183	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845841	10268	32424	300	99

Description

6500730684 ymca:b0984 hypothetical protein:hypothetical 78.7 kd lipoprotein in appa-cspi intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0984 b0984 Escherichia coli 562 -11534542 4000708793 ymca (de:precursor) (db:swissprot) YMCA_ECOLI P75882 ESCHERICHIA COLI 562 -11534542 7000688150 yegh yegh protein precursor (cl:vibrio cholerae otng protein) (db:pir2.dat) F64839 F64839 Escherichia coli 562 -11534542 7500951271 ymca orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 90 of 400 of the completegenome.) (nt:f698; this 698 aa orf is 64 pct identical (7 gaps)) (le:5355) (re:7451) (di:complement) AE000200 AE000200 g1787219 Escherichia coli 562 -11534542 5000691920 hypothetical 78.5 kd protein in pgi-xyle (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf_id:o226#1; similar to swissprot accession) (le:11768) (re:13864) (di:complement) D90735 D90735 g4062544 Escherichia coli 562 -11534542 7502852130 hypothetical 78.5 kd protein in pgi-xyle (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf_id:o226#1; similar to swissprot accession) (le:344) (re:2440) (di:complement) D90736 D90736 g4062701 Escherichia coli 562 -11534542

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845842	10269	32425	1818	605

Description

6500730685 ymcb:b0985 hypothetical protein:hypothetical 27.3 kd protein in appa-cspi intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0985 b0985 Escherichia coli 562 -11534543 4000708192 ymcb (de:hypothetical 27.3 kd protein in appa-csph intergenic region precursor) (db:swissprot) YMCB_ECOLI P75883 ESCHERICHIA COLI 562 -11534543 7000688151 ymcb ymcb protein (cl:hypothetical protein b0985) (db:pir2.dat) G64839 G64839 Escherichia coli 562 -11534543 7500951272 ymcb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 90 of 400 of the completegenome.) (nt:f248; this 248 aa orf is 42 pct identical (1 gap)) (le:7451) (re:8197) (di:complement) AE000200 AE000200 g1787220 Escherichia coli 562 -11534543 5000691921 (de:(ecoli_950) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_950 ECOLI_950 Escherichia coli 562 10123108

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845849	10270	32426	672	223

Description

GTC ORF with score 166 to: (fn:unknown) (sr:xenopus laevis (library: lambda gt11) embryo stage 24/25 (tailbud) (db:genpept-vrt) (de:xenopus laevis ribonucleoprotein mrna, complete cds.) (nt:a protein most similar to the a/b type hmrnp) (le:41) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845898	10271	32427	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845900	10272	32428	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845903	10273	32429	399	132

Description

6500730686 ymcc:b0986 hypothetical protein:hypothetical 24.3 kd lipoprotein in appa-cspi intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0986 b0986 Escherichia coli 562 -11534544 4000708792 ymcc (de:precursor) (db:swissprot) YMCC_ECOLI P75884 ESCHERICHIA COLI 562 -11534544 7000688152 ymcc ymcc protein precursor (cl:hypothetical protein b1706) (db:pir2.dat) H64839 Escherichia coli 562 -11534544 7500951273 ymcc putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 90 of 400 of the completegenome.) (nt:f214; this 214 aa orf is 38 pct identical (4 gaps)) (le:8194) (re:8838) (di:complement) AE000200 AE000200 g1787221 Escherichia coli 562 -11534544 5000691922 hypothetical 25.0 kd lipoprotein in pgi-xyle (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf_id:o226#3; similar to swissprot accession) (le:14607) (re:15251) (di:complement) D90735 D90735 g4062546 Escherichia coli 562 -11534544 7502852131 hypothetical 25.0 kd lipoprotein in pgi-xyle (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf_id:o226#3; similar to swissprot accession) (le:3183) (re:3827) (di:complement) D90736 D90736 g4062703 Escherichia coli 562 -11534544

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845904	10274	32430	1875	624

Description

5000691923 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0987 b0987 Escherichia coli 562 -11534545
7500951274 ymcd (de:hypothetical 10.2 kd protein in appa-csph intergenic region) (db:swissprot) YMCD_ECOLI P75885 ESCHERICHIA COLI 562 -11534545
7000691133 ymcd probable membrane protein ymcd (db:pir2.dat) A64840 A64840 Escherichia coli 562 -11534545 7500951276 ymcd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 90 of 400 of the completegenome.) (nt:f107; this 107 aa orf is 40 pct identical (3 gaps)) (le:8945) (re:9268) (di:complement) AE000200 AE000200 g1787222 Escherichia coli 562 -11534545 7502852132 integumentary mucin c.1 fim-c.1 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf_id:o226#4; similar to pir accession number) (le:15358) (re:15681) (di:complement) D90735 D90735 g4062547 Escherichia coli 562 -11534545
7502852133 integumentary mucin c.1 fim-c.1 . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf_id:o226#4; similar to pir accession number) (le:3934) (re:4257) (di:complement) D90736 D90736 g4062704 Escherichia coli 562 -11534545 6500730687 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0987 b0987 Escherichia coli 562 -11534545

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845913	10275	32431	1413	470

Description

6500730688 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0989 b0989 Escherichia coli 562 -11534546
7500879497 csph:csph (de:cold shock-like protein csph) (db:swissprot) CSPH_ECOLI P56253 ESCHERICHIA COLI 562 -11534546 7000691134 csph:csph cold shock protein homolog csph (cl:major cold shock protein:cold shock domain homology) (db:pir2.dat) C64840 C64840 Escherichia coli 562 -11534546
4000713799 csph csph (db:genpept-bct1) (de:escherichia coli major cold-shock proteins csph (csph) and csph(csph) genes, complete cds.) (nt:major cold-shock protein) (le:652) (re:864) (di:direct) AF003591 AF003591 g2226345 Escherichia coli 562 -11534546 7500879500 csph cold shock-like protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 90 of 400 of the completegenome.) (nt:f70; 75 pct identical to cold shock-like) (le:10469) (re:10681) (di:complement) AE000200 AE000200 g2367112 Escherichia coli 562 -11534546

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845922	10276	32432	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845923	10277	32433	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845928	10278	32434	606	201

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845939	10279	32435	540	179

Description

6500730689 yccm:b0992 hypothetical protein:hypothetical 40.1 kd protein in sfa-tors intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0992 b0992 Escherichia coli 562 -11534547 110635 yccm (de:hypothetical 40.1 kd protein in sfa-tors intergenic region) (db:swissprot) YCCM_ECOLI P52636 ESCHERICHIA COLI 562 -11534547 7000687424 yccm probable ferredoxin-like protein yccm (db:pir2.dat) F64840 F64840 Escherichia coli 562 -11534547 7500921627 yccm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 91 of 400 of the completegenome.) (nt:f357; this 357 aa orf is 28 pct identical (33 gaps)) (le:1062) (re:2135) (di:complement) AE000201 AE000201 gl787226 Escherichia coli 562 -11534547 5000691926 yccm hypothetical protein in sfa 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf_id:o226#11; similar to swissprot accession) (le:6784) (re:7857) (di:complement) D90736 D90736 g4062709 Escherichia coli 562 -11534547

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845945	10280	32436	864	287

Description

6500730690 yccd:b0999 hypothetical 11.5 protein in tord-cbpa intergenic region:orf-2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0999 b0999 Escherichia coli 562 -11534548 110625 yccd (de:hypothetical 11.5 protein in tord-cbpa intergenic region (orf-2)) (db:swissprot) YCCD_ECOLI P36660 ESCHERICHIA COLI 562 -11534548 7000687420 yccd yccd protein (db:pir2.dat) E64841 E64841 Escherichia coli 562 -11534548 7500921618 yccd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 92 of 400 of the completegenome.) (nt:f101; 100 pct identical to yccd_ecoli sw: p36660) (le:106) (re:411) (di:complement) AE000202 AE000202 gl787234 Escherichia coli 562 -11534548 5000691930 yccd hypothetical 11.5 protein in tord-cbpa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf_id:o227#6; similar to swissprot accession) (le:8047) (re:8352) (di:complement) D90737 D90737 g4062555 Escherichia coli 562 -11534548 7502852134 yccd hypothetical 11.5 protein in tord-cbpa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf_id:o227#6; similar to swissprot accession) (le:17045) (re:17350) (di:complement) D90736 D90736 g4062712 Escherichia coli 562 -11534548

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845955	10281	32437	1818	605

Description

GTC ORF with score 709 to: (db:genpept) (de:aureobasidium pullulans multidrug resistance protein 1 (mdr1) gene,promoter region and complete cds.) (nt:atp-binding cassette (abc) transporter protein) (le:542) (re:4450) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501845968	10282	32438	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845972	10283	32439	867	288

Description

6500730691 ycce:b1001 hypothetical protein in cbpa-agp intergenic region:hypothetical 48.4 kd protein in cbpa-agp intergenic region:orf-d (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1001 b1001 Escherichia coli 562 -11534549 110626 ycce (de:hypothetical 48.4 kd protein in cbpa-agp intergenic region (orf-d)) (db:swissprot) YCCE_ECOLI P36661 ESCHERICHIA COLI 562 -11534549 7000687421 ycce ycce protein (db:pir2.dat) G64841 G64841 Escherichia coli 562 -11534549 7500921619 ycce orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:o418; 100 pct identical to fragment ycce_ecoli) (le:1592) (re:2848) (di:direct) AE000202 AE000202 g1787236 Escherichia coli 562 -11534549 5000691931 ycce hypothetical protein in cbpa-agp intergenic (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf_id:o227#8; similar to swissprot accession) (le:9533) (re:10789) (di:direct) D90737 D90737 g4062556 Escherichia coli 562 -11534549

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845977	10284	32440	672	224

Description

6500730692 yccj:b1003 hypothetical 8.5 kd protein in agp 3region:hypothetical 8.5 kd protein in agp-wrba intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1003 b1003 Escherichia coli 562 -11534550 110631 yccj (de:hypothetical 8.5 kd protein in agp-wrba intergenic region) (db:swissprot) YCCJ_ECOLI P46131 ESCHERICHIA COLI 562 -11534550 7000687423 yccj yccj protein (db:pir2.dat) A64842 A64842 Escherichia coli 562 -11534550 7500921621 yccj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:f75; 100 pct identical to yccj_ecoli sw: p46131) (le:4420) (re:4647) (di:complement) AE000202 AE000202 g1787238 Escherichia coli 562 -11534550 5000691932 yccj hypothetical 8.5 kd protein in agp 3region. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf_id:o228#1; similar to swissprot accession) (le:12361) (re:12588) (di:complement) D90737 D90737 g4062557 Escherichia coli 562 -11534550 7502852135 yccj hypothetical 8.5 kd protein in agp 3region. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept) (de:escherichia coli genomic dna. (23.0 - 23.4 min).) (nt:orf_id:o228#1; similar to swissprot accession) (le:825) (re:1052) (di:complement) D90738 D90738 g4062566 Escherichia coli 562 -11534550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845991	10285	32441	1854	617

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501845999	10286	32442	552	184

Description

5000691933 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1005 b1005 Escherichia coli 562 -11534551
7000691135 ycdf ycdf protein (db:pir2.dat) C64842 C64842 Escherichia coli 562 -11534551 7500921648 ycdf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completengenome.) (nt:o76; this 76 aa orf is 29 pct identical (2 gaps)) (le:5474) (re:5704) (di:direct) AE000202 AE000202 g1787240 Escherichia coli 562 -11534551 7500921646 ycdf (de:hypothetical 8.8 kd protein in wrba-puta intergenic region) (db:swissprot) YCDF_ECOLI P75891 ESCHERICHIA COLI 562 -11534551 6500730693 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1005 b1005 Escherichia coli 562 -11534551

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846024	10287	32443	1080	359

Description

6500730694 ycdg:b1006 hypothetical protein:hypothetical 48.1 kd protein in wrba-puta intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1006 b1006 Escherichia coli 562 -11534552
5500686494 ycdg (de:hypothetical 48.1 kd protein in wrba-puta intergenic region) (db:swissprot) YCDG_ECOLI P75892 ESCHERICHIA COLI 562 -11534552
7000687429 ycdg probable transport protein ycdg:probable permease ycdg (cl:uracil transport protein uraa) (db:pir2.dat) D64842 D64842 Escherichia coli 562 -11534552 7500921649 ycdg putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completengenome.) (nt:f464; this 464 aa orf is 41 pct identical (30 gaps)) (le:6067) (re:7461) (di:complement) AE000202 AE000202 g1787241 Escherichia coli 562 -11534552 5000691934 (de:(ecoli_969) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_969 ECOLI_969 Escherichia coli 562 10123117

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846036	10288	32444	645	214

Description

5000691935 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1007 b1007 Escherichia coli 562 -11534553
7000691136 probable monooxygenase b1007 (cl:4-hydroxyphenylacetate 3-monooxygenase small chain) (db:pir2.dat) E64842 E64842 Escherichia coli 562 -11534553 7500959930 b1007 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:f152; 33 pct identical (0 gaps) to 33 residues of) (le:7416) (re:7874) (di:complement) AE000202 AE000202 g1787242 Escherichia coli 562 -11534553 6500730695 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1007 b1007 Escherichia coli 562 -11534553

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846037	10289	32445	645	215

Description

5000691936 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1008 b1008 Escherichia coli 562 -11534554
7000691137 hypothetical protein b1008 (db:pir2.dat) F64842 F64842 Escherichia coli 562 -11534554 7500959931 b1008 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:f196; this 196 aa orf is 26 pct identical (25 gaps)) (le:7921) (re:8511) (di:complement) AE000202 AE000202 g1787243 Escherichia coli 562 -11534554 7502852136 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf_id:o228#6) (le:15862) (re:16452) (di:complement) D90737 D90737 g4062562 Escherichia coli 562 -11534554 7502852137 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept) (de:escherichia coli genomic dna. (23.0 - 23.4 min).) (nt:orf_id:o228#6) (le:4326) (re:4916) (di:complement) D90738 D90738 g4062571 Escherichia coli 562 -11534554 6500730696 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1008 b1008 Escherichia coli 562 -11534554

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846038	10290	32446	681	226

Description

5000691937 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1009 b1009 Escherichia coli 562 -11534555
7000691138 probable hydrolase b1009 (db:pir2.dat) G64842 G64842 Escherichia coli 562 -11534555 7500959932 b1009 putative acetyltransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:f266; this 266 aa orf is 38 pct identical (3 gaps)) (le:8521) (re:9321) (di:complement) AE000202 AE000202 g1787244 Escherichia coli 562 -11534555 7502852138 bcho bcho protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf_id:o228#7; similar to pir accession number) (le:16462) (re:17262) (di:complement) D90737 D90737 g4062563 Escherichia coli 562 -11534555 7502852139 bcho bcho protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept) (de:escherichia coli genomic dna. (23.0 - 23.4 min).) (nt:orf_id:o228#7; similar to pir accession number) (le:4926) (re:5726) (di:complement) D90738 D90738 g4062572 Escherichia coli 562 -11534555 6500730697 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1009 b1009 Escherichia coli 562 -11534555

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846063	10291	32447	705	234

Description

5000691938 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1010 b1010 Escherichia coli 562 -11534556
7000689511 probable translation initiation regulator b1010 (cl:hypothetical protein hi0719) (db:pir2.dat) H64842 H64842 Escherichia coli 562 -11534556 7500955818 b1010 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:f128; residues 3-119 are 35 pct identical to) (le:9329) (re:9715) (di:complement) AE000202 AE000202 g1787245 Escherichia coli 562 -11534556 7502852140 hypothetical protein 1 vnfa 5 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #227) (db:genpept) (de:escherichia coli genomic dna. (22.8 - 23.1 min).) (nt:orf_id:o228#8; similar to pir accession number) (le:17270) (re:17656) (di:complement) D90737 D90737 g4062564 Escherichia coli 562 -11534556 7502852141 hypothetical protein 1 vnfa 5 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept) (de:escherichia coli genomic dna. (23.0 - 23.4 min).) (nt:orf_id:o228#8; similar to pir accession number) (le:5734) (re:6120) (di:complement) D90738 D90738 g4062573 Escherichia coli 562 -11534556 6500730698 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1010 b1010 Escherichia coli 562 -11534556

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846064	10292	32448	354	118
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846070	10293	32449	372	123
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846071	10294	32450	1617	538
<u>Description</u>				

5000691939 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1011 b1011 Escherichia coli 562 -11534557
7000691139 hypothetical protein b1011 (cl:hypothetical protein b1011) (db:pir2.dat) A64843 A64843 Escherichia coli 562 -11534557 7500955931 b1011 putative synthetase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:f244; this 244 aa orf is 25 pct identical (17 gaps)) (le:9727) (re:10461) (di:complement) AE000202 AE000202 g1787246 Escherichia coli 562 -11534557 6500730699 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1011 b1011 Escherichia coli 562 -11534557

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846083	10295	32451	351	116
<u>Description</u>				

5000691940 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1012 b1012 Escherichia coli 562 -11534558
7000691140 hypothetical protein b1012 (db:pir2.dat) B64843 B64843 Escherichia coli 562 -11534558 7500959933 b1012 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 92 of 400 of the completegenome.) (nt:f382; this 382 aa orf is 23 pct identical (14 gaps)) (le:10419) (re:11567) (di:complement) AE000202 AE000202 g1787247 Escherichia coli 562 -11534558 7502852142 yxek hypothetical 49.3 kd protein in idh-deor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept) (de:escherichia coli genomic dna. (23.0 - 23.4 min).) (nt:orf_id:o228#10; similar to swissprot accession) (le:6824) (re:7972) (di:complement) D90738 D90738 g4062575 Escherichia coli 562 -11534558 6500730700 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1012 b1012 Escherichia coli 562 -11534558

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846085	10296	32452	318	105

Description

GTC ORF with score 173 to: (sr:n.crassa (strain 74-or23-1a) dna, clone pcon10a) (db:genpept-pln1) (de:n.crassa conidation-specific protein genes con-10 (complete cds.)and con-13 (3' flank).) (nt:conidation-specific protein con-10) (le:1745:1859:2021) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846114	10297	32453	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846116	10298	32454	183	60

Description

6500730701 ycdc:b1013 hypothetical protein:hypothetical transcriptional regulator in wrba-puta intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1013 b1013 Escherichia coli 562 -11534559 1500686229 ycdc (de:hypothetical transcriptional regulator in wrba-puta intergenic region) (db:swissprot) YCDC_ECOLI P75899 ESCHERICHIA COLI 562 -11534559 7000687428 ycdc probable transcription regulator ycdc (db:pir2.dat) C64843 C64843 Escherichia coli 562 -11534559 7500921645 ycdc putative tet operon regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 93 of 400 of the completegenome.) (nt:o212; this 212 aa orf is 22 pct identical (1 gap)) (le:146) (re:784) (di:direct) AE000203 AE000203 g1787249 Escherichia coli 562 -11534559 5000691941 yixd orfa 3 of hemy (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept) (de:escherichia coli genomic dna. (23.0 - 23.4 min).) (nt:orf_id:o228#11; similar to pir accession number) (le:8203) (re:8841) (di:direct) D90738 D90738 g4062576 Escherichia coli 562 -11534559

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846117	10299	32455	231	76

Description

5000691942 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1016 b1016 Escherichia coli 562 -11534560
7000691141 hypothetical protein b1016 (db:pir2.dat) F64843 F64843
Escherichia coli 562 -11534560 7500959934 b1016 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 93 of 400 of the completegenome.) (nt:o39; this 39 aa orf is 38 pct identical (1 gap)) (le:7251) (re:7370) (di:direct) AE000203 AE000203
g1787252 Escherichia coli 562 -11534560 6500730702 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1016 b1016 Escherichia coli 562 -11534560

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846118	10300	32456	210	69

Description

5000691943 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1017 b1017 Escherichia coli 562 -11534561
7000691142 probable peroxidase b1017 (db:pir2.dat) G64843 G64843
Escherichia coli 562 -11534561 7500959935 b1017 putative cytochrome (fn:putative carrier; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 93 of 400 of the completegenome.) (nt:o243; this 243 aa orf is 31 pct identical (11 gaps)) (le:7358) (re:8089) (di:direct) AE000203 AE000203
g1787253 Escherichia coli 562 -11534561 6500730703 hypothetical protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #228) (db:genpept) (de:escherichia coli genomic dna. (23.0 - 23.4 min).) (nt:orf_id:o229#1; similar to pir accession number) (le:15415) (re:16146) (di:direct) D90738 D90738 g4062578 Escherichia coli 562 -11534561
7502852143 hypothetical protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #229) (db:genpept) (de:escherichia coli genomic dna. (23.3 - 23.6 min).) (nt:orf_id:o229#1; similar to pir accession number) (le:849) (re:1580) (di:direct) D90739 D90739 g4062582 Escherichia coli 562 -11534561

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846119	10301	32457	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846133	10302	32458	255	84

Description

5000691944 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1018 b1018 Escherichia coli 562 -11534562
 7500921650 ycd0 (de:hypothetical 41.1 kd protein in putp-phoh intergenic region) (db:swissprot) YCDO_ECOLI P75902 ESCHERICHIA COLI 562 -11534562
 7000691143 ycd0 ycd0 protein (db:pir2.dat) H64843 H64843 Escherichia coli 562 -11534562 7500921652 ycd0 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 93 of 400 of the completegenome.) (nt:o375; this 375 aa orf is 45 pct identical (4 gaps)) (le:8147) (re:9274) (di:direct) AE000203 AE000203 g1787254 Escherichia coli 562 -11534562 6500730704 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1018 b1018 Escherichia coli 562 -11534562

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846166	10303	32459	627	208

Description

6500730705 ycdb:b1019 hypothetical protein in phoh 5region:hypothetical 46.8 kd protein in putp-phoh intergenic region precursor:orf1 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1019 b1019 Escherichia coli 562 -11534563 110644 ycdb (de:(orf1)) (db:swissprot) YCDB_ECOLI P31545 ESCHERICHIA COLI 562 -11534563 7000687427 ycdb ycdb protein precursor (cl:hypothetical protein ycdb) (db:pir2.dat) A64844 A64844 Escherichia coli 562 -11534563 7500921644 ycdb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 93 of 400 of the completegenome.) (nt:o423; 100 pct identical to 228 aa fragment of) (le:9280) (re:10551) (di:direct) AE000203 AE000203 g1787255 Escherichia coli 562 -11534563 5000691945 ycdb orf1 5 of phoh. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #229) (db:genpept) (de:escherichia coli genomic dna. (23.3 - 23.6 min).) (nt:orf_id:o229#3; similar to pir accession number) (le:2771) (re:4042) (di:direct) D90739 D90739 g4062584 Escherichia coli 562 -11534563

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846176	10304	32460	2190	730

Description

6500730706 ycdp:b1021 hypothetical protein:hypothetical 16.1 kd protein in phoh-csgg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1021 b1021 Escherichia coli 562 -11534564
 4000709320 ycdp (de:hypothetical 16.1 kd protein in phoh-csgg intergenic region) (db:swissprot) YCDP_ECOLI P75904 ESCHERICHIA COLI 562 -11534564
 7000687430 ycdp probable membrane protein ycdp (db:pir2.dat) C64844 C64844 Escherichia coli 562 -11534564 7500921653 ycdp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 94 of 400 of the completegenome.) (nt:f137; this 137 aa orf is 23 pct identical (6 gaps)) (le:1317) (re:1730) (di:complement) AE000204 AE000204 g1787258 Escherichia coli 562 -11534564 5000691946 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #229) (db:genpept) (de:escherichia coli genomic dna. (23.3 - 23.6 min).) (nt:orf_id:o229#5) (le:5501) (re:5914) (di:complement) D90739 D90739 g4062585 Escherichia coli 562 -11534564

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846178	10305	32461	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846179	10306	32462	1467	489

Description

GTC ORF with score 101 to: (sr:homo sapiens male myeloblast cell_line kg-1 cdna to mrna) (db:genpept-pri2) (de:human mrna for kiaa0035 gene, partial cds.) (nt:similar to rat nucleolar phosphoprotein of 140kd) (le:<1) (re:2126) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846191	10307	32463	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846192	10308	32464	1248	416

Description

6500730707 ycdq:b1022 hypothetical protein:hypothetical 50.8 kd protein in phoh-csgg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1022 b1022 Escherichia coli 562 -11534565
 4000709321 ycdq (de:hypothetical 50.8 kd protein in phoh-csgg intergenic region) (db:swissprot) YCDQ_ECOLI P75905 ESCHERICHIA COLI 562 -11534565
 7000687431 ycdq probable glycosyltransferase ycdq (db:pir2.dat) D64844 D64844 Escherichia coli 562 -11534565 7500921654 ycdq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 94 of 400 of the completgenome.) (nt:f441; this 441 aa orf is 26 pct identical (25 gaps)) (le:1732) (re:3057) (di:complement) AE000204 AE000204 g1787259 Escherichia coli 562 -11534565 5000691947 glycosyl transferase lgtD homolog (sr:escherichia coli(strain:k12) dna, clone:kohara clone #229) (db:genpept) (de:escherichia coli genomic dna. (23.3 - 23.6 min).) (nt:orf_id:o229#6; similar to pir accession number) (le:5916) (re:7241) (di:complement) D90739 D90739 g4062586 Escherichia coli 562 -11534565

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846196	10309	32465	447	148

Description

6500730708 ycdr:b1023 hypothetical protein:hypothetical 77.4 kd lipoprotein in phoh-csgg intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1023 b1023 Escherichia coli 562 -11534566 4000709322 ycdr (de:precursor) (db:swissprot) YCDR_ECOLI P75906 ESCHERICHIA COLI 562 -11534566 7000687432 ycdr ycdr protein precursor (db:pir2.dat) E64844 E64844 Escherichia coli 562 -11534566 7500921655 ycdr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 94 of 400 of the completgenome.) (nt:f672; this 672 aa orf is 33 pct identical (4 gaps)) (le:3050) (re:5068) (di:complement) AE000204 AE000204 g1787260 Escherichia coli 562 -11534566 5000691948 (de:(ecoli_986) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_986 ECOLI_986 Escherichia coli 562 10123130

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846202	10310	32466	564	187

Description

GTC ORF with score 115 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmid 9819.) (nt:small region of similarity to nadh-ubiquinone) (le:3007) (re:3876) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846203	10311	32467	489	162

Description

GTC ORF with score 116 to: (sr:baker's yeast strain=s288c (ab972))
(db:genpept-pln1) (de:saccharomyces cerevisiae chromosome iv cosmid 9819.)
(nt:small region of similarity to nadh-ubiquinone) (le:3007) (re:3876)
(di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846205	10312	32468	255	84

Description

6500730709 ycds:b1024 hypothetical protein:hypothetical 92.2 kd protein in
phoh-csgg intergenic region precursor (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b1024 b1024 Escherichia coli 562
-11534567 4000709323 ycds (de:hypothetical 92.2 kd protein in phoh-csgg
intergenic region precursor) (db:swissprot) YCDS_ECOLI P75907 ESCHERICHIA
COLI 562 -11534567 7000687433 ycds ycds protein precursor (db:pir2.dat)
F64844 F64844 Escherichia coli 562 -11534567 7500921656 ycds putative outer
membrane protein (fn:putative membrane; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 94 of 400 of the completegenome.)
(nt:f807; this 807 aa orf is 27 pct identical (4 gaps)) (le:5077) (re:7500)
(di:complement) AE000204 AE000204 g1787261 Escherichia coli 562 -11534567
5000691949 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #229)
(db:genpept) (de:escherichia coli genomic dna. (23.3 - 23.6 min).)
(nt:orf_id:o230#1) (le:9260) (re:11683) (di:complement) D90739 D90739
g4062589 Escherichia coli 562 -11534567 7502852144 (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #230) (db:genpept) (de:escherichia
coli genomic dna. (23.5 - 23.8 min).) (nt:orf_id:o230#1) (le:112) (re:2535)
(di:complement) D90740 D90740 g4062592 Escherichia coli 562 -11534567

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846263	10313	32469	1170	390

Description

6500730710 ycdt:b1025 hypothetical protein:hypothetical 51.8 kd protein in phoh-csgg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1025 b1025 Escherichia coli 562 -11534568
 4000709324 ycdt (de:hypothetical 51.8 kd protein in phoh-csgg intergenic region) (db:swissprot) YCDT_ECOLI P75908 ESCHERICHIA COLI 562 -11534568
 7000687434 ycdt probable membrane protein ycdt (cl:hypothetical protein b1785) (db:pir2.dat) G64844 G64844 Escherichia coli 562 -11534568
 7500921657 ycdt orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl1655 section 94 of 400 of the completegenome.) (nt:o452; this 452 aa orf is 31 pct identical (20 gaps)) (le:8087) (re:9445) (di:direct) AE000204 AE000204 g1787262 Escherichia coli 562 -11534568 5000691950 (de:(ecoli_988) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_988 ECOLI_988 Escherichia coli 562 10123132

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846273	10314	32470	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846277	10315	32471	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846279	10316	32472	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846299	10317	32473	615	205

Description

GTC ORF with score 110 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 8083.) (nt:similar to kluyveromyces lactis deoxyribonucleic) (le:23775) (re:26219) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846308	10318	32474	1227	409

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846329	10319	32475	756	251

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846330	10320	32476	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846334	10321	32477	576	191

Description

5000691951 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1028 b1028 Escherichia coli 562 -11534569
7000691145 hypothetical protein b1028 (db:pir2.dat) B64845 B64845
Escherichia coli 562 -11534569 7500959941 b1028 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
95 of 400 of the complete genome.) (nt:0107; this 107 aa orf is 27 pct
identical (0 gaps)) (le:69) (re:392) (di:direct) AE000205 AE000205 g1787266
Escherichia coli 562 -11534569 6500730711 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1028 b1028
Escherichia coli 562 -11534569

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846338	10322	32478	258	85

Description

6500730712 ycdy:b1029 hypothetical protein:hypothetical 38.7 kd protein in phoh-csgg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1029 b1029 Escherichia coli 562 -11534570
 4000709325 ycdy (de:hypothetical 38.7 kd protein in phoh-csgg intergenic region) (db:swissprot) YCDU_ECOLI P75910 ESCHERICHIA COLI 562 -11534570
 7000687435 ycdy probable membrane protein ycdy (db:pir2.dat) C64845 C64845 Escherichia coli 562 -11534570 7500921658 ycdy orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of 400 of the completegenome.) (nt:o328; this 328 aa orf is 19 pct identical (4 gaps)) (le:389) (re:1375) (di:direct) AE000205 AE000205 g1787267 Escherichia coli 562 -11534570 5000691952 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #230) (db:genpept) (de:escherichia coli genomic dna. (23.5 - 23.8 min).) (nt:orf_id:o230#5) (le:6089) (re:7075) (di:direct) D90740 D90740 g4062596 Escherichia coli 562 -11534570

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846339	10323	32479	360	119

Description

5000691953 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1030 b1030 Escherichia coli 562 -11534571
 7000691146 hypothetical protein b1030 (db:pir2.dat) D64845 D64845 Escherichia coli 562 -11534571 7500959942 b1030 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of 400 of the completegenome.) (nt:o83; this 83 aa orf is 25 pct identical (7 gaps)) (le:1494) (re:1745) (di:direct) AE000205 AE000205 g1787268 Escherichia coli 562 -11534571 6500730713 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1030 b1030 Escherichia coli 562 -11534571

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846341	10324	32480	222	73

Description

6500730714 ycdv:b1031 hypothetical protein:hypothetical 15.0 kd protein in phoh-csgg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1031 b1031 Escherichia coli 562 -11534572 7000687436 ycdv ycdv protein (db:pir2.dat) E64845 E64845 Escherichia coli 562 -11534572 7500921659 ycdv putative ribosomal protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of 400 of the completegenome.) (nt:o137; this 137 aa orf is 27 pct identical (1 gap)) (le:1513) (re:1926) (di:direct) AE000205 AE000205 g1787269 Escherichia coli 562 -11534572 4000709326 ycdv (de:hypothetical 15.0 kd protein in phoh-csgg intergenic region) (db:swissprot) YCDV_ECOLI P75912 ESCHERICHIA COLI 562 -11534572 5000691954 (de:(ecoli_994) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_994 ECOLI_994 Escherichia coli 562 10123136

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846348	10325	32481	591	196

Description

6500730715 ycdw:b1033 hypothetical protein:putative 2-hydroxyacid dehydrogenase in phoh-csgg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1033 b1033 Escherichia coli 562 -11534573 4000709327 ycdw (de:putative 2-hydroxyacid dehydrogenase in phoh-csgg intergenic region) (db:swissprot) YCDW_ECOLI P75913 ESCHERICHIA COLI 562 -11534573 7000687437 ycdw probable 2-hydroxyacid dehydrogenase ycdw (db:pir2.dat) F64845 F64845 Escherichia coli 562 -11534573 7500921660 ycdw putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of 400 of the completegenome.) (nt:o325; this 325 aa orf is 32 pct identical (2 gaps)) (le:2393) (re:3370) (di:direct) AE000205 AE000205 g1787270 Escherichia coli 562 -11534573 5000691955 (de:(ecoli_995) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_995 ECOLI_995 Escherichia coli 562 10123137

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846350	10326	32482	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846352	10327	32483	225	74

Description

6500730716 ycdx:b1034 hypothetical protein:hypothetical 26.9 kd protein in phoh-csgg intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1034 b1034 Escherichia coli 562 -11534574 4000709328 ycdx (de:hypothetical 26.9 kd protein in phoh-csgg intergenic region precursor) (db:swissprot) YCDX_ECOLI P75914 ESCHERICHIA COLI 562 -11534574 7000687438 ycdx ycdx protein (db:pir2.dat) G64845 G64845 Escherichia coli 562 -11534574 7500921661 ycdx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of 400 of the completegenome.) (nt:o245) (le:3425) (re:4162) (di:direct) AE000205 AE000205 g1787271 Escherichia coli 562 -11534574 5000691956 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #230) (db:genpept) (de:escherichia coli genomic dna. (23.5 - 23.8 min).) (nt:orf_id:o231#2) (le:8944) (re:9681) (di:direct) D90740 D90740 g4062598 Escherichia coli 562 -11534574 7502852145 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231) (db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).) (nt:orf_id:o231#2) (le:2145) (re:2882) (di:direct) D90741 D90741 g4062607 Escherichia coli 562 -11534574

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846353	10328	32484	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846366	10329	32485	330	110

Description

6500730717 ycdy:b1035 hypothetical protein:hypothetical 20.7 kd protein in phoh-csgg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1035 b1035 Escherichia coli 562 -11534575
4000708193 ycdy (de:hypothetical 20.7 kd protein in phoh-csgg intergenic region) (db:swissprot) YCDY_ECOLI P75915 ESCHERICHIA COLI 562 -11534575
7000687439 ycdy ycdy protein (cl:escherichia coli ycdy protein) (db:pir2.dat) H64845 H64845 Escherichia coli 562 -11534575 7500921662 ycdy putative oxidoreductase component (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of 400 of the completegenome.) (nt:ol84; this 184 aa orf is 40 pct identical (12 gaps)) (le:4186) (re:4740) (di:direct) AE000205 AE000205 g1787272 Escherichia coli 562 -11534575 5000691957 hypothetical protein hi1543 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #230) (db:genpept) (de:escherichia coli genomic dna. (23.5 - 23.8 min).) (nt:orf_id:o231#3; similar to pir accession number) (le:9705) (re:10259) (di:direct) D90740 D90740 g4062599 Escherichia coli 562 -11534575 7502852146 hypothetical protein hi1543 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231) (db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).) (nt:orf_id:o231#3; similar to pir accession number) (le:2906) (re:3460) (di:direct) D90741 D90741 g4062608 Escherichia coli 562 -11534575

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846367	10330	32486	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846368	10331	32487	900	299

Description

6500730718 ycdz:b1036 hypothetical protein:hypothetical 18.8 kd protein in phoh-csgg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b1036 b1036 Escherichia coli 562 -11534576
4000709329 ycdz (de:hypothetical 18.8 kd protein in phoh-csgg intergenic region) (db:swissprot) YCDZ_ECOLI P75916 ESCHERICHIA COLI 562 -11534576
7000687440 ycdz probable membrane protein ycdz (db:pir2.dat) A64846 A64846 Escherichia coli 562 -11534576 7500921664 ycdz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of 400 of the completegenome.) (nt:o179; this 179 aa orf is 27 pct identical (12 gaps)) (le:4794) (re:5333) (di:direct) AE000205 AE000205 g1787273 Escherichia coli 562 -11534576 5000691958 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #230) (db:genpept) (de:escherichia coli genomic dna. (23.5 - 23.8 min).) (nt:orf_id:o231#4) (le:10313) (re:10852) (di:direct) D90740 D90740 g4062600 Escherichia coli 562 -11534576 7502852147 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231) (db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).) (nt:orf_id:o231#4) (le:3514) (re:4053) (di:direct) D90741 D90741 g4062609 Escherichia coli 562 -11534576

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846394	10332	32488	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846396	10333	32489	1311	436

6500730719 csgc:b1043 hypothetical protein:putative curli production protein
csgc precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1043 b1043 Escherichia coli 562 -11534577 110646
csgc (de:putative curli production protein csgc precursor) (db:swissprot)
CSGC_ECOLI P52107 ESCHERICHIA COLI 562 -11534577 7000684916 csgc csgc
protein precursor (db:pir2.dat) S70789 S70789 Escherichia coli 562 -11534577
7500879454 orfc putative curli production protein (db:genpept-bct1)
(de:e.coli csgg, csge, csge, csge, csge, csge, and orfc genes.) (le:4243)
(re:4575) (di:direct) ECCSGABDG X90754 g1147565 Escherichia coli 562
-11534577 232590 csgc putative curli production protein (fn:putative
structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 95 of 400 of the completegenome.) (nt:o110; this 110 aa orf
is 32 pct identical (3 gaps)) (le:9507) (re:9839) (di:direct) AE000205
AE000205 g1787280 Escherichia coli 562 -11534577 5000691964 ycde putative
curli production protein precursor (sr:escherichia coli(strain:k12) dna,
clone:kohara clone #231) (db:genpept) (de:escherichia coli genomic dna.
(23.7 - 24.0 min).) (nt:orf_id:o232#1; similar to swissprot accession)
(le:8227) (re:8559) (di:direct) D90741 D90741 g4062614 Escherichia coli 562
-11534577 7502852148 ycde putative curli production protein precursor
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept)
(de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf_id:o232#1;
similar to swissprot accession) (le:245) (re:577) (di:direct) D90742 D90742
q4062620 Escherichia coli 562 -11534577

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846403	10334	32490	396	131

Description

5000691965 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1044 b1044 Escherichia coli 562 -11534578
7502852149 ymda (de:hypothetical 11.2 kd protein in csgc-mdog intergenic region precursor) (db:swissprot) YMDA_ECOLI P75917 ESCHERICHIA COLI 562 -11534578 7000691147 hypothetical protein b1044 precursor (db:pir2.dat) A64847 A64847 Escherichia coli 562 -11534578 7500959943 b1044 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of 400 of the completengenome.) (nt:o103; this 103 aa orf is 44 pct identical (0 gaps)) (le:9960) (re:10271) (di:direct) AE000205 AE000205 g1787281 Escherichia coli 562 -11534578 7502852150 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231) (db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).) (nt:orf_id:o232#2) (le:10016) (re:10327) (di:direct) D90741 D90741 g4062615 Escherichia coli 562 -11534578 7502852151 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf_id:o232#2) (le:2034) (re:2345) (di:direct) D90742 D90742 g4062621 Escherichia coli 562 -11534578 6500730720 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1044 b1044 Escherichia coli 562 -11534578

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846418	10335	32491	186	61

Description

5000691966 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1045 b1045 Escherichia coli 562 -11534579
7000691148 hypothetical protein b1045 (db:pir2.dat) B64847 B64847 Escherichia coli 562 -11534579 7500959944 b1045 putative polyprotein (fn:orf; unknown function) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 96 of 400 of the completengenome.) (nt:o177; this 177 aa orf is 31 pct identical (4 gaps)) (le:78) (re:611) (di:direct) AE000206 AE000206 g1787283 Escherichia coli 562 -11534579 7502852152 orf2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231) (db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).) (nt:orf_id:o232#3; similar to pir accession number) (le:10422) (re:10955) (di:direct) D90741 D90741 g4062616 Escherichia coli 562 -11534579 7502852153 orf2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf_id:o232#3; similar to pir accession number) (le:2440) (re:2973) (di:direct) D90742 D90742 g4062622 Escherichia coli 562 -11534579 6500730721 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1045 b1045 Escherichia coli 562 -11534579

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846420	10336	32492	2343	781

Description

6500730722 ymdc:b1046 hypothetical protein:hypothetical 55.9 kd protein in csga-mdog intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1046 b1046 Escherichia coli 562 -11534580
5500686624 ymdc (de:hypothetical 55.9 kd protein in csgc-mdog intergenic region) (db:swissprot) YMDC_ECOLI P75919 ESCHERICHIA COLI 562 -11534580
7000688153 ymdc ymdc protein (db:pir2.dat) C64847 C64847 Escherichia coli 562 -11534580 7500951288 ymdc putative synthase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 96 of 400 of the completegenome.) (nt:o493; this 493 aa orf is 31 pct identical (13 gaps)) (le:553) (re:2034) (di:direct) AE000206 AE000206 g1787284 Escherichia coli 562 -11534580 5000691967 cls novobiocin resistance-related protein nov (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231) (db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).) (nt:orf_id:o232#4; similar to pir accession number) (le:10897) (re:12378) (di:direct) D90741 D90741 g4062617 Escherichia coli 562 -11534580
7502852154 cls novobiocin resistance-related protein nov (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf_id:o232#4; similar to pir accession number) (le:2915) (re:4396) (di:direct) D90742 D90742 g4062623 Escherichia coli 562 -11534580

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846444	10337	32493	477	158

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846452	10338	32494	1539	512

Description

5000691968 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1047 b1047 Escherichia coli 562 -11534581
7500951289 ymdd (de:hypothetical 44.7 kd protein in csgc-modg intergenic region) (db:swissprot) YMDD_ECOLI P75920 ESCHERICHIA COLI 562 -11534581
7000691149 ymdd probable membrane protein ymdd (db:pir2.dat) D64847 D64847 Escherichia coli 562 -11534581 7500951291 ymdd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 96 of 400 of the completegenome.) (nt:f385; this 385 aa orf is 24 pct identical (21 gaps)) (le:2042) (re:3199) (di:complement) AE000206 AE000206 g1787285 Escherichia coli 562 -11534581 7502852155 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231) (db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).) (nt:orf_id:o232#5) (le:12386) (re:13543) (di:complement) D90741 D90741 g4062618 Escherichia coli 562 -11534581 7502852156 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf_id:o232#5) (le:4404) (re:5561) (di:complement) D90742 D90742 g4062624 Escherichia coli 562 -11534581 6500730723 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1047 b1047 Escherichia coli 562 -11534581

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846453	10339	32495	372	123

Description

6500730724 ycek:b1050 hypothetical protein in mdoh-msyb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1050 b1050 Escherichia coli 562 -11534582 7000691836 ycek ycek protein precursor (cl:hypothetical protein hi0650) (db:pir2.dat) G64847 G64847 Escherichia coli 562 -11534582 7500960350 ycek orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 96 of 400 of the completegenome.) (nt:o75; 100 pct identical to ycek_ecoli sw: p45806 but) (le:7837) (re:8064) (di:direct) AE000206 AE000206 g1787288 Escherichia coli 562 -11534582 5000691969 (de:(ecoli_1012) (pn:hypothetical 7) (gn:ycek) (gtcfc:13.7:14.1) (ec:) (ycek_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1012 ECOLI_1012 Escherichia coli 562 10123145

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846482	10340	32496	492	164
<u>Description</u>				
5000691970 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1052 b1052 Escherichia coli 562 -11534583				
7000691150 hypothetical protein b1052 (db:pir2.dat) A64848 A64848				
Escherichia coli 562 -11534583 7500959945 b1052 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 96 of 400 of the completegenome.) (nt:f32; this 32 aa orf is 44 pct identical (1 gap)) (le:8469) (re:8567) (di:complement) AE000206 AE000206				
g1787290 Escherichia coli 562 -11534583 6500730725 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1052 b1052 Escherichia coli 562 -11534583				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846485	10341	32497	396	131
<u>Description</u>				
6500730726 ycee:b1053 hypothetical 43.9 kd protein in msyb-htrb intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1053 b1053 Escherichia coli 562 -11534584 7500921680 ycee (de:hypothetical 43.9 kd protein in msyb-htrb intergenic region (orf1)) (db:swissprot) YCEE_ECOLI P25744 ESCHERICHIA COLI 562 -11534584 164388 ycee probable membrane protein b1053 (cl:escherichia coli probable integral membrane protein) (db:pir2.dat) B42290 B42290 Escherichia coli 562 -11534584 5000691971 orf1 (db:genpept-bct1) (de:e.coli orf1 and msyb gene for membrane protein and multicopysuppressor of secy24 mutation protein.) (le:496) (re:1722) (di:direct) ECMSYB X59939 g42029 Escherichia coli 562 -11534584 233414 ycee putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 96 of 400 of the completegenome.) (nt:f408; 100 pct identical to ycee_ecoli sw: p25744) (le:8522) (re:9748) (di:complement) AE000206 AE000206 g1787291 Escherichia coli 562 -11534584 7502852157 ycee probable integral membrane protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf_id:o233#2; similar to pir accession number) (le:10884) (re:12110) (di:complement) D90742 D90742 g4062627 Escherichia coli 562 -11534584 7502852158 ycee probable integral membrane protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf_id:o233#2; similar to pir accession number) (le:630) (re:1856) (di:complement) D90743 D90743 g4062636 Escherichia coli 562 -11534584 110664 ycee (de:hypothetical 43.9 kd protein in msyb-htrb intergenic region (orf1)) (db:swissprot) YCEE_ECOLI P25744 ESCHERICHIA COLI 562 -11534584				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846502	10342	32498	936	311

Description

6500730727 ycea:b1055 hypothetical 40.0 kd protein in htrb 5region:orf39.9 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1055 b1055 Escherichia coli 562 -11534585 7500921672 ycea (de:hypothetical 40.0 kd protein in htrb-dini intergenic region (orf39.9)) (db:swissprot) YCEA_ECOLI P24188 ESCHERICHIA COLI 562 -11534585 7000690939 ycea ycea protein (cl:escherichia coli ycea protein) (db:pir2.dat) D64848 D64848 Escherichia coli 562 -11534585 7500921674 ycea orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 97 of 400 of the completegenome.) (nt:o350; 99 pct identical to ycea_ecoli sw: p24188) (le:143) (re:1195) (di:direct) AE000207 AE000207 g1787294 Escherichia coli 562 -11534585 5000691973 ycea hypothetical protein 39.9 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf_id:o233#4; similar to pir accession number) (le:13427) (re:14479) (di:direct) D90742 D90742 g4062629 Escherichia coli 562 -11534585 7502852159 ycea hypothetical protein 39.9 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf_id:o233#4; similar to pir accession number) (le:3173) (re:4225) (di:direct) D90743 D90743 g4062637 Escherichia coli 562 -11534585

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846505	10343	32499	312	103

Description

6500730728 ycei:b1056 hypothetical 18.7 kd protein in htrb 5region:18.7 kd protein in htrb-dini intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1056 b1056 Escherichia coli 562 -11534586 110669 ycei (de:18.7 kd protein in htrb-dini intergenic region precursor) (db:swissprot) YCEI_ECOLI P37904 ESCHERICHIA COLI 562 -11534586 7000687445 ycei ycei protein precursor (db:pir2.dat) E64848 E64848 Escherichia coli 562 -11534586 7500921685 ycei orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 97 of 400 of the completegenome.) (nt:f191; 100 pct identical to ycei_ecoli sw: p37904) (le:1237) (re:1812) (di:complement) AE000207 AE000207 g1787295 Escherichia coli 562 -11534586 5000691974 ycei 18.7 kd protein in htrb 5region precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf_id:o233#5; similar to swissprot accession) (le:14521) (re:15096) (di:complement) D90742 D90742 g4062630 Escherichia coli 562 -11534586 7502852160 ycei 18.7 kd protein in htrb 5region precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf_id:o233#5; similar to swissprot accession) (le:4267) (re:4842) (di:complement) D90743 D90743 g4062638 Escherichia coli 562 -11534586

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846506	10344	32500	333	110

Description

5000691975 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1057 b1057 Escherichia coli 562 -11534587
7000691151 probable membrane protein b1057 (db:pir2.dat) F64848 F64848 Escherichia coli 562 -11534587 7500959946 b1057 putative cytochrome (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 97 of 400 of the completegenome.) (nt:f188; this 188 aa orf is 30 pct identical (1 gap)) (le:1816) (re:2382) (di:complement) AE000207 AE000207 g1787296 Escherichia coli 562 -11534587 7502852161 cybb cytochrome b561 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #232) (db:genpept) (de:escherichia coli genomic dna. (23.8 - 24.2 min).) (nt:orf_id:o233#6; similar to pir accession number) (le:15100) (re:15666) (di:complement) D90742 D90742 g4062631 Escherichia coli 562 -11534587 7502852162 cybb cytochrome b561 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf_id:o233#6; similar to pir accession number) (le:4846) (re:5412) (di:complement) D90743 D90743 g4062639 Escherichia coli 562 -11534587 6500730729 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1057 b1057 Escherichia coli 562 -11534587

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846512	10345	32501	420	139

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846517	10346	32502	1065	354

Description

5000691976 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1058 b1058 Escherichia coli 562 -11534588
7500921686 yceo (de:hypothetical 5.9 kd protein in waam-sola intergenic region) (db:swissprot) YCEO_ECOLI P75926 ESCHERICHIA COLI 562 -11534588
7000691152 yceo yceo protein (db:pir2.dat) G64848 G64848 Escherichia coli 562 -11534588 7500921688 yceo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 97 of 400 of the completegenome.) (nt:f46; this 46 aa orf is 38 pct identical (0 gaps)) (le:2643) (re:2783) (di:complement) AE000207 AE000207 g1787297 Escherichia coli 562 -11534588 6500730730 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1058 b1058 Escherichia coli 562 -11534588

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846538	10347	32503	432	143

Description

5000691978 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1060 b1060 Escherichia coli 562 -11534589
 7500921689 ycep (de:hypothetical 9.7 kd protein in sola-dini intergenic region) (db:swissprot) YCEP_ECOLI P75927 ESCHERICHIA COLI 562 -11534589
 7000691153 ycep ycep protein (db:pir2.dat) A64849 A64849 Escherichia coli 562 -11534589 7500921691 ycep orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 97 of 400 of the completengenome.) (nt:f84; this 84 aa orf is 22 pct identical (4 gaps)) (le:4037) (re:4291) (di:complement) AE000207 AE000207 g1787299 Escherichia coli 562 -11534589 6500730731 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1060 b1060 Escherichia coli 562 -11534589

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846547	10348	32504	2433	811

Description

6500730732 yceb:b1063 hypothetical 20.5 kd protein in pyrc 3region:20.5 kd protein in pyrc-grxb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1063 b1063 Escherichia coli 562 -11534590 7500921675 yceb (de:20.5 kd protein in pyrc-grxb intergenic region) (db:swissprot) YCEB_ECOLI P09995 ESCHERICHIA COLI 562 -11534590 135163 yceb yceb protein (db:pir1.dat) (mp:23 min) QQECP5 B25008 Escherichia coli 562 -11534590 5000691980 (db:genpept-bct1) (de:e. coli pyrc gene for dihydroorotase.) (nt:urf) (le:215) (re:775) (di:direct) ECPYRC X04469 g42606 Escherichia coli 562 -11534590 237974 yceb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 97 of 400 of the completengenome.) (nt:f186; 99 pct identical to yceb_ecoli sw: p09995) (le:6049) (re:6609) (di:complement) AE000207 AE000207 g1787302 Escherichia coli 562 -11534590 7502852163 yceb hypothetical 20.5 kd protein in pyrc 3region. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf_id:o233#11; similar to swissprot accession) (le:9079) (re:9639) (di:complement) D90743 D90743 g4062643 Escherichia coli 562 -11534590 7502852164 (db:genpept) (de:e. coli pyrc gene for dihydroorotase.) (nt:urf) (le:215) (re:775) (di:direct) ECPYRC X04469 g42606 Escherichia coli 562 -11534590 110658 yceb (de:20.5 kd protein in pyrc-grxb intergenic region) (db:swissprot) YCEB_ECOLI P09995 ESCHERICHIA COLI 562 -11534590

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846556	10349	32505	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846564	10350	32506	381	126

Description

5000691981 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1065 b1065 Escherichia coli 562 -11534591
 7000691154 probable permease b1065 (db:pir2.dat) F64849 F64849 Escherichia coli 562 -11534591 7500959947 ycel orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 97 of 400 of the completengenome.) (nt:f412; this 412 aa orf is 23 pct identical (17 gaps)) (le:7454) (re:8692) (di:complement) AE000207 AE000207 g1787304 Escherichia coli 562 -11534591 7502852165 yqjv hypothetical 44.7 kd protein in glng-ansr (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf_id:o233#13; similar to swissprot accession) (le:10484) (re:11722) (di:complement) D90743 D90743 g4062645 Escherichia coli 562 -11534591
 6500730733 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1065 b1065 Escherichia coli 562 -11534591

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846565	10351	32507	996	331

Description

6500730734 yceh:b1067 hypothetical protein in rimj 3 region:hypothetical 24.2 kd protein in rimj-mvim intergenic region:g20.3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1067 b1067 Escherichia coli 562 -11534592 110668 yceh (de:hypothetical 24.2 kd protein in rimj-mvim intergenic region (g20.3)) (db:swissprot) YCEH_ECOLI P29217 ESCHERICHIA COLI 562 -11534592 7000687444 yceh yceh protein (db:pir2.dat) H64849 H64849 Escherichia coli 562 -11534592 7500921684 yceh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 97 of 400 of the completengenome.) (nt:o215; 100 pct identical to n-ter 109 aa of) (le:9493) (re:10140) (di:direct) AE000207 AE000207 g1787306 Escherichia coli 562 -11534592 5000691982 yceh hypothetical 25.6 kd protein in rimj 3region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf_id:o233#15; similar to swissprot accession) (le:12523) (re:13170) (di:direct) D90743 D90743 g4062646 Escherichia coli 562 -11534592

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846578	10352	32508	573	190

Description

5000691987 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1085 b1085 Escherichia coli 562 -11534593
7000691155 hypothetical protein b1085 (db:pir2.dat) B64852 B64852
Escherichia coli 562 -11534593 7500959948 b1085 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
99 of 400 of the completegenome.) (nt:ol24) (le:6133) (re:6507) (di:direct)
AE000209 AE000209 g1787326 Escherichia coli 562 -11534593 6500730735
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1085 b1085 Escherichia coli 562 -11534593

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846596	10353	32509	267	88

Description

GTC ORF with score 98 to: (sr:caenorhabditis elegans strain-bristol n2)
(db:genpept-inv) (de:caenorhabditis elegans cosmid c14f11.) (nt:repeated
leucine-rich (lrr); coded for by c.) (le:1575:1876:2149) (re:1694:2081:2344)
(di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846600	10354	32510	822	273

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846601	10355	32511	615	204

Description

6500730736 ycec:b1086 hypothetical 36.0 kd protein in rne-rpmf intergenic region:orfx (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1086 b1086 Escherichia coli 562 -11534594 110660 rluc (ec:4.2.1.70) (de:(pseudouridylate synthase) (uracil hydrolyase)) (db:swissprot) RLUC_ECOLI P23851 ESCHERICHIA COLI 562 -11534594 7000687441 ycec probable pseudouridylate synthase ycec (db:pir2.dat) C64852 C64852 Escherichia coli 562 -11534594 7500921676 ycec orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 99 of 400 of the completegenome.) (nt:o319; 100 pct identical to ycec_ecoli sw: p23851) (le:6625) (re:7584) (di:direct) AE000209 AE000209 g1787327 Escherichia coli 562 -11534594 5000691988 ycec hypothetical 36.0 kd protein in rne-rpmf (sr:escherichia coli(strain:k12) dna, clone:kohara clone #234) (db:genpept) (de:escherichia coli genomic dna. (24.5 - 24.8 min).) (nt:orf_id:o235#4; similar to swissprot accession) (le:11894) (re:12853) (di:direct) D90744 D90744 g4062660 Escherichia coli 562 -11534594

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846603	10356	32512	672	223

Description

GTC ORF with score 186 to: (fn:ensures cocoon cohesion by sticking silk) (sr:greater wax moth) (db:genpept-inv) (de:galleria mellonella sericin-1 (ser-1) mrna, partial cds.) (nt:similar to bombyx mori sericins; water-soluble silk) (le:<1) (re:350) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846623	10357	32513	2313	770

Description

6500730737 ycef:b1087 hypothetical 23.2 kd protein in rne-rpmf intergenic region:orfy (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1087 b1087 Escherichia coli 562 -11534595 110665 ycef (de:hypothetical 23.2 kd protein in rne-rpmf intergenic region (orfy)) (db:swissprot) YCEF_ECOLI P27244 ESCHERICHIA COLI 562 -11534595 7000687442 ycef ycef protein (cl:septum formation protein maf) (db:pir2.dat) D64852 D64852 Escherichia coli 562 -11534595 7500921681 orfy (fn:unknown) (sr:escherichia coli (strain k-12) (library: kohara) dna) (db:genpept-bct1) (de:escherichia coli orfx, (3' end), orfy, (complete cds), and g30kprotein (5' end) genes.) (le:296) (re:919) (di:complement) ECOG30K M96791 g146051 Escherichia coli 562 -11534595 234421 ycef orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 99 of 400 of the completgenome.) (nt:f207; 100 pct identical to ycef_ecoli sw: p27244) (le:7696) (re:8319) (di:complement) AE000209 AE000209 g1787328 Escherichia coli 562 -11534595 5000691989 ycef hypothetical 23.2 kd protein in rne-rpmf (sr:escherichia coli(strain:k12) dna, clone:kohara clone #234) (db:genpept) (de:escherichia coli genomic dna. (24.5 - 24.8 min).) (nt:orf_id:o235#5; similar to swissprot accession) (le:12965) (re:13588) (di:complement) D90744 D90744 g4062661 Escherichia coli 562 -11534595

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846635	10358	32514	426	141

Description

6500730738 yced:g30k:b1088 hypothetical 19.3 kd protein in rne-rpmf intergenic region:g30k (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1088 b1088 Escherichia coli 562 -11534596 110662 yced:g30k (de:hypothetical 19.3 kd protein in rne-rpmf intergenic region (g30k)) (db:swissprot) YCED_ECOLI P14189 ESCHERICHIA COLI 562 -11534596 163266 yced probable membrane protein yced (db:pir2.dat) (mp:23 min) JV0047 JV0047 Escherichia coli 562 -11534596 7500921678 (sr:e.coli dna, clone pay2-5) (db:genpept-bct1) (de:e.coli g30k protein and ribosomal protein l32 (rpmf) genes,complete cds.) (nt:g30k protein) (le:295) (re:816) (di:direct) ECORPMFA M29698 g147711 Escherichia coli 562 -11534596 235876 yced orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 99 of 400 of the completgenome.) (nt:o173; 100 pct identical to yced_ecoli sw: p14189) (le:8479) (re:9000) (di:direct) AE000209 AE000209 g1787329 Escherichia coli 562 -11534596 5000691990 g30k hypothetical 19.3 kd protein in rne-rpmf (sr:escherichia coli(strain:k12) dna, clone:kohara clone #234) (db:genpept) (de:escherichia coli genomic dna. (24.5 - 24.8 min).) (nt:orf_id:o235#6; similar to swissprot accession) (le:13748) (re:14269) (di:direct) D90744 D90744 g4062662 Escherichia coli 562 -11534596

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846638	10359	32515	804	267

Description

6500730739 ycfh:b1100 hypothetical protein in holb-ptsg intergenic region:hypothetical 29.8 kd protein in holb-ptsg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1100 b1100 Escherichia coli 562 -11534597 110756 ycfh (de:hypothetical 29.8 kd protein in holb-ptsg intergenic region) (db:swissprot) YCFH_ECOLI P37346 ESCHERICHIA COLI 562 -11534597 7000687451 ycfh probable metal-dependent hydrolase:ycfh (cl:hypothetical protein hi0454) (ec:3.-.-.-) (db:pir2.dat) A64854 A64854 Escherichia coli 562 -11534597 7500921730 ycfh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 100 of 400 of the completegenome.) (nt:o265; 99 pct identical to fragment ycfh_ecoli) (le:8082) (re:8879) (di:direct) AE000210 AE000210 g1787342 Escherichia coli 562 -11534597 5000691992 ycfh hypothetical protein in holb 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf_id:o236#9; similar to swissprot accession) (le:7419) (re:8216) (di:direct) D90745 D90745 g4062666 Escherichia coli 562 -11534597

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846639	10360	32516	189	62

Description

6500730740 ycff:b1103 hypothetical protein in fhue-ndh intergenic region:hypothetical 13.2 kd protein hit-like protein in fhue 5region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1103 b1103 Escherichia coli 562 -11534598 110754 ycff (de:hypothetical 13.2 kd protein hit-like protein in fhue 5'region) (db:swissprot) YCFF_ECOLI P36950 ESCHERICHIA COLI 562 -11534598 7000687450 ycff histidine triad-like protein ycff:pl:p4 bis 5-adenosyl tetraphosphate-binding histidine triad protein:14k (cl:protein kinase c inhibitor:histidine triad homology) (db:pir2.dat) (mp:16 min) JC5685 JC5685 Escherichia coli 562 -11534598 7500921729 ycff orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completegenome.) (nt:o119; this 119 aa orf is 74 pct identical (0 gaps)) (le:197) (re:556) (di:direct) AE000211 AE000211 g1787346 Escherichia coli 562 -11534598 5000691993 hypothetical protein hi0961 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf_id:o237#2; similar to pir accession number) (le:12527) (re:12886) (di:direct) D90745 D90745 g4062667 Escherichia coli 562 -11534598 7502852166 hypothetical protein hi0961 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf_id:o237#2; similar to pir accession number) (le:3826) (re:4185) (di:direct) D90746 D90746 g4062673 Escherichia coli 562 -11534598

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846641	10361	32517	246	82

Description

GTC ORF with score 340 to: (sr:n.crassa (strain 74a) dna) (db:genpept-pln1) (de:n.crassa vacuolar atpase 67-kd subunit (vma-1) gene, complete cds.) (nt:vacuolar atpase vma-1) (le:1155:1295:1406:1493) (re:1163:1331:1427:1541) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846651	10362	32518	843	280

Description

5000691994 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1104 b1104 Escherichia coli 562 -11534599
7500921734 ycf1 (de:hypothetical 14.0 kd protein in fhue-ndh intergenic region) (db:swissprot) YCF1_ECOLI P75946 ESCHERICHIA COLI 562 -11534599
7000691156 ycf1 ycf1 protein precursor (db:pir2.dat) E64854 E64854
Escherichia coli 562 -11534599 7500921736 ycf1 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completengenome.) (nt:o125) (le:559) (re:936) (di:direct)
AE000211 AE000211 g1787347 Escherichia coli 562 -11534599 7502852167 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf_id:o237#3) (le:12889) (re:13266) (di:direct) D90745 D90745 g4062668 Escherichia coli 562 -11534599 7502852168 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf_id:o237#3) (le:4188) (re:4565) (di:direct) D90746 D90746 g4062674 Escherichia coli 562 -11534599 6500730741 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1104 b1104 Escherichia coli 562 -11534599

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846658	10363	32519	339	112

Description

5000691995 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1105 b1105 Escherichia coli 562 -11534600
7500921737 ycfm (de:hypothetical 22.5 kd protein in fhue-ndh intergenic region) (db:swissprot) YCFM_ECOLI P75947 ESCHERICHIA COLI 562 -11534600
7000691157 ycfm ycfm protein precursor (db:pir2.dat) F64854 F64854
Escherichia coli 562 -11534600 7500921739 ycfm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completengenome.) (nt:o213; this 213 aa orf is 43 pct identical (8 gaps)) (le:950) (re:1591) (di:direct) AE000211 AE000211 g1787348 Escherichia coli 562 -11534600 6500730742 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1105 b1105 Escherichia coli 562 -11534600

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846663	10364	32520	312	103

Description

5000691996 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1106 b1106 Escherichia coli 562 -11534601
7500921740 ycfn (de:hypothetical 32.4 kd protein in fhue-ndh intergenic region) (db:swissprot) YCFN_ECOLI P75948 ESCHERICHIA COLI 562 -11534601
7000691158 ycfn ycfn protein (db:pir2.dat) G64854 G64854 Escherichia coli 562 -11534601 7500921742 ycfn putative beta-glucosidase ec 3.2.1.21 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completegenome.) (nt:o274; this 274 aa orf is 32 pct identical (1 gap)) (le:1572) (re:2396) (di:direct) AE000211 AE000211 g1787349 Escherichia coli 562 -11534601 7502852169 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf_id:o237#5) (le:13902) (re:14726) (di:direct) D90745 D90745 g4062670 Escherichia coli 562 -11534601 7502852170 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf_id:o237#5) (le:5201) (re:6025) (di:direct) D90746 D90746 g4062676 Escherichia coli 562 -11534601 6500730743 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1106 b1106 Escherichia coli 562 -11534601

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846666	10365	32521	1011	336

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846668	10366	32522	729	242

Description

5000691997 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1107 b1107 Escherichia coli 562 -11534602
 7500921743 ycfo (de:hypothetical 37.6 kd protein in fhue-ndh intergenic region) (db:swissprot) YCFO_ECOLI P75949 ESCHERICHIA COLI 562 -11534602
 7000691159 ycfo probable glucosidase:ycfo (ec:3.2.1.-) (db:pir2.dat) H64854 H64854 Escherichia coli 562 -11534602 7500921745 ycfo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completegenome.) (nt:o341; this 341 aa orf is 52 pct identical (8 gaps)) (le:2407) (re:3432) (di:direct) AE000211 AE000211 g1787350 Escherichia coli 562 -11534602 7502852171 hypothetical protein hi0959 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf_id:o237#6; similar to pir accession number) (le:14737) (re:15762) (di:direct) D90745 D90745 g4062671 Escherichia coli 562 -11534602
 7502852172 hypothetical protein hi0959 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf_id:o237#6; similar to pir accession number) (le:6036) (re:7061) (di:direct) D90746 D90746 g4062677 Escherichia coli 562 -11534602 6500730744 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1107 b1107 Escherichia coli 562 -11534602

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846685	10367	32523	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846693	10368	32524	1002	333

Description

GTC ORF with score 185 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pksl1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846706	10369	32525	369	122

Description

5000691998 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1108 b1108 Escherichia coli 562 -11534603
7500921747 ycfp (de:hypothetical 23.3 kd protein in fhue-ndh intergenic region) (db:swissprot) YCFP_ECOLI P75950 ESCHERICHIA COLI 562 -11534603
7000691160 ycfp ycfp protein (db:pir2.dat) A64855 A64855 Escherichia coli 562 -11534603 7500921749 ycfp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completengenome.) (nt:o199; this 199 aa orf is 26 pct identical (5 gaps)) (le:3398) (re:3997) (di:direct) AE000211 AE000211 g1787351 Escherichia coli 562 -11534603 7502852173 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #236) (db:genpept) (de:escherichia coli genomic dna. (24.8 - 25.2 min).) (nt:orf_id:o237#7) (le:15728) (re:16327) (di:direct) D90745 D90745 g4062672 Escherichia coli 562 -11534603 7502852174 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf_id:o237#7) (le:7027) (re:7626) (di:direct) D90746 D90746 g4062678 Escherichia coli 562 -11534603
6500730745 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1108 b1108 Escherichia coli 562 -11534603

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846707	10370	32526	585	194

Description

5000692000 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1111 b1111 Escherichia coli 562 -11534604
7000691161 ycfq probable transcription regulator ycfq (db:pir2.dat) D64855 D64855 Escherichia coli 562 -11534604 7500921752 ycfq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completengenome.) (nt:f236; this 236 aa orf is 28 pct identical (12 gaps)) (le:6512) (re:7222) (di:complement) AE000211 AE000211 g1787354 Escherichia coli 562 -11534604 7502852175 soca3 soca3 protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf_id:o237#10; similar to pir accession number) (le:10141) (re:10851) (di:complement) D90746 D90746 g4062680 Escherichia coli 562 -11534604
7500921750 ycfq (de:hypothetical transcriptional regulator in ndh-mfd intergenic region) (db:swissprot) YCFQ_ECOLI P75952 ESCHERICHIA COLI 562 -11534604 6500730746 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1111 b1111 Escherichia coli 562 -11534604

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846710	10371	32527	525	174

Description

5000692001 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1112 b1112 Escherichia coli 562 -11534605
7500921753 ycfR (de:hypothetical 8.8 kd protein in ndh-mfd intergenic region precursor) (db:swissprot) YCFR_ECOLI P75953 ESCHERICHIA COLI 562 -11534605 7000691162 ycfR ycfR protein precursor (cl:conserved hypothetical protein b3238) (db:pir2.dat) E64855 E64855 Escherichia coli 562 -11534605
7500921755 ycfR orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completegenome.) (nt:o85; this 85 aa orf is 47 pct identical (1 gap)) (le:7385) (re:7642) (di:direct) AE000211 AE000211 g1787355 Escherichia coli 562 -11534605 7502852176 hypothetical 8.6 kd protein in ding/rarb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf_id:o238#1; similar to swissprot accession) (le:11014) (re:11271) (di:direct) D90746 D90746 g4062681 Escherichia coli 562 -11534605 7502852177 hypothetical 8.6 kd protein in ding/rarb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf_id:o238#1; similar to swissprot accession) (le:760) (re:1017) (di:direct) D90747 D90747 g4062685 Escherichia coli 562 -11534605
6500730747 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1112 b1112 Escherichia coli 562 -11534605

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846715	10372	32528	504	167

Description

5000692002 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1113 b1113 Escherichia coli 562 -11534606
7500921756 ycfs (de:hypothetical 34.6 kd protein in ndh-mfd intergenic region precursor) (db:swissprot) YCFS_ECOLI P75954 ESCHERICHIA COLI 562 -11534606 7000691163 ycfs ycfs protein precursor (cl:conserved hypothetical protein b0819) (db:pir2.dat) F64855 F64855 Escherichia coli 562 -11534606
7500921758 ycfs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completegenome.) (nt:f320; this 320 aa orf is 48 pct identical (8 gaps)) (le:7724) (re:8686) (di:complement) AE000211 AE000211 g1787356 Escherichia coli 562 -11534606 7502852178 erfk protein erfk/srfk precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf_id:o238#2; similar to swissprot accession) (le:11353) (re:12315) (di:complement) D90746 D90746 g4062682 Escherichia coli 562 -11534606 7502852179 erfk protein erfk/srfk precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf_id:o238#2; similar to swissprot accession) (le:1099) (re:2061) (di:complement) D90747 D90747 g4062686 Escherichia coli 562 -11534606 6500730748 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1113 b1113 Escherichia coli 562 -11534606

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846716	10373	32529	591	196

Description

5000692003 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1115 b1115 Escherichia coli 562 -11534607
 7500921759 ycft (de:hypothetical 40.8 kd protein in mfd-cobb intergenic region) (db:swissprot) YCFT_ECOLI P75955 ESCHERICHIA COLI 562 -11534607
 7000691164 ycft probable membrane protein ycft (db:pir2.dat) H64855 H64855 Escherichia coli 562 -11534607 7500921761 ycft orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completegenome.) (nt:f357; this 357 aa orf is 20 pct identical (25 gaps)) (le:94) (re:1167) (di:complement) AE000212 AE000212 g1787359 Escherichia coli 562 -11534607 7502852180 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf_id:o238#4) (le:16033) (re:17106) (di:complement) D90746 D90746 g4062683 Escherichia coli 562 -11534607 7502852181 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf_id:o238#4) (le:5779) (re:6852) (di:complement) D90747 D90747 g4062687 Escherichia coli 562 -11534607 6500730749 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1115 b1115 Escherichia coli 562 -11534607

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846737	10374	32530	198	65

Description

5000692004 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1116 b1116 Escherichia coli 562 -11534608
 5500686496 ycfu (de:hypothetical 43.3 kd protein in mfd-cobb intergenic region) (db:swissprot) YCFU_ECOLI P75956 ESCHERICHIA COLI 562 -11534608
 7000687454 ycfu probable membrane protein ycfu (cl:hypothetical protein hi1555) (db:pir2.dat) A64856 A64856 Escherichia coli 562 -11534608
 7500921762 ycfu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completegenome.) (nt:o399; this 399 aa orf is 45 pct identical (8 gaps)) (le:1429) (re:2628) (di:direct) AE000212 AE000212 g1787360 Escherichia coli 562 -11534608 6500730750 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1116 b1116 Escherichia coli 562 -11534608

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846747	10375	32531	687	228

Description

5000692005 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1117 b1117 Escherichia coli 562 -11534609
 7000687455 ycfv probable abc-type transport protein ycfv (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) B64856 B64856 Escherichia coli 562 -11534609 7500921764 ycfv putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completengenome.) (nt:o228; residues 10-216 are 65 pct identical to) (le:2636) (re:3322) (di:direct) AE000212 AE000212 g1787361 Escherichia coli 562 -11534609 5500686497 ycfv (de:hypothetical abc transporter atp-binding protein ycfv) (db:swissprot) YCFV_ECOLI P75957 ESCHERICHIA COLI 562 -11534609 6500730751 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1117 b1117 Escherichia coli 562 -11534609

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846748	10376	32532	345	114

Description

5000692006 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1118 b1118 Escherichia coli 562 -11534610
 5500686498 ycfw (de:hypothetical 45.3 kd protein in mfd-cobb intergenic region) (db:swissprot) YCFW_ECOLI P75958 ESCHERICHIA COLI 562 -11534610
 7000687456 ycfw probable permease ycfw (db:pir2.dat) C64856 C64856 Escherichia coli 562 -11534610 7500921765 ycfw putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completengenome.) (nt:o414; this 414 aa orf is 51 pct identical (6 gaps)) (le:3322) (re:4566) (di:direct) AE000212 AE000212 g1787362 Escherichia coli 562 -11534610 7502852182 hypothetical protein hi1548 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf_id:o238#7; similar to pir accession number) (le:9007) (re:10251) (di:direct) D90747 D90747 g4062690 Escherichia coli 562 -11534610
 6500730752 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1118 b1118 Escherichia coli 562 -11534610

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846751	10377	32533	312	103

Description

6500730753 ycfx:b1119 hypothetical protein:hypothetical 33.0 kd protein in mfd-cobb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1119 b1119 Escherichia coli 562 -11534611
 4000709695 ycfx (de:hypothetical 33.0 kd protein in mfd-cobb intergenic region) (db:swissprot) YCFX_ECOLI P75959 ESCHERICHIA COLI 562 -11534611
 7000687457 ycfx ycfx protein (cl:conserved hypothetical protein hi0182:glucose kinase homology) (db:pir2.dat) D64856 D64856 Escherichia coli 562 -11534611 7500921767 ycfx putative nagc-like transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completegenome.) (nt:o303; this 303 aa orf is 50 pct identical (1 gap)) (le:4595) (re:5506) (di:direct) AE000212 AE000212 g1787363 Escherichia coli 562 -11534611 5000692007 hypothetical protein hi0182 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf_id:o238#8; similar to pir accession number) (le:10280) (re:11191) (di:direct) D90747 D90747 g4062691 Escherichia coli 562 -11534611

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846762	10378	32534	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846772	10379	32535	666	221

Description

5000692008 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1120 b1120 Escherichia coli 562 -11534612
 7000691165 hypothetical protein b1120 (cl:conserved hypothetical protein b1120) (db:pir2.dat) E64856 E64856 Escherichia coli 562 -11534612
 7500959949 cobb putative nicotinic acid (fn:putative enzyme; biosynthesis of cofactors,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completegenome.) (nt:o279; this 279 aa orf is 31 pct identical (8 gaps)) (le:5522) (re:6361) (di:direct) AE000212 AE000212 g1787364 Escherichia coli 562 -11534612 7502852183 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf_id:o238#9) (le:11207) (re:12046) (di:direct) D90747 D90747 g4062692 Escherichia coli 562 -11534612
 6500730754 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1120 b1120 Escherichia coli 562 -11534612

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846780	10380	32536	399	132

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846796	10381	32537	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846799	10382	32538	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846815	10383	32539	657	218

Description

5000692009 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1121 b1121 Escherichia coli 562 -11534613 7500879008 cobb (ec:2.4.2.21) (de:phosphoribosyltransferase) (db:swissprot) COBB_ECOLI P75961 ESCHERICHIA COLI 562 -11534613 7000691166 cobb probable nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransfrase (db:pir2.dat) F64856 F64856 Escherichia coli 562 -11534613 7500879010 b1121 homolog of virulence factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completegenome.) (nt:f262; this 262 aa orf is 40 pct identical (3 gaps)) (le:6481) (re:7269) (di:complement) AE000212 AE000212 g1787365 Escherichia coli 562 -11534613 7502852184 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf_id:o238#10) (le:12166) (re:12954) (di:complement) D90747 D90747 g4062693 Escherichia coli 562 -11534613 6500730755 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1121 b1121 Escherichia coli 562 -11534613

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846820	10384	32540	993	330

Description

5000692010 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1122 b1122 Escherichia coli 562 -11534614
7500951310 ymfa (de:hypothetical 17.8 kd protein in cobb-potd intergenic region) (db:swissprot) YMFA_ECOLI P75962 ESCHERICHIA COLI 562 -11534614
7000691167 probable membrane protein ymfa (db:pir2.dat) G64856 G64856 Escherichia coli 562 -11534614 7500951312 ymfa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 102 of 400 of the completegenome.) (nt:f156; this 156 aa orf is 36 pct identical (0 gaps)) (le:7266) (re:7736) (di:complement) AE000212 AE000212 g1787366 Escherichia coli 562 -11534614 7502852185 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #238) (db:genpept) (de:escherichia coli genomic dna. (25.2 - 25.6 min).) (nt:orf_id:o238#11) (le:12951) (re:13421) (di:complement) D90747 D90747 g4062694 Escherichia coli 562 -11534614 6500730756 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1122 b1122 Escherichia coli 562 -11534614

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846834	10385	32541	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846843	10386	32542	189	62

Description

6500730757 ycfb:b1128 hypothetical protein in pept-phoq intergenic region:hypothetical 42.6 kd protein in pept-phoq intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1128 b1128 Escherichia coli 562 -11534615 7000690983 ycfb ycfb protein (db:pir2.dat) E64857 E64857 Escherichia coli 562 -11534615 7500959848 ycfb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 103 of 400 of the completegenome.) (nt:f376; 100 pct identical to fragment ycfb_ecoli) (le:1430) (re:2560) (di:complement) AE000213 AE000213 g1787373 Escherichia coli 562 -11534615 5000692011 (de:(ecoli_1090) (pn:hypothetical protein in pept-phoq intergenic region:fragment) (gn:ycfb) (gtcfc:13.7:14.1) (ec:) (ycfb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1090 ECOLI_1090 Escherichia coli 562 10123178

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846844	10387	32543	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846847	10388	32544	939	312

Description

6500730758 ycfc:b1132 hypothetical 22.9 kd protein in purb
5region:hypothetical 22.9 kd protein in purb-icda intergenic region:orf-23
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1132
b1132 Escherichia coli 562 -11534616 7500921726 ycfc (de:hypothetical 22.9
kd protein in purb-icda intergenic region (orf-23)) (db:swissprot)
YCFC_ECOLI P25746 ESCHERICHIA COLI 562 -11534616 163473 ycfc ycfc protein
(db:pir2.dat) S19211 S19211 Escherichia coli 562 -11534616 5000692012
orf-23 (db:genpept-bct1) (de:e.coli orf-15, orf-23, purb and phop (5'end)
genes.) (le:731) (re:1372) (di:direct) ECPURB X59307 g581207 Escherichia
coli 562 -11534616 237959 ycfc orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 103 of 400 of the
completengenome.) (nt:f213; 99 pct identical to ycfc_ecoli sw: p25746)
(le:6301) (re:6942) (di:complement) AE000213 AE000213 g1787377 Escherichia
coli 562 -11534616 7502852186 ycfc hypothetical protein 23. (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #239) (db:genpept) (de:escherichia
coli genomic dna. (25.6 - 25.9 min).) (nt:orf_id:o240#3; similar to pir
accession number) (le:8224) (re:8865) (di:complement) D90748 D90748 g4062696
Escherichia coli 562 -11534616 7502852187 ycfc hypothetical protein 23.
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept)
(de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o240#3;
similar to pir accession number) (le:2541) (re:3182) (di:complement) D90749
D90749 g4062714 Escherichia coli 562 -11534616 110749 ycfc (de:hypothetical
22.9 kd protein in purb-icda intergenic region (orf-23)) (db:swissprot)
YCFC_ECOLI P25746 ESCHERICHIA COLI 562 -11534616

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846848	10389	32545	396	131

Description

6500730759 ycfb:b1133 hypothetical protein in purb 5 region:hypothetical
42.6 kd protein in purb-icda intergenic region:orf-15 (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1133 b1133
Escherichia coli 562 -11534617 110747 trmu:asue (ec:2.1.1.61) (de:(ec
2.1.1.61)) (db:swissprot) TRMU_ECOLI P25745 ESCHERICHIA COLI 562 -11534617
7000687449 ycfb probable atpase ycfb (cl:probable membrane protein ydl033c)
(db:pir2.dat) B64858 B64858 Escherichia coli 562 -11534617 7500893413 ycfb
orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 103 of 400 of the completgenome.) (nt:f383; 100
pct identical to fragment ycfb_ecoli) (le:6978) (re:8129) (di:complement)
AE000213 AE000213 g1787378 Escherichia coli 562 -11534617 5000692013
(de:(ecoli_1095) (pn:hypothetical protein in purb 5"region:orf-15:fragment)
(gn:ycfb) (gtcfc:13.7:14.1) (ec:) (ycfb_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_1095 ECOLI_1095 Escherichia coli 562
10123179

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846860	10390	32546	1065	354

Description

5000692014 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1134 b1134 Escherichia coli 562 -11534618
7000691168 probable dntp pyrophosphohydrolase b1134 (cl:mutt domain
homology) (db:pir2.dat) C64858 C64858 Escherichia coli 562 -11534618
7500959950 b1134 putative phosphohydrolase (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 103
of 400 of the completgenome.) (nt:f153; this 153 aa orf is 45 pct identical
(3 gaps)) (le:8138) (re:8599) (di:complement) AE000213 AE000213 g1787379
Escherichia coli 562 -11534618 7502852188 hypothetical protein ygl067w
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #239) (db:genpept)
(de:escherichia coli genomic dna. (25.6 - 25.9 min).) (nt:orf_id:o240#5;
similar to pir accession number) (le:10061) (re:10522) (di:complement)
D90748 D90748 g4062698 Escherichia coli 562 -11534618 7502852189
hypothetical protein ygl067w (sr:escherichia coli(strain:k12) dna,
clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna.
(25.7 - 26.1 min).) (nt:orf_id:o240#5; similar to pir accession number)
(le:4378) (re:4839) (di:complement) D90749 D90749 g4062716 Escherichia coli
562 -11534618 6500730760 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b1134 b1134 Escherichia coli 562
-11534618

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846861	10391	32547	1314	437

Description

6500730761 ymfc:b1135 hypothetical protein:hypothetical 23.7 kd protein in trmu-icda intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1135 b1135 Escherichia coli 562 -11534619
 7000688154 ymfc probable pseudouridylate synthase ymfc (db:pir2.dat) D64858 D64858 Escherichia coli 562 -11534619 7500951316 ymfc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 103 of 400 of the completegenome.) (nt:f207; this 207 aa orf is 66 pct identical (1 gap)) (le:8609) (re:9232) (di:complement) AE000213 AE000213 g1787380 Escherichia coli 562 -11534619 4000709931 ymfc (de:hypothetical 23.7 kd protein in trmu-icda intergenic region) (db:swissprot) YMFC_ECOLI P75966 ESCHERICHIA COLI 562 -11534619 5000692015 (de:(ecoli_1097) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1097 ECOLI_1097 Escherichia coli 562 10123181

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846869	10392	32548	1206	401

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846885	10393	32549	192	63

Description

5000692016 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1137 b1137 Escherichia coli 562 -11534620
 7500951318 ymfd (de:hypothetical 25.1 kd protein in icda-lit intergenic region) (db:swissprot) YMFD_ECOLI P75967 ESCHERICHIA COLI 562 -11534620
 7000691169 ymfd ymfd protein (db:pir2.dat) F64858 F64858 Escherichia coli 562 -11534620 7500951320 ymfd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:f221; phage stats; this 221 aa orf is 27 pct) (le:277) (re:942) (di:complement) AE000214 AE000214 g1787383 Escherichia coli 562 -11534620 6500730762 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1137 b1137 Escherichia coli 562 -11534620

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846886	10394	32550	351	116

Description

5000692017 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1138 b1138 Escherichia coli 562 -11534621
7500951321 ymfe (de:hypothetical 27.6 kd protein in icda-lit intergenic region) (db:swissprot) YMFE_ECOLI P75968 ESCHERICHIA COLI 562 -11534621
7000691170 ymfe probable membrane protein ymfe (db:pir2.dat) G64858 G64858 Escherichia coli 562 -11534621 7500951323 ymfe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:f234; f234; phage; this 234 aa orf is 29 pct) (le:943) (re:1647) (di:complement) AE000214 AE000214 g1787384 Escherichia coli 562 -11534621 6500730763 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1138 b1138 Escherichia coli 562 -11534621

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846892	10395	32551	279	92

Description

5000692018 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1140 b1140 Escherichia coli 562 -11534622
7500884182 inte (de:prophage lambda integrase (int(lambda)) (prophage e14 integrase)) (db:swissprot) INTE_ECOLI P75969 ESCHERICHIA COLI 562 -11534622
7000691171 hypothetical protein b1140 (cl:phage lambda integrase) (db:pir2.dat) A64859 A64859 Escherichia coli 562 -11534622 7500884184 inte prophage e14 integrase (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:f375; phage stats; this 375 aa orf is 60 pct) (le:3089) (re:4216) (di:complement) AE000214 AE000214 g1787386 Escherichia coli 562 -11534622 7502852190 int integrase. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o240#9; similar to swissprot accession) (le:10230) (re:11357) (di:complement) D90749 D90749 g4062718 Escherichia coli 562 -11534622 6500730764 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1140 b1140 Escherichia coli 562 -11534622

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846898	10396	32552	693	230

Description

5000692019 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1141 b1141 Escherichia coli 562 -11534623
 7000691172 hypothetical protein b1141 (db:pir2.dat) B64859 B64859
 Escherichia coli 562 -11534623 7500959951 b1141 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:f81; phage stats; this 81 aa orf is 36 pct) (le:4197) (re:4442) (di:complement) AE000214 AE000214 g1787387
 Escherichia coli 562 -11534623 7502852191 xis excisionase. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o240#10; similar to swissprot accession) (le:11338) (re:11583) (di:complement) D90749 D90749 g4062719 Escherichia coli 562 -11534623 6500730765 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1141 b1141 Escherichia coli 562 -11534623

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846906	10397	32553	1140	379

Description

5000692020 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1142 b1142 Escherichia coli 562 -11534624
 7500951324 ymfh (de:hypothetical 11.0 kd protein in inte-pin intergenic region) (db:swissprot) YMFH_ECOLI P75971 ESCHERICHIA COLI 562 -11534624
 7000691173 hypothetical protein b1142 (db:pir2.dat) C64859 C64859
 Escherichia coli 562 -11534624 7500951326 ymfh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:f103; phage stats; this 103 aa orf is 35 pct) (le:4479) (re:4790) (di:complement) AE000214 AE000214 g1787388
 Escherichia coli 562 -11534624 6500730766 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1142 b1142
 Escherichia coli 562 -11534624

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846918	10398	32554	486	161

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846922	10399	32555	375	124

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846924	10400	32556	765	254

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846940	10401	32557	663	220

Description

5000692021 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1143 b1143 Escherichia coli 562 -11534625
 7500951327 ymfi (de:hypothetical 14.5 kd protein in inte-pin intergenic region) (db:swissprot) YMFI_ECOLI P75972 ESCHERICHIA COLI 562 -11534625
 7000691174 hypothetical protein b1143 (db:pir2.dat) D64859 D64859 Escherichia coli 562 -11534625 7500951329 ymfi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:o128; phage stats; this 128 aa orf is 27 pct) (le:4862) (re:5248) (di:direct) AE000214 AE000214 g1787389
 Escherichia coli 562 -11534625 6500730767 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1143 b1143 Escherichia coli 562 -11534625

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501846941	10402	32558	285	94

Description

5000692022 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1144 b1144 Escherichia coli 562 -11534626
 7500951330 ymfj (de:hypothetical 10.5 kd protein in inte-pin intergenic region) (db:swissprot) YMFJ_ECOLI P75973 ESCHERICHIA COLI 562 -11534626
 7000691175 hypothetical protein b1144 (db:pir2.dat) E64859 E64859 Escherichia coli 562 -11534626 7500951332 ymfj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:f94; phage stats; this 94 aa orf is 33 pct) (le:5186) (re:5470) (di:complement) AE000214 AE000214 g1787390
 Escherichia coli 562 -11534626 6500730768 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1144 b1144 Escherichia coli 562 -11534626

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846945	10403	32559	471	156

Description

5000692023 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1145 b1145 Escherichia coli 562 -11534627
7000691176 hypothetical protein b1145 (db:pir2.dat) F64859 F64859
Escherichia coli 562 -11534627 7500959952 b1145 putative phage repressor (fn:is, phage, tn; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:f224; phage stats; this 224 aa orf is 42 pct) (le:5669) (re:6343) (di:complement) AE000214 AE000214 g1787391 Escherichia coli 562 -11534627 7502852192 repressor protein c2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o241#1; similar to pir accession number) (le:12810) (re:13484) (di:complement) D90749 D90749 g4062720 Escherichia coli 562 -11534627 7502852193 repressor protein c2 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o241#1; similar to pir accession number) (le:457) (re:1131) (di:complement) D90750 D90750 g4062731 Escherichia coli 562 -11534627 6500730769 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1145 b1145 Escherichia coli 562 -11534627

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846949	10404	32560	297	98

Description

5000692024 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1146 b1146 Escherichia coli 562 -11534628
7000691177 hypothetical protein b1146 (db:pir2.dat) G64859 G64859
Escherichia coli 562 -11534628 7500959953 b1146 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:o167; phage stats) (le:6131) (re:6634) (di:direct) AE000214 AE000214 g1787392 Escherichia coli 562 -11534628 6500730770 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1146 b1146 Escherichia coli 562 -11534628

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501846989	10405	32561	399	132

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847001	10406	32562	903	300

Description

5000692025 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1147 b1147 Escherichia coli 562 -11534629
7500951333 ymfl (de:hypothetical 20.7 kd protein in inte-pin intergenic region) (db:swissprot) YMFL_ECOLI P75976 ESCHERICHIA COLI 562 -11534629
7000691178 hypothetical protein b1147 (db:pir2.dat) H64859 H64859 Escherichia coli 562 -11534629 7500951335 ymfl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:o189; phage stats; this 189 aa orf is 30 pct) (le:6666) (re:7235) (di:direct) AE000214 AE000214 g1787393 Escherichia coli 562 -11534629 7502852194 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o241#3) (le:13807) (re:14376) (di:direct) D90749 D90749 g4062722 Escherichia coli 562 -11534629 7502852195 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o241#3) (le:1454) (re:2023) (di:direct) D90750 D90750 g4062733 Escherichia coli 562 -11534629 6500730771 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1147 b1147 Escherichia coli 562 -11534629

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847011	10407	32563	258	85

Description

5000692026 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1148 b1148 Escherichia coli 562 -11534630
7500951336 ymfm (de:hypothetical 12.2 kd protein in inte-pin intergenic region) (db:swissprot) YMFM_ECOLI P75977 ESCHERICHIA COLI 562 -11534630
7000691179 ymfm ymfm protein (db:pir2.dat) A64860 A64860 Escherichia coli 562 -11534630 7500951338 ymfm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:o112; this 112 aa orf is 32 pct identical (2 gaps)) (le:7232) (re:7570) (di:direct) AE000214 AE000214 g1787394 Escherichia coli 562 -11534630 6500730772 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1148 b1148 Escherichia coli 562 -11534630

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847012	10408	32564	303	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847015	10409	32565	192	63

Description

5000692027 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1149 b1149 Escherichia coli 562 -11534631
7500951339 ymfn (de:hypothetical 50.9 kd protein in inte-pin intergenic region) (db:swissprot) YMFN_ECOLI P75978 ESCHERICHIA COLI 562 -11534631
7000691180 ymfn ymfn protein (db:pir2.dat) B64860 B64860 Escherichia coli 562 -11534631 7500951341 ymfn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:o455; this 455 aa orf is 36 pct identical (4 gaps)) (le:7580) (re:8947) (di:direct) AE000214 AE000214 g1787395 Escherichia coli 562 -11534631 7502852196 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o241#5) (le:14721) (re:16088) (di:direct) D90749 D90749 g4062724 Escherichia coli 562 -11534631 7502852197 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o241#5) (le:2368) (re:3735) (di:direct) D90750 D90750 g4062735 Escherichia coli 562 -11534631
6500730773 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1149 b1149 Escherichia coli 562 -11534631

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847025	10410	32566	1662	553

Description

5000692028 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1150 b1150 Escherichia coli 562 -11534632
7500951345 ymfr (de:hypothetical 6.4 kd protein in inte-pin intergenic region) (db:swissprot) YMFR_ECOLI P75979 ESCHERICHIA COLI 562 -11534632
7000691181 hypothetical protein b1150 (db:pir2.dat) C64860 C64860 Escherichia coli 562 -11534632 7500951347 ymfr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:o60; this 60 aa orf is 36 pct identical (3 gaps)) (le:8959) (re:9141) (di:direct) AE000214 AE000214 g1787396 Escherichia coli 562 -11534632 7502852198 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o241#6) (le:16100) (re:16282) (di:direct) D90749 D90749 g4062725 Escherichia coli 562 -11534632 7502852199 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o241#6) (le:3747) (re:3929) (di:direct) D90750 D90750 g4062736 Escherichia coli 562 -11534632 6500730774 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1150 b1150 Escherichia coli 562 -11534632

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847049	10411	32567	207	68

Description

5000692029 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1151 b1151 Escherichia coli 562 -11534633
7500951342 ymfo (de:hypothetical 17.6 kd protein in inte-pin intergenic region) (db:swissprot) YMFO_ECOLI P75980 ESCHERICHIA COLI 562 -11534633
7000691182 hypothetical protein b1151 (db:pir2.dat) D64860 D64860 Escherichia coli 562 -11534633 7500951344 ymfo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:o157) (le:9141) (re:9614) (di:direct) AE000214 AE000214 g1787397 Escherichia coli 562 -11534633 7502852200 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o241#7) (le:16282) (re:16755) (di:direct) D90749 D90749 g4062726 Escherichia coli 562 -11534633 7502852201 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o241#7) (le:3929) (re:4402) (di:direct) D90750 D90750 g4062737 Escherichia coli 562 -11534633 6500730775 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1151 b1151 Escherichia coli 562 -11534633

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847051	10412	32568	516	171

Description

GTC ORF with score 325 to: (sr:human) (db:genpept-pri2) (de:homo sapiens chromosome 9, p1 clone 11659, complete sequence.) (nt:hypothetical 38.8 kda putative membrane protein;) (le:79490:80053:80387) (re:79627:80181:80466) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847054	10413	32569	852	283

Description

5000692030 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1152 b1152 Escherichia coli 562 -11534634
7502852202 ymfp (de:hypothetical 28.2 kd protein in inte-pin intergenic region) (db:swissprot) YMFP_ECOLI P75981 ESCHERICHIA COLI 562 -11534634
7000691183 hypothetical protein b1152 (db:pir2.dat) E64860 E64860 Escherichia coli 562 -11534634 7500959954 b1152 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:o263; 34 pct identical (11 gaps) to 248 residues) (le:9541) (re:10332) (di:direct) AE000214 AE000214 g1787398 Escherichia coli 562 -11534634 6500730776 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1152 b1152 Escherichia coli 562 -11534634

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847056	10414	32570	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847060	10415	32571	630	209

Description

5000692031 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1153 b1153 Escherichia coli 562 -11534635
7502852203 ymfq (de:hypothetical 21.6 kd protein in inte-pin intergenic region precursor) (db:swissprot) YMFQ_ECOLI P75982 ESCHERICHIA COLI 562 -11534635 7000691184 hypothetical protein b1153 (db:pir2.dat) F64860 F64860 Escherichia coli 562 -11534635 7500959955 b1153 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:o194; 27 pct identical (8 gaps) to 160 residues) (le:10323) (re:10907) (di:direct) AE000214 AE000214 g1787399 Escherichia coli 562 -11534635 7502852204 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o241#9) (le:17464) (re:18048) (di:direct) D90749 D90749 g4062728 Escherichia coli 562 -11534635 7502852205 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o241#9) (le:5111) (re:5695) (di:direct) D90750 D90750 g4062739 Escherichia coli 562 -11534635 6500730777 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1153 b1153 Escherichia coli 562 -11534635

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847081	10416	32572	1179	392

Description

6500730778 ycfk:b1154 hypothetical protein in pin 5 region:hypothetical 22.0 kd protein in icda-pin intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1154 b1154 Escherichia coli 562 -11534636 110760 ycfk (de:hypothetical 22.0 kd protein in icda-pin intergenic region) (db:swissprot) YCFK_ECOLI P45581 ESCHERICHIA COLI 562 -11534636 7000687453 ycfk hypothetical protein in pin 5 region (db:pir2.dat) G64860 G64860 Escherichia coli 562 -11534636 7500921733 ycfk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completgenome.) (nt:o209; 100 pct identical to 112 aa of ycfk_ecoli) (le:10911) (re:11540) (di:direct) AE000214 AE000214 g1787400 Escherichia coli 562 -11534636 5000692032 ycfk hypothetical 13.1 kd protein in pin 5region. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o241#10; similar to swissprot accession) (le:18052) (re:18681) (di:direct) D90749 D90749 g4062729 Escherichia coli 562 -11534636 7502852206 ycfk hypothetical 13.1 kd protein in pin 5region. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o241#10; similar to swissprot accession) (le:5699) (re:6328) (di:direct) D90750 D90750 g4062740 Escherichia coli 562 -11534636

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847084	10417	32573	732	243

Description

5000692033 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1155 b1155 Escherichia coli 562 -11534637 7502852207 ymfs (de:hypothetical 15.4 kd protein in inte-pin intergenic region) (db:swissprot) YMFS_ECOLI P09154 ESCHERICHIA COLI 562 -11534637 7000691185 hypothetical protein b1155 (db:pir2.dat) H64860 H64860 Escherichia coli 562 -11534637 7500959956 b1155 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completgenome.) (nt:o137; residues 44-130 are 98 pct identical to) (le:11542) (re:11955) (di:direct) AE000214 AE000214 g1787401 Escherichia coli 562 -11534637 6500730779 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1155 b1155 Escherichia coli 562 -11534637

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847085	10418	32574	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847089	10419	32575	264	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847093	10420	32576	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847096	10421	32577	1359	452

Description

6500730780 ycfe:b1157 hypothetical protein: hypothetical protein in pin 5region:fragment (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1157 b1157 Escherichia coli 562 -11534638 7000691186 hypothetical protein b1157 (cl:phage p1 major tail fiber protein s) (db:pir2.dat) (mp:25 min) B64861 B64861 Escherichia coli 562 -11534638 7500955723 b1157 putative tail fiber protein (fn:is, phage, tn; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:f179; residues 14-164 are 100 pct identical to) (le:12529) (re:13068) (di:complement) AE000214 AE000214 g1787403 Escherichia coli 562 -11534638 5000692035 ycfe hypothetical protein p-min (sr:escherichia coli(strain:k12) dna, clone:kohara clone #240) (db:genpept) (de:escherichia coli genomic dna. (25.7 - 26.1 min).) (nt:orf_id:o241#13; similar to pir accession number) (le:19670) (re:20209) (di:complement) D90749 D90749 g4062730 Escherichia coli 562 -11534638 7502852208 ycfe hypothetical protein p-min (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o241#13; similar to pir accession number) (le:7317) (re:7856) (di:complement) D90750 D90750 g4062741 Escherichia coli 562 -11534638

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847099	10422	32578	792	263

Description

5000692036 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1160 b1160 Escherichia coli 562 -11534639
7500921798 ycgw (de:hypothetical 12.1 kd protein in icdc-mine intergenic region) (db:swissprot) YCGW_ECOLI P75987 ESCHERICHIA COLI 562 -11534639
7000691187 ycgw ycgw protein (db:pir2.dat) E64861 E64861 Escherichia coli 562 -11534639 7500921800 ycgw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:f107; this 107 aa orf is 29 pct identical (5 gaps)) (le:1418) (re:1741) (di:complement) AE000215 AE000215 g1787407 Escherichia coli 562 -11534639 6500730781 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1160 b1160 Escherichia coli 562 -11534639

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847107	10423	32579	1491	496

Description

6500730782 ycgx:b1161 hypothetical protein:hypothetical 15.8 kd protein in icdc-mine intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1161 b1161 Escherichia coli 562 -11534640
4000708194 ycgx (de:hypothetical 15.8 kd protein in icdc-mine intergenic region) (db:swissprot) YCGX_ECOLI P75988 ESCHERICHIA COLI 562 -11534640
7000687462 ycgx ycgx protein (cl:ydfp protein) (db:pir2.dat) F64861 F64861 Escherichia coli 562 -11534640 7500921801 ycgx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:f134) (le:2441) (re:2845) (di:complement) AE000215 AE000215 g1787408 Escherichia coli 562 -11534640
5000692037 (de:(ecoli_1123) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1123 ECOLI_1123 Escherichia coli 562 10123203

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847114	10424	32580	846	281

Description

5000692038 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1162 b1162 Escherichia coli 562 -11534641
7500921778 ycge (de:hypothetical transcriptional regulator in icdc-mine intergenic region) (db:swissprot) YCGE_ECOLI P75989 ESCHERICHIA COLI 562 -11534641 7000691188 ycge probable transcription regulator ycge (cl:hypothetical protein b1162) (db:pir2.dat) G64861 G64861 Escherichia coli 562 -11534641 7500921780 ycge putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:f243; 49 pct identical to n-terminal 235 aa of) (le:3066) (re:3797) (di:complement) AE000215 AE000215 g1787409 Escherichia coli 562 -11534641 7502852209 yehv hypothetical transcriptional regulator in (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o241#17; similar to swissprot accession) (le:11526) (re:12257) (di:complement) D90750 D90750 g4062743 Escherichia coli 562 -11534641 6500730783 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1162 b1162 Escherichia coli 562 -11534641

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847131	10425	32581	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847132	10426	32582	879	292

Description

5000692039 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1163 b1163 Escherichia coli 562 -11534642
7000691189 hypothetical protein b1163 (db:pir2.dat) H64861 H64861
Escherichia coli 562 -11534642 7500959957 b1163 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:f403; this 403 aa orf is 28 pct identical (9 gaps)) (le:4002) (re:5213) (di:complement) AE000215 AE000215 g1787410 Escherichia coli 562 -11534642 7502852210 hypothetical protein 1 ntrc 3 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o242#1; similar to pir accession number) (le:12462) (re:13673) (di:complement) D90750 D90750 g4062744 Escherichia coli 562 -11534642
7502852211 hypothetical protein 1 ntrc 3 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (nt:orf_id:o242#1; similar to pir accession number) (le:599) (re:1810) (di:complement) D90751 D90751 g4062748 Escherichia coli 562 -11534642 6500730784 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1163 b1163 Escherichia coli 562 -11534642

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847133	10427	32583	1278	425

Description

5000692040 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1164 b1164 Escherichia coli 562 -11534643
7500921805 ycgz (de:hypothetical 8.8 kd protein in icdc-mine intergenic region) (db:swissprot) YCGZ_ECOLI P75991 ESCHERICHIA COLI 562 -11534643
7000691190 ycgz ycgz protein (db:pir2.dat) A64862 A64862 Escherichia coli 562 -11534643 7500921807 ycgz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:o78; this 78 aa orf is 31 pct identical (4 gaps)) (le:5527) (re:5763) (di:direct) AE000215 AE000215 g1787411 Escherichia coli 562 -11534643 6500730785 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1164 b1164 Escherichia coli 562 -11534643

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847140	10428	32584	1176	391

Description

5000692041 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1165 b1165 Escherichia coli 562 -11534644
7500951355 ymga (de:hypothetical 10.3 kd protein in icdc-mine intergenic region) (db:swissprot) YMGA_ECOLI P75992 ESCHERICHIA COLI 562 -11534644
7000691191 ymga ymga protein (db:pir2.dat) B64862 B64862 Escherichia coli 562 -11534644 7500951357 ymga orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:o90; this 90 aa orf is 23 pct identical (1 gap)) (le:5806) (re:6078) (di:direct) AE000215 AE000215 g1787412 Escherichia coli 562 -11534644 6500730786 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1165 b1165 Escherichia coli 562 -11534644

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847144	10429	32585	438	145

Description

5000692042 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1166 b1166 Escherichia coli 562 -11534645
7500951358 ymgb (de:hypothetical 9.7 kd protein in icdc-mine intergenic region) (db:swissprot) YMGB_ECOLI P75993 ESCHERICHIA COLI 562 -11534645
7000691192 ymgb ymgb protein (db:pir2.dat) C64862 C64862 Escherichia coli 562 -11534645 7500951360 ymgb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:o88; this 88 aa orf is 29 pct identical (6 gaps)) (le:6107) (re:6373) (di:direct) AE000215 AE000215 g1787413 Escherichia coli 562 -11534645 6500730787 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1166 b1166 Escherichia coli 562 -11534645

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847148	10430	32586	750	249

Description

5000692043 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1167 b1167 Escherichia coli 562 -11534646
7500951361 ymgc (de:hypothetical 9.7 kd protein in icdc-mine intergenic region) (db:swissprot) YMGC_ECOLI P75994 ESCHERICHIA COLI 562 -11534646
7000691193 ymgc ymgc protein (db:pir2.dat) D64862 D64862 Escherichia coli 562 -11534646 7500951363 ymgc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:o82; this 82 aa orf is 33 pct identical (3 gaps)) (le:6486) (re:6734) (di:direct) AE000215 AE000215 gl787414 Escherichia coli 562 -11534646 7502852212 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o242#2) (le:14946) (re:15194) (di:direct) D90750 D90750 g4062745 Escherichia coli 562 -11534646 7502852213 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (nt:orf_id:o242#2) (le:3083) (re:3331) (di:direct) D90751 D90751 g4062749 Escherichia coli 562 -11534646
6500730788 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1167 b1167 Escherichia coli 562 -11534646

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847165	10431	32587	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847168	10432	32588	249	83

Description

5000692044 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1168 b1168 Escherichia coli 562 -11534647
7000691194 probable membrane protein b1168 (db:pir2.dat) E64862 E64862 Escherichia coli 562 -11534647 7500959958 b1168 putative proteases (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:o521 was o322 and 0191; this 322 aa orf is 30 pct) (le:7024) (re:8589) (di:direct) AE000215 AE000215 g1787415 Escherichia coli 562 -11534647 7502852214 hypothetical 60.8 kd protein in ssb-soxs (sr:escherichia coli(strain:k12) dna, clone:kohara clone #241) (db:genpept) (de:escherichia coli genomic dna. (26.0 - 26.3 min).) (nt:orf_id:o242#3; similar to swissprot accession) (le:15484) (re:17049) (di:direct) D90750 D90750 g4062746 Escherichia coli 562 -11534647 7502852215 hypothetical 60.8 kd protein in ssb-soxs (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (nt:orf_id:o242#3; similar to swissprot accession) (le:3621) (re:5186) (di:direct) D90751 D90751 g4062750 Escherichia coli 562 -11534647 6500730789 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1168 b1168 Escherichia coli 562 -11534647

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847169	10433	32589	2070	690

Description

5000692045 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1169 b1169 Escherichia coli 562 -11534648
7000691195 hypothetical protein b1169 (db:pir2.dat) F64862 F64862 Escherichia coli 562 -11534648 7500959959 b1169 putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 105 of 400 of the completegenome.) (nt:o506 was o411 and o104; this 411 aa orf is 18 pct) (le:9339) (re:10859) (di:direct) AE000215 AE000215 g1787416 Escherichia coli 562 -11534648 6500730790 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1169 b1169 Escherichia coli 562 -11534648

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847177	10434	32590	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847190	10435	32591	408	135

Description

5000692046 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1170 b1170 Escherichia coli 562 -11534649
7000691196 hypothetical protein b1170 (db:pir2.dat) G64862 G64862
Escherichia coli 562 -11534649 7500959960 b1170 putative part of putative atp-binding component (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.) (nt:o338; this 338 aa orf is 35 pct identical (5 gaps)) (le:73) (re:1089) (di:direct) AE000216 AE000216 g1787418 Escherichia coli 562 -11534649 6500730791 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1170 b1170 Escherichia coli 562 -11534649

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847198	10436	32592	1218	405

Description

5000692047 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1171 b1171 Escherichia coli 562 -11534650
7500951364 ymgd (de:hypothetical 12.1 kd protein in icdc-mine intergenic region precursor) (db:swissprot) YMGD_ECOLI P75998 ESCHERICHIA COLI 562 -11534650 7000691197 hypothetical protein b1171 (db:pir2.dat) H64862 H64862 Escherichia coli 562 -11534650 7500951366 b1171 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.) (nt:f111; this 111 aa orf is 26 pct identical (4 gaps)) (le:1172) (re:1507) (di:complement) AE000216 AE000216 g1787419 Escherichia coli 562 -11534650 7502852216 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (nt:orf_id:o243#2) (le:8640) (re:8975) (di:complement) D90751 D90751 g4062751 Escherichia coli 562 -11534650 7502852217 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf_id:o243#2) (le:4196) (re:4531) (di:complement) D90752 D90752 g4062761 Escherichia coli 562 -11534650 6500730792 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1171 b1171 Escherichia coli 562 -11534650

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847210	10437	32593	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847226	10438	32594	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847232	10439	32595	210	69

Description

GTC ORF with score 171 to: (db:genpept-bct1) (de:synechococcus pcc7942 clpp2/x operon, atp-dependent clp protease, proteolytic subunit (clpp2) and atp-dependent clp protease, regulatory subunit (clpx) genes, complete cds.) (nt:clpp2; second clpp gene) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847245	10440	32596	489	162

Description

5000692048 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1172 b1172 Escherichia coli 562 -11534651
7000691198 hypothetical protein b1172 (db:pir2.dat) A64863 A64863
Escherichia coli 562 -11534651 7500959961 b1172 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the complete genome.) (nt:f94; this 94 aa orf is 40 pct identical (3 gaps)) (le:1511) (re:1795) (di:complement) AE000216 AE000216 g1787420 Escherichia coli 562 -11534651 6500730793 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1172 b1172 Escherichia coli 562 -11534651

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847251	10441	32597	381	126

Description

5000692049 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1173 b1173 Escherichia coli 562 -11534652
7000691199 hypothetical protein b1173 (db:pir2.dat) B64863 B64863
Escherichia coli 562 -11534652 7500959962 b1173 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the complete genome.) (nt:o70; this 70 aa orf is 60 pct identical (0 gaps)) (le:2562) (re:2774) (di:direct) AE000216 AE000216 g1787421 Escherichia coli 562 -11534652 6500730794 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1173 b1173 Escherichia coli 562 -11534652

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847253	10442	32598	309	102

Description

5000692050 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1177 b1177 Escherichia coli 562 -11534653
7500921781 ycgj (de:hypothetical 13.4 kd protein in minc-shea intergenic region precursor) (db:swissprot) YCGJ_ECOLI P76001 ESCHERICHIA COLI 562 -11534653 7000691200 ycgj ycgj protein precursor (db:pir2.dat) F64863 F64863 Escherichia coli 562 -11534653 7500921783 ycgj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.) (nt:o122; this 122 aa orf is 27 pct identical (7 gaps)) (le:5467) (re:5835) (di:direct) AE000216 AE000216 g1787425 Escherichia coli 562 -11534653 7502852218 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (nt:orf_id:o243#9) (le:12935) (re:13303) (di:direct) D90751 D90751 g4062754 Escherichia coli 562 -11534653 7502852219 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf_id:o243#9) (le:8491) (re:8859) (di:direct) D90752 D90752 g4062764 Escherichia coli 562 -11534653 6500730795 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1177 b1177 Escherichia coli 562 -11534653

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847292	10443	32599	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847295	10444	32600	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847299	10445	32601	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847310	10446	32602	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847318	10447	32603	336	112

Description

5000692051 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1178 b1178 Escherichia coli 562 -11534654
7500921784 ycgk (de:hypothetical 14.9 kd protein in minc-shea intergenic region precursor) (db:swissprot) YCGK_ECOLI P76002 ESCHERICHIA COLI 562 -11534654 7000691201 ycgk ycgk protein precursor (db:pir2.dat) G64863 G64863 Escherichia coli 562 -11534654 7500921786 ycgk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the completgenome.) (nt:f133; this 133 aa orf is 22 pct identical (2 gaps)) (le:5938) (re:6339) (di:complement) AE000216 AE000216 g1787426 Escherichia coli 562 -11534654 7502852220 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (nt:orf_id:o243#10) (le:13406) (re:13807) (di:complement) D90751 D90751 g4062755 Escherichia coli 562 -11534654 7502852221 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf_id:o243#10) (le:8962) (re:9363) (di:complement) D90752 D90752 g4062765 Escherichia coli 562 -11534654 6500730796 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1178 b1178 Escherichia coli 562 -11534654

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847323	10448	32604	567	188

Description

5000692052 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1179 b1179 Escherichia coli 562 -11534655
7500921787 ycgl (de:hypothetical 12.4 kd protein in minc-shea intergenic region) (db:swissprot) YCGL_ECOLI P76003 ESCHERICHIA COLI 562 -11534655
7000689513 ycgl ycgl protein (cl:hypothetical protein b1179) (db:pir2.dat) H64863 H64863 Escherichia coli 562 -11534655 7500921789 ycgl
orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.) (nt:o108; this 108 aa orf is 42 pct identical (0 gaps)) (le:6548) (re:6874) (di:direct) AE000216 AE000216 g1787427 Escherichia coli 562 -11534655 7502852222
hypothetical protein hil446 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (nt:orf_id:o243#11; similar to pir accession number) (le:14016) (re:14342) (di:direct) D90751 D90751 g4062756 Escherichia coli 562 -11534655 7502852223 hypothetical protein hil446 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf_id:o243#11; similar to pir accession number) (le:9572) (re:9898) (di:direct) D90752 D90752 g4062766 Escherichia coli 562 -11534655 6500730797 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1179 b1179 Escherichia coli 562 -11534655

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847329	10449	32605	747	248
<u>Description</u>				
5000692053 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1180 b1180 Escherichia coli 562 -11534656				
7000691202 probable 2-hydroxyhepta-2:4-diene-1:7-dioate isomerase b1180 (cl:2-hydroxyhepta-2,4-diene-1,7-dioate isomerase) (db:pir2.dat) A64864 A64864 Escherichia coli 562 -11534656 7500959963 b1180 putative isomerase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.) (nt:o219; this 219 aa orf is 43 pct identical (1 gap)) (le:6946) (re:7605) (di:direct) AE000216 AE000216 gl787428 Escherichia coli 562 -11534656 7502852224 zk688.3 protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (nt:orf_id:o243#12; similar to pir accession number) (le:14414) (re:15073) (di:direct) D90751 D90751 g4062757 Escherichia coli 562 -11534656 7502852225 zk688.3 protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf_id:o243#12; similar to pir accession number) (le:9970) (re:10629) (di:direct) D90752 D90752 g4062767 Escherichia coli 562 -11534656 6500730798 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1180 b1180 Escherichia coli 562 -11534656				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847339	10450	32606	780	259
<u>Description</u>				
5000692054 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1181 b1181 Escherichia coli 562 -11534657				
7000691203 ycgN ycgN protein (cl:hypothetical protein hi1355) (db:pir2.dat) B64864 B64864 Escherichia coli 562 -11534657 7500921793 ycgN				
orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the completegenome.) (nt:o158; this 158 aa orf is 46 pct identical (3 gaps)) (le:7667) (re:8143) (di:direct) AE000216 AE000216 g1787429 Escherichia coli 562 -11534657 7502852226				
hypothetical protein hi1355 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna. (26.2 - 26.6 min).) (nt:orf_id:o244#1; similar to pir accession number) (le:15135) (re:15611) (di:direct) D90751 D90751 g4062758 Escherichia coli 562 -11534657 7502852227 hypothetical protein hi1355 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept) (de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf_id:o244#1; similar to pir accession number) (le:10691) (re:11167) (di:direct) D90752 D90752 g4062768 Escherichia coli 562 -11534657 7502852228 hypothetical protein hi1355 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept) (de:escherichia coli genomic dna. (26.5 - 26.8 min).) (nt:orf_id:o244#1; similar to pir accession number) (le:546) (re:1022) (di:direct) D90753 D90753 g4062771 Escherichia coli 562 -11534657 7500921791 ycgN				
(de:hypothetical 18.6 kd protein in minc-shea intergenic region) (db:swissprot) YCGN_ECOLI P76005 ESCHERICHIA COLI 562 -11534657 6500730799				
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1181 b1181 Escherichia coli 562 -11534657				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847340	10451	32607	642	214

Description

6500730800 hlye:hpr:b1182 hypothetical protein:hemolysin
e:hemolysin-inducing protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1182 b1182 Escherichia coli 562 -11534658
7000685538 hlye:hpr hemolysin e:hemolysin-inducing protein (db:pir2.dat)
C64864 C64864 Escherichia coli 562 -11534658 1500686948 shea silent
hemolysin (db:genpept-bct1) (de:e.coli shea gene.) (le:70) (re:987)
(di:direct) ECSHEA X98615 g2058309 Escherichia coli 562 -11534658
7500883393 hlye hemolytic protein hly (sr:escherichia coli strain=x11-blue)
(db:genpept-bct1) (de:escherichia coli hemolytic protein hly (hlye) gene,
complete cds.) (nt:hemolysin; hemolytic on sheep blood agar when) (le:142)
(re:1059) (di:direct) ECU57430 U57430 g1518605 Escherichia coli 562
-11534658 239734 hlye hemolysin e (fn:phenotype; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 106 of 400 of the
completeness genome.) (nt:f305 was f220 and f73; this 220 aa orf is 29 pct)
(le:8350) (re:9267) (di:complement) AE000216 AE000216 g1787430 Escherichia
coli 562 -11534658 5000692055 (sr:escherichia coli(strain:k12) dna,
clone:kohara clone #242) (db:genpept) (de:escherichia coli genomic dna.
(26.2 - 26.6 min).) (nt:orf_id:o244#2) (le:15818) (re:16735) (di:complement)
D90751 D90751 g4062759 Escherichia coli 562 -11534658 7502852229
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #243) (db:genpept)
(de:escherichia coli genomic dna. (26.3 - 26.7 min).) (nt:orf_id:o244#2)
(le:11374) (re:12291) (di:complement) D90752 D90752 g4062769 Escherichia
coli 562 -11534658 7502852230 (sr:escherichia coli(strain:k12) dna,
clone:kohara clone #244) (db:genpept) (de:escherichia coli genomic dna.
(26.5 - 26.8 min).) (nt:orf_id:o244#2) (le:1229) (re:2146) (di:complement)
D90753 D90753 g4062772 Escherichia coli 562 -11534658 500685122
hlye:hpr:shea:cly (de:hemolysin shea) (latent pore-forming 34 kd
haemolysin)) (db:swissprot) HLYE_ECOLI P77335 ESCHERICHIA COLI 562 -11534658

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847347	10452	32608	804	267

Description

6500730801 ycgb:b1188 hypothetical protein in fadr-dada intergenic region:hypothetical 60.8 kd protein in fadr-dada intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1188 b1188 Escherichia coli 562 -11534659 110770 ycgb (de:hypothetical 60.8 kd protein in fadr-dada intergenic region) (db:swissprot) YCGB_ECOLI P29013 ESCHERICHIA COLI 562 -11534659 7000687460 ycgb:dadr ycgb protein (db:pir2.dat) A64865 A64865 Escherichia coli 562 -11534659 7500921776 ycgb putative sporulation protein (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 107 of 400 of the completengenome.) (nt:f510; 99 pct identical to ycgb_ecoli sw: p29013 but) (le:2636) (re:4168) (di:complement) AE000217 AE000217 g1787437 Escherichia coli 562 -11534659 5000692056 dadr dadr protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept) (de:escherichia coli genomic dna. (26.5 - 26.8 min).) (nt:orf_id:o244#8; similar to pir accession number) (le:7455) (re:8987) (di:complement) D90753 D90753 g4062773 Escherichia coli 562 -11534659

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847352	10453	32609	480	159

Description

5000692057 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1191 b1191 Escherichia coli 562 -11534660 7000691204 probable na+/h+-exchanging protein b1191 (db:pir2.dat) D64865 D64865 Escherichia coli 562 -11534660 7500959964 b1191 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 107 of 400 of the completengenome.) (nt:f536; this 536 aa orf is 26 pct identical (30 gaps)) (le:7262) (re:8872) (di:complement) AE000217 AE000217 g1787440 Escherichia coli 562 -11534660 7502852231 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #244) (db:genpept) (de:escherichia coli genomic dna. (26.5 - 26.8 min).) (nt:orf_id:o245#1) (le:12081) (re:13691) (di:complement) D90753 D90753 g4062774 Escherichia coli 562 -11534660 7502852232 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #245) (db:genpept) (de:escherichia coli genomic dna. (26.8 - 27.1 min).) (nt:orf_id:o245#1) (le:1233) (re:2843) (di:complement) D90754 D90754 g4062776 Escherichia coli 562 -11534660 6500730802 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1191 b1191 Escherichia coli 562 -11534660

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847353	10454	32610	678	225

Description

GTC ORF with score 119 to: (or:Glycine max) (sr:soybean) (db:genpept-pln1) (de:glycine max low molecular weight heat shock protein hsp22.3(gmhsp22.3) mrna, complete cds.) (nt:low molecular weight heat shock protein) (le:39) (re:632) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847374	10455	32611	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847389	10456	32612	321	106

Description

5000692058 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1192 b1192 Escherichia coli 562 -11534661
7000691205 hypothetical protein b1192 (db:pir2.dat) E64865 E64865
Escherichia coli 562 -11534661 7500959965 b1192 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 107 of 400 of the completegenome.) (nt:f304; this 304 aa orf is 31 pct identical (1 gap)) (le:9093) (re:10007) (di:complement) AE000217 AE000217 g1787441 Escherichia coli 562 -11534661 7502852233 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #245) (db:genpept) (de:escherichia coli genomic dna. (26.8 - 27.1 min).) (nt:orf_id:o245#2) (le:3064) (re:3978) (di:complement) D90754 D90754 g4062777 Escherichia coli 562 -11534661
6500730803 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1192 b1192 Escherichia coli 562 -11534661

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847392	10457	32613	384	127

Description

5000692059 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1193 b1193 Escherichia coli 562 -11534662
7500885689 mlte:sltz (ec:3.2.1.-) (de:hydrolase e) (db:swissprot) MLTE_ECOLI P76009 ESCHERICHIA COLI 562 -11534662 7000691206 mlte:sltz murein hydrolase e::membrane-bound lytic murein transglycosylase e (ec:3.2.1.-) (db:pir2.dat) F64865 F64865 Escherichia coli 562 -11534662
7500885691 mlte murein transglycosylase e (fn:enzyme; murein sacculus, peptidoglycan) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 107 of 400 of the completegenome.) (nt:o241; this 241 aa orf is 40 pct identical (0 gaps)) (le:9993) (re:10718) (di:direct) AE000217 AE000217 g1787442 Escherichia coli 562 -11534662 7502852234 hypothetical protein hi0761 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #245) (db:genpept) (de:escherichia coli genomic dna. (26.8 - 27.1 min).) (nt:orf_id:o245#3; similar to pir accession number) (le:3964) (re:4689) (di:direct) D90754 D90754 g4062778 Escherichia coli 562 -11534662
6500730804 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1193 b1193 Escherichia coli 562 -11534662

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847394	10458	32614	462	153

Description

5000692060 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1194 b1194 Escherichia coli 562 -11534663
7500921795 ycgr (de:hypothetical 27.9 kd protein in mlte-trea intergenic region) (db:swissprot) YCGR_ECOLI P76010 ESCHERICHIA COLI 562 -11534663
7000691207 ycgr ycgr protein (db:pir2.dat) G64865 G64865 Escherichia coli 562 -11534663 7500921797 ycgr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 107 of 400 of the completegenome.) (nt:f244; this 244 aa orf is 31 pct identical (0 gaps)) (le:10720) (re:11454) (di:complement) AE000217 AE000217 g1787443 Escherichia coli 562 -11534663 6500730805 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1194 b1194 Escherichia coli 562 -11534663

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847396	10459	32615	183	60

Description

6500730806 ycgz:tag:b1195 hypothetical protein:transglycosylase associated protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1195 b1195 Escherichia coli 562 -11534664 7000691208 ymge:tag transglycosylase-associated protein ymge (cl:conserved hypothetical protein hi1364) (db:pir2.dat) H64865 H64865 Escherichia coli 562 -11534664
7500959966 ymge orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 108 of 400 of the completengenome.) (nt:o84; this 84 aa orf is 35 pct identical (3 gaps)) (le:131) (re:385) (di:direct) AE000218 AE000218 g1787445 Escherichia coli 562 -11534664 5000692061 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #245) (db:genpept) (de:escherichia coli genomic dna. (26.8 - 27.1 min).) (nt:orf_id:o245#5) (le:5626) (re:5880) (di:direct) D90754 D90754 g4062780 Escherichia coli 562 -11534664

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847397	10460	32616	285	94

Description

5000692062 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1196 b1196 Escherichia coli 562 -11534665
7500921802 ycgz (de:hypothetical 16.7 kd protein in mlte-trea intergenic region) (db:swissprot) YCGY_ECOLI P76012 ESCHERICHIA COLI 562 -11534665
7000691209 ycgz ycgz protein (db:pir2.dat) A64866 A64866 Escherichia coli 562 -11534665 7500921804 ycgz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 108 of 400 of the completengenome.) (nt:o146; this 146 aa orf is 28 pct identical (3 gaps)) (le:563) (re:1003) (di:direct) AE000218 AE000218 g1787446 Escherichia coli 562 -11534665 6500730807 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1196 b1196 Escherichia coli 562 -11534665

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847402	10461	32617	501	166

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847403	10462	32618	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847405	10463	32619	465	154

Description

6500730808 ycgcb1198 hypothetical protein in trea 5region:hypothetical 51.6 kd protein in trea-ptb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1198 b1198 Escherichia coli 562 -11534666 110771 ycgcb1198 (de:hypothetical 51.6 kd protein in trea-ptb intergenic region) (db:swissprot) YCGC_ECOLI P37349 ESCHERICHIA COLI 562 -11534666 7000687461 ycgcb1198 trehalase precursor (cl:phosphotransferase system phosphohistidine-containing protein homology) (db:pir2.dat) C64866 C64866 Escherichia coli 562 -11534666 7500921777 ycgcb1198 putative pts system enzyme i (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 108 of 400 of the completegenome.) (nt:f473; 100 pct identical to fragment ycgcb1198) (le:3099) (re:4520) (di:complement) AE000218 AE000218 g1787448 Escherichia coli 562 -11534666 5000692063 ycgcb1198 hypothetical protein in trea 5region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #245) (db:genpept) (de:escherichia coli genomic dna. (26.8 - 27.1 min).) (nt:orf_id:o245#7; similar to swissprot accession) (le:9793) (re:11214) (di:complement) D90754 D90754 g4062781 Escherichia coli 562 -11534666

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847422	10464	32620	1416	472

Description

5000692064 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1199 b1199 Escherichia coli 562 -11534667 7000691210 hypothetical protein b1199 (db:pir2.dat) D64866 D64866 Escherichia coli 562 -11534667 7500959967 b1199 putative dihydroxyacetone kinase ec 2.7.1.2 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 108 of 400 of the completegenome.) (nt:f210; 30 pct identical (16 gaps) to 181 residues) (le:4528) (re:5160) (di:complement) AE000218 AE000218 g1787449 Escherichia coli 562 -11534667 6500730809 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1199 b1199 Escherichia coli 562 -11534667

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847448	10465	32621	2226	741

Description

GTC ORF with score 1991 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0221 gene, complete cds.) (nt:similar to yeast prematurely terminated mrna decay) (le:210) (re:3599) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847466	10466	32622	2436	811

Description

5000692065 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1200 b1200 Escherichia coli 562 -11534668
7000691211 hypothetical protein b1200 (db:pir2.dat) E64866 E64866 Escherichia coli 562 -11534668 7500959968 b1200 putative dihydroxyacetone kinase ec 2.7.1.2 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 108 of 400 of the completegenome.) (nt:f366; 35 pct identical (32 gaps) to 355 residues) (le:5171) (re:6271) (di:complement) AE000218 AE000218 g1787450 Escherichia coli 562 -11534668
6500730810 hypothetical protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #245) (db:genpept) (de:escherichia coli genomic dna. (26.8 - 27.1 min).) (nt:orf_id:o246#2; similar to pir accession number) (le:11865) (re:12965) (di:complement) D90754 D90754 g4062783 Escherichia coli 562 -11534668

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847474	10467	32623	318	105

Description

5000692066 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1201 b1201 Escherichia coli 562 -11534669
7000691212 probable transcription regulator b1201 (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) F64866 F64866 Escherichia coli 562 -11534669 7500959969 b1201 putative sensor-type regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 108 of 400 of the completegenome.) (nt:o642; this 642 aa orf is 71 pct identical (0 gaps)) (le:6460) (re:8388) (di:direct) AE000218 AE000218 g1787451 Escherichia coli 562 -11534669 7502852235 dhar glycerol metabolism operon regulatory protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #245) (db:genpept) (de:escherichia coli genomic dna. (26.8 - 27.1 min).) (nt:orf_id:o246#3; similar to swissprot accession) (le:13154) (re:15082) (di:direct) D90754 D90754 g4062784 Escherichia coli 562 -11534669 6500730811 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1201 b1201 Escherichia coli 562 -11534669

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847477	10468	32624	564	187

Description

5000692067 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1202 b1202 Escherichia coli 562 -11534670
 7000691213 probable membrane protein b1202 (db:pir2.dat) G64866 G64866 Escherichia coli 562 -11534670 7500959970 b1202 putative adhesion and penetration protein (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 108 of 400 of the completegenome.) (nt:f955; this 955 aa orf is 27 pct identical (74 gaps)) (le:8488) (re:11355) (di:complement) AE000218 AE000218 gl787452 Escherichia coli 562 -11534670 6500730812 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1202 b1202 Escherichia coli 562 -11534670

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847481	10469	32625	405	134

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847490	10470	32626	1911	636

Description

GTC ORF with score 113 to: (sr:pisum sativum (strain alaska) (clone: na481-5) (clone library) (db:genpept-pln1) (de:pisum sativum l. (clone na-481-5) mrna, complete cds.) (nt:protein localized in the nucleoli of pea nuclei;) (le:75) (re:1910) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847513	10471	32627	255	84

Description

6500730813 ychf:gtp1:b1203 hypothetical gtp-binding protein in pth 3 region:probable gtp-binding protein in trea-pth intergenic region:orf-3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1203 b1203 Escherichia coli 562 -11534671 7000687464 ychf:gtp1 probable gtp-binding protein ychf (cl:yeast probable purine nucleotide-binding protein ybr025c) (db:pir2.dat) H64866 H64866 Escherichia coli 562 -11534671 7500921817 ychf putative gtp-binding protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.) (nt:f363; 100 pct identical to fragment ychf_ecoli) (le:415) (re:1506) (di:complement) AE000219 AE000219 g1787454 Escherichia coli 562 -11534671 5000692068 gtp1 probable gtp-binding protein in pth 3region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf_id:o247#1; similar to swissprot accession) (le:983) (re:2074) (di:complement) D90756 D90756 g4062787 Escherichia coli 562 -11534671 110784 ychf:gtp1 (de:probable gtp-binding protein in trea-pth intergenic region (orf-3)) (db:swissprot) YCHF_ECOLI P31216 ESCHERICHIA COLI 562 -11534671

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847516	10472	32628	354	117

Description

6500730814 ychh:b1205 hypothetical 10.5 kd protein in pth-prs intergenic region:orf-2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1205 b1205 Escherichia coli 562 -11534672 304611 ychh (de:hypothetical 10.5 kd protein in pth-prs intergenic region (orf-2)) (db:swissprot) YCHH_ECOLI P31807 ESCHERICHIA COLI 562 -11534672 7000687465 ychh probable membrane protein ychh (db:pir2.dat) B64867 B64867 Escherichia coli 562 -11534672 5000692069 orf-2 (fn:unknown) (db:genpept-bct1) (de:e.coli pth gene for peptidyl-trna hydrolase.) (le:147) (re:425) (di:complement) ECPTHG X61941 g311422 Escherichia coli 562 -11534672 237943 ychh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.) (nt:o92; 100 pct identical to ychh_ecoli sw: p31807) (le:2485) (re:2763) (di:direct) AE000219 AE000219 g1787456 Escherichia coli 562 -11534672 7502852236 ychh hypothetical 10.5 kd protein in pth-prs (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf_id:o247#3; similar to swissprot accession) (le:3053) (re:3331) (di:direct) D90756 D90756 g4062788 Escherichia coli 562 -11534672 110788 ychh (de:hypothetical 10.5 kd protein in pth-prs intergenic region (orf-2)) (db:swissprot) YCHH_ECOLI P31807 ESCHERICHIA COLI 562 -11534672

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847540	10473	32629	1425	474

Description

6500730815 ychm:b1206 hypothetical protein in pth-prs intergenic region:hypothetical 58.4 kd protein in pth-prsa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1206 b1206 Escherichia coli 562 -11534673 110794 ychm (de:hypothetical 58.4 kd protein in pth-prsa intergenic region) (db:swissprot) YCHM_ECOLI P40877 ESCHERICHIA COLI 562 -11534673 7000687467 ychm probable sulfate transport protein ychm (db:pir2.dat) C64867 C64867 Escherichia coli 562 -11534673 7500921819 ychm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.) (nt:f550; 98 pct identical to fragment ychm_ecoli) (le:2818) (re:4470) (di:complement) AE000219 AE000219 g1787457 Escherichia coli 562 -11534673 5000692070 ychm hypothetical protein in pth-prsa intergenic (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf_id:o247#4; similar to swissprot accession) (le:3386) (re:5038) (di:complement) D90756 D90756 g4062789 Escherichia coli 562 -11534673

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847541	10474	32630	1137	378

Description

6500730816 ychb:b1208 hypothetical 30.9 kd protein in hemm-prs intergenic region:hypothetical 30.9 kd protein in hemm-prsa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1208 b1208 Escherichia coli 562 -11534674 110779 ychb (de:hypothetical 30.9 kd protein in hemm-prsa intergenic region) (db:swissprot) YCHB_ECOLI P24209 ESCHERICHIA COLI 562 -11534674 162619 ychb hypothetical 30.9k protein hemm-prs intergenic region (db:pir2.dat) (mp:26 min) B47706 B47706 Escherichia coli 562 -11534674 238743 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli orf1 and orf2 gene, complete cds; prs gene, 5' end; hemagene, putative cds.) (nt:orf2) (le:844) (re:1695) (di:direct) ECOPRSA M77237 g147382 Escherichia coli 562 -11534674 235573 ychb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.) (nt:f283; 100 pct identical to ychb_ecoli sw: p24209) (le:5720) (re:6571) (di:complement) AE000219 AE000219 g1787459 Escherichia coli 562 -11534674 7500921812 orfy (db:genpept-bct2) (de:escherichia coli kdsa operon genes, complete cds.) (le:169) (re:1020) (di:complement) ECU18555 U18555 g968927 Escherichia coli 562 -11534674 5000692071 ychb 31k hypothetical protein 5 of prs (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf_id:o247#6; similar to pir accession number) (le:6288) (re:7139) (di:complement) D90756 D90756 g4062791 Escherichia coli 562 -11534674

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847559	10475	32631	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847560	10476	32632	726	241

Description

5000692073 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1213 b1213 Escherichia coli 562 -11534675 163459 probable membrane protein b1213 (db:pir2.dat) I83571 I83571 Escherichia coli 562 -11534675 238748 b1213 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 109 of 400 of the completengenome.) (nt:o130; this 130 aa orf is 29 pct identical (7 gaps)) (le:10618) (re:11010) (di:direct) AE000219 AE000219 g1787464 Escherichia coli 562 -11534675 7500959853 orf2 (db:genpept-bct2) (de:escherichia coli kdsa operon genes, complete cds.) (le:5066) (re:5458) (di:direct) ECU18555 U18555 g968932 Escherichia coli 562 -11534675 7502852237 hypothetical protein 2 kdsa 3 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf_id:o248#3; similar to pir accession number) (le:11186) (re:11578) (di:direct) D90756 D90756 g4062792 Escherichia coli 562 -11534675 7502852238 hypothetical protein 2 kdsa 3 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf_id:o248#3; similar to pir accession number) (le:2048) (re:2440) (di:direct) D90757 D90757 g4062795 Escherichia coli 562 -11534675 6500730817 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1213 b1213 Escherichia coli 562 -11534675

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847562	10477	32633	414	137

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847572	10478	32634	474	157
<u>Description</u>				
6500730818 ycha:b1214 hypothetical protein in hemk-kdsa (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1214 b1214 Escherichia coli 562 -11534676 163419 ycha ycha protein (db:pir2.dat) I83572 I83572 Escherichia coli 562 -11534676 238749 ycha orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.) (nt:o269; 99 pct identical to ycha_ecoli sw: p20101 but) (le:11014) (re:11823) (di:direct) AE000219 AE000219 g1787465 Escherichia coli 562 -11534676 7500959845 orf1 (db:genpept-bct2) (de:escherichia coli kdsa operon genes, complete cds.) (le:5462) (re:6271) (di:direct) ECU18555 U18555 g968933 Escherichia coli 562 -11534676 5000692074 hypothetical protein 1 kdsa 3 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf_id:o248#4; similar to pir accession number) (le:11582) (re:12391) (di:direct) D90756 D90756 g4062793 Escherichia coli 562 -11534676 7502852239 hypothetical protein 1 kdsa 3 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf_id:o248#4; similar to pir accession number) (le:2444) (re:3253) (di:direct) D90757 D90757 g4062796 Escherichia coli 562 -11534676				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847579	10479	32635	669	222
<u>Description</u>				
6500730819 ychn:b1219 hypothetical 12.7 kd protein in chac-narl intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1219 b1219 Escherichia coli 562 -11534677 110795 ychn (de:hypothetical 12.7 kd protein in chac-narl intergenic region) (db:swissprot) YCHN_ECOLI P39164 ESCHERICHIA COLI 562 -11534677 7000687468 ychn ychn protein (cl:escherichia coli ychn protein) (db:pir2.dat) H64868 H64868 Escherichia coli 562 -11534677 7500921820 ychn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 110 of 400 of the completegenome.) (nt:f117; 99 pct identical to ychn_ecoli sw: p39164) (le:3392) (re:3745) (di:complement) AE000220 AE000220 g1787471 Escherichia coli 562 -11534677 5000692077 ychn hypothetical 12.7 kd protein in chac-narl (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf_id:o248#9; similar to swissprot accession) (le:8370) (re:8723) (di:complement) D90757 D90757 g4062797 Escherichia coli 562 -11534677				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847582	10480	32636	966	321

Description

6500730820 ychp:ycho:b1220 hypothetical protein in narl 5region:hypothetical 47.0 kd protein in chac-narl intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1220 b1220 Escherichia coli 562 -11534678 110796 ycho (de:hypothetical 47.0 kd protein in chac-narl intergenic region) (db:swissprot) YCHO_ECOLI P39165 ESCHERICHIA COLI 562 -11534678 7000687469 ychp:ycho ychp protein (db:pir2.dat) A64869 A64869 Escherichia coli 562 -11534678 7500921821 ychp putative factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 110 of 400 of the completegenome.) (nt:o417; 100 pct identical to fragment ychp_ecoli) (le:4071) (re:5324) (di:direct) AE000220 AE000220 g1787472 Escherichia coli 562 -11534678 5000692078 ychp hypothetical protein in narl 5region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf_id:o248#10; similar to swissprot accession) (le:9049) (re:10302) (di:direct) D90757 D90757 g4062798 Escherichia coli 562 -11534678

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847589	10481	32637	450	149

Description

5000692079 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1228 b1228 Escherichia coli 562 -11534679 7000691214 hypothetical protein b1228 (db:pir2.dat) A64870 A64870 Escherichia coli 562 -11534679 7500959971 b1228 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 111 of 400 of the completegenome.) (nt:o91; 35 pct identical (3 gaps) to 54 residues of) (le:7133) (re:7408) (di:direct) AE000221 AE000221 g1787481 Escherichia coli 562 -11534679 6500730821 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1228 b1228 Escherichia coli 562 -11534679

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847599	10482	32638	918	305

Description

6500730822 ychj:b1233 hypothetical 17.0 kd protein in hnr-puru intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1233 b1233 Escherichia coli 562 -11534680 110789 ychj (de:hypothetical 17.0 kd protein in hnr-puru intergenic region) (db:swissprot) YCHJ_ECOLI P37052 ESCHERICHIA COLI 562 -11534680 7000687466 ychj ychj protein (cl:hypothetical protein hi0277) (db:pir2.dat) D64870 D64870 Escherichia coli 562 -11534680 224711 ychj (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min).) (nt:orf_id:o249#9; similar to (swissprot accession) (le:5670) (re:6128) (di:complement) D90852 D90852 g1805510 Escherichia coli 562 -11534680 301351 ychj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 111 of 400 of the complete genome.) (nt:f152; 96 pct identical to ychj_ecoli sw: p37052) (le:9098) (re:9556) (di:complement) AE000221 AE000221 g1787484 Escherichia coli 562 -11534680 5000692080 ychj hyothetical protein purt region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #249) (db:genpept) (de:escherichia coli genomic dna. (27.6 - 27.9 min).) (nt:orf_id:o250#7; similar to pir accession number) (le:10013) (re:10471) (di:complement) D90758 D90758 g4062802 Escherichia coli 562 -11534680 7502852240 ychj hyothetical protein purt region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf_id:o250#7; similar to pir accession number) (le:5670) (re:6128) (di:complement) D90759 D90759 g4062806 Escherichia coli 562 -11534680

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847604	10483	32639	429	142

Description

6500730823 ychk:b1234 hypothetical 34.4 kd protein in hnr-puru intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1234 b1234 Escherichia coli 562 -11534681 110792 ychk (de:hypothetical 34.4 kd protein in hnr-puru intergenic region) (db:swissprot) YCHK_ECOLI P37053 ESCHERICHIA COLI 562 -11534681 164202 ychk probable membrane protein ychk (db:pir2.dat) B36871 B36871 Escherichia coli 562 -11534681 224712 orf34 5 of tgs (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min).) (nt:orf_id:o249#10; similar to (pir accession number) (le:6202) (re:7146) (di:direct) D90852 D90852 g1805511 Escherichia coli 562 -11534681 301352 ychk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 111 of 400 of the completegenome.) (nt:o314; 99 pct identical to ychk_ecoli sw: p37053) (le:9630) (re:10574) (di:direct) AE000221 AE000221 g1787485 Escherichia coli 562 -11534681 5000692081 rrsa orf34 5 of tgs. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #249) (db:genpept) (de:escherichia coli genomic dna. (27.6 - 27.9 min).) (nt:orf_id:o250#8; similar to pir accession number) (le:10545) (re:11489) (di:direct) D90758 D90758 g4062803 Escherichia coli 562 -11534681 7502852241 rrsa orf34 5 of tgs. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf_id:o250#8; similar to pir accession number) (le:6202) (re:7146) (di:direct) D90759 D90759 g4062807 Escherichia coli 562 -11534681

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847611	10484	32640	657	219

Description

6500730824 ychg:b1239 hypothetical 22.2 kd protein in tdk-adhe intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1239 b1239 Escherichia coli 562 -11534682 301357 ychg (de:hypothetical 22.2 kd protein in tdk-adhe intergenic region) (db:swissprot) YCHG_ECOLI P30192 ESCHERICHIA COLI 562 -11534682 163229 ychg ychg protein (db:pir2.dat) I76912 I76912 Escherichia coli 562 -11534682 224717 hypothetical protein hns-adhe intergenic (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min).) (nt:orf_id:o250#3; similar to (pir accession number) (le:11422) (re:12012) (di:complement) D90852 D90852 g1805516 Escherichia coli 562 -11534682 238359 ychg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 112 of 400 of the completegenome.) (nt:f196; 100 pct identical to ychg_ecoli sw: p30192) (le:4260) (re:4850) (di:complement) AE000222 AE000222 g1787491 Escherichia coli 562 -11534682 5000692083 (db:genpept-bct2) (de:e.coli genes for h-n-s thymidine kinase alcohol dehydrogenase.) (nt:orf) (le:1909) (re:2499) (di:complement) ECTKAD X67326 g43080 Escherichia coli 562 -11534682 7502852242 ychg hypothetical protein hns-adhe intergenic (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf_id:o251#5; similar to pir accession number) (le:11422) (re:12012) (di:complement) D90759 D90759 g4062808 Escherichia coli 562 -11534682 110787 ychg (de:hypothetical 22.2 kd protein in tdk-adhe intergenic region) (db:swissprot) YCHG_ECOLI P30192 ESCHERICHIA COLI 562 -11534682

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847617	10485	32641	237	78

Description

5000692084 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1240 b1240 Escherichia coli 562 -11534683 7000691215 hypothetical protein b1240 (db:pir2.dat) C64871 C64871 Escherichia coli 562 -11534683 7500959972 b1240 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 112 of 400 of the completegenome.) (nt:f76; f76; broken; this 76 aa orf is 42 pct) (le:4802) (re:5032) (di:complement) AE000222 AE000222 g1787492 Escherichia coli 562 -11534683 7502852243 (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf_id:o251#6) (le:11964) (re:12194) (di:complement) D90759 D90759 g4062809 Escherichia coli 562 -11534683 6500730825 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1240 b1240 Escherichia coli 562 -11534683

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847621	10486	32642	468	155

Description

6500730826 yche:b1242 hypothetical protein in adhe-oppa intergenic region:hypothetical 23.5 kd protein in adhe-oppa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1242 b1242 Escherichia coli 562 -11534684 110783 yche (de:hypothetical 23.5 kd protein in adhe-oppa intergenic region) (db:swissprot) YCHE_ECOLI P25743 ESCHERICHIA COLI 562 -11534684 7000687463 yche probable membrane protein yche (cl:conserved hypothetical protein mj1677) (db:pir2.dat) E64871 E64871 Escherichia coli 562 -11534684 7500921814 yche putative channel protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 112 of 400 of the completegenome.) (nt:o215; 100 pct identical to yche_ecoli sw: p25743) (le:8432) (re:9079) (di:direct) AE000222 AE000222 g1787494 Escherichia coli 562 -11534684 5000692085 yche::gene hypothetical 23.5 kda protein in adhe-opaa (db:genpept) (de:escherichia coli oppa & yche genes.) (le:897) (re:1544) (di:complement) ECADHGENE X59501 g4210346 Escherichia coli 562 -11534684

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847622	10487	32643	366	121

Description

5000692086 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1248 b1248 Escherichia coli 562 -11534685 7000691216 hypothetical protein b1248 (cl:hypothetical protein hil450) (db:pir2.dat) C64872 C64872 Escherichia coli 562 -11534685 7500959973 b1248 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 113 of 400 of the completegenome.) (nt:f135; this 135 aa orf is 48 pct identical (1 gap)) (le:3995) (re:4402) (di:complement) AE000223 AE000223 g1787501 Escherichia coli 562 -11534685 6500730827 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1248 b1248 Escherichia coli 562 -11534685

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847627	10488	32644	465	155

Description

6500730828 ycii:b1251 hypothetical protein in kch-tonb intergenic region
 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1251
 b1251 Escherichia coli 562 -11534686 7000691834 ycii ycii protein
 (db:pir2.dat) F64872 F64872 Escherichia coli 562 -11534686 7500960349 ycii
 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia
 coli k-12 mg1655 section 113 of 400 of the completegenome.) (nt:f130; 100
 pct identical to ycii_ecoli sw: p31070) (le:7743) (re:8135) (di:complement)
 AE000223 AE000223 g1787504 Escherichia coli 562 -11534686 5000692087
 (de:(ecoli_1211) (pn:hypothetical 10) (gn:ycii) (gtcfc:13.7:14.1) (ec:)
 (ycii_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
 ECOLI_1211 ECOLI_1211 Escherichia coli 562 10123244

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501847645	10489	32645	1860	620

Description

6500730829 ycia:b1253 hypothetical 14.2 kd protein in tonb
3region:hypothetical 14.2 kd protein in tonb-trpa intergenic region
precursor:p14 protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1253 b1253 Escherichia coli 562 -11534687 110800
ycia (de:(p14 protein)) (db:swissprot) YCIA_ECOLI P04379 ESCHERICHIA COLI
562 -11534687 164227 ycia ycia protein precursor:14.2k protein
(db:pir2.dat) (mp:28 min) A05224 A05224 Escherichia coli 562 -11534687
223459 ycia (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#252(28.1-28.4 min.)) (nt:orf_id:o252#11; similar to (swissprot accession)
(le:10169) (re:10567) (di:complement) D90763 D90763 g1742042 Escherichia
coli 562 -11534687 238853 (sr:e.coli k12 (strain mo), clone prz540)
(db:genpept-bct1) (de:e.coli tonb and p14 genes, complete cds.) (nt:p14
protein (p14 gene; putative); putative) (le:1096) (re:1494) (di:complement)
ECOTONB K00431 g455187 Escherichia coli 562 -11534687 238861 ycia
(db:genpept-bct1) (de:escherichia coli ecor 1 (ycid) gene, partial cds, and
(ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative
potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.)
(le:2294) (re:2692) (di:direct) ECU24195 U24195 g902382 Escherichia coli 562
-11534687 238869 ycia (db:genpept-bct1) (de:escherichia coli ecor 4 (ycid)
gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb),
(ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls)
genes, complete cds.) (le:2294) (re:2692) (di:direct) ECU24196 U24196
g902391 Escherichia coli 562 -11534687 238877 ycia (db:genpept-bct1)
(de:escherichia coli ecor 16 (ycid) gene, partial cds, and (ycic), (ycib),
(ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch),
and cardiolipin synthase (cls) genes, complete cds.) (le:2294) (re:2692)
(di:direct) ECU24197 U24197 g902400 Escherichia coli 562 -11534687 238885
ycia (db:genpept-bct1) (de:escherichia coli ecor 28 (ycid) gene, partial
cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative
potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.)
(le:2294) (re:2692) (di:direct) ECU24198 U24198 g902409 Escherichia coli 562
-11534687 238893 ycia (db:genpept-bct1) (de:escherichia coli ecor 31 (ycid)
gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb),
(ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls)
genes, complete cds.) (le:2294) (re:2692) (di:direct) ECU24199 U24199
g902418 Escherichia coli 562 -11534687 238901 ycia (db:genpept-bct1)
(de:escherichia coli ecor 37 (ycid) gene, partial cds, and (ycic), (ycib),
(ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch),
and cardiolipin synthase (cls) genes, complete cds.) (le:2294) (re:2692)
(di:direct) ECU24200 U24200 g902427 Escherichia coli 562 -11534687 238909
ycia (db:genpept-bct1) (de:escherichia coli ecor 46 (ycid) gene, partial
cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative
potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.)
(le:2294) (re:2692) (di:direct) ECU24201 U24201 g902436 Escherichia coli 562
-11534687 238917 ycia (db:genpept-bct1) (de:escherichia coli ecor 50 (ycid)

-11534687 238917 ycia (db:genpept-bct1) (de:escherichia coli ecor 50 (ycid)
~~gene, partial cds, and (ycic), (ycih), (ycia), membrane protein (tonb),~~

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501847666	10490	32646	906	301

Description

6500730830 ycib:b1254 hypothetical 20.8 kd protein in tonb-trpa intergenic region:orf6 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1254 b1254 Escherichia coli 562 -11534688 238852 ycib (de:hypothetical 20.8 kd protein in tonb-trpa intergenic region (orf6)) (db:swissprot) YCIB_ECOLI P21366 ESCHERICHIA COLI 562 -11534688 163507 ycib probable membrane protein ycib (sr:strain k12, , strain k12) (sr:strain k12,) (db:pir2.dat) (mp:28 min) S07799 S07799 Escherichia coli 562 -11534688 223460 ycib (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #252(28.1-28.4 min.)) (nt:orf_id:o252#12; similar to (pir accession number) (le:10672) (re:11211) (di:complement) D90763 D90763 g1742043 Escherichia coli 562 -11534688 5000692089 (db:genpept-bct1) (de:e. coli dna for intervening region between trp operon and tonbgene.) (nt:orf6 protein (aa 1-179)) (le:3201) (re:3740) (di:direct) ECTRTOI X13583 g43213 Escherichia coli 562 -11534688 238860 ycib (db:genpept-bct1) (de:escherichia coli ecor 1 (ycid) gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:1650) (re:2189) (di:direct) ECU24195 U24195 g902381 Escherichia coli 562 -11534688 238868 ycib (db:genpept-bct1) (de:escherichia coli ecor 4 (ycid) gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:1650) (re:2189) (di:direct) ECU24196 U24196 g902390 Escherichia coli 562 -11534688 238892 ycib (db:genpept-bct1) (de:escherichia coli ecor 16 (ycid) gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:1650) (re:2189) (di:direct) ECU24197 U24197 g902399 Escherichia coli 562 -11534688 238900 ycib (db:genpept-bct1) (de:escherichia coli ecor 37 (ycid) gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:1650) (re:2189) (di:direct) ECU24200 U24200 g902426 Escherichia coli 562 -11534688 238908 ycib (db:genpept-bct1) (de:escherichia coli ecor 46 (ycid) gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:1650) (re:2189) (di:direct) ECU24201 U24201 g902435 Escherichia coli 562 -11534688 238932 ycib (db:genpept-bct1) (de:escherichia coli ecor 50 (ycid) gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:1650) (re:2189) (di:direct) ECU24202 U24202 g902444 Escherichia coli 562 -11534688 238940 ycib (db:genpept-bct1) (de:escherichia coli ecor 71 (ycid) gene, partial cds, and (ycic), (ycib), (ycia), membrane protein (tonb), (ycii), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.) (le:1650) (re:2189) (di:direct) ECU24205 U24205 g902471 Escherichia coli 562 -11534688 300263 ycib (db:genpept-bct1) (de:escherichia coli k12 (ycid) gene, partial cds, and (ycic),

(de:escherichia coli k12 (ycid) gene, partial cds, and (ycic),
~~(ycib), (ycia), membrane protein (tonb), (ycii), putative potassium~~

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847671	10491	32647	417	138

Description

6500730831 ycic:b1255 hypothetical protein in tonb-trpa intergenic region
 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1255
 b1255 Escherichia coli 562 -11534689 7000691843 ycic probable membrane
 protein ycic (cl:ycic protein) (db:pir2.dat) (mp:28 min) B64873 B64873
 Escherichia coli 562 -11534689 223461 ycic (sr:escherichia coli
 (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
 (de:e.coli genomic dna, kohara clone #252(28.1-28.4 min.).)
 (nt:orf_id:o252#13; similar to (swissprot accession) (le:11241) (re:11984)
 (di:complement) D90763 D90763 g1742044 Escherichia coli 562 -11534689
 300264 ycic orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
 (de:escherichia coli k-12 mg1655 section 113 of 400 of the completegenome.)
 (nt:f247; 93 pct identical to ycic_ecoli sw: p21365;) (le:10094) (re:10837)
 (di:complement) AE000223 AE000223 g1787508 Escherichia coli 562 -11534689
 5000692090 (de:(ecoli_1215) (pn:hypothetical 26) (gn:ycic)
 (gtcfc:13.7:14.1) (ec:) (ycic_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli)) ECOLI_1215 ECOLI_1215 Escherichia coli 562
 10119482

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847673	10492	32648	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847679	10493	32649	513	170

Description

6500730832 ycid:b1256 hypothetical 22.9 kd protein in tonb-trpa intergenic region:hypothetical 22.9 kd protein in tonb-trpa intergenic region
precursor:orf4 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1256 b1256 Escherichia coli 562 -11534690 300265
ompw (de:outer membrane protein w precursor) (db:swissprot) OMPW_ECOLI
P21364 ESCHERICHIA COLI 562 -11534690 163496 ycid ycid protein precursor
(db:pir2.dat) (mp:28 min) S07797 S07797 Escherichia coli 562 -11534690
223462 ycid outer membrane protein precursor. (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #252(28.1-28.4 min..))
(nt:orf_id:o252#14; similar to (swissprot accession) (le:12341) (re:12979)
(di:direct) D90763 D90763 g1742045 Escherichia coli 562 -11534690
5000692091 (db:genpept-bct1) (de:e. coli dna for intervening region between
trp operon and tonbgene.) (nt:orf4 protein (aa 1-212)) (le:1433) (re:2071)
(di:complement) ECTRTOI X13583 g43211 Escherichia coli 562 -11534690 238430
ycid putative outer membrane protein (fn:putative membrane; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 114 of 400 of the
completegenome.) (nt:o212; 100 pct identical to ycid_ecoli sw: p21364)
(le:209) (re:847) (di:direct) AE000224 AE000224 g1787510 Escherichia coli
562 -11534690 110808 ycid (de:(orf4)) (db:swissprot) YCID_ECOLI P21364
ESCHERICHIA COLI 562 -11534690

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847696	10494	32650	681	226

Description

6500730833 ycie:b1257 hypothetical 19.0 kd protein in tonb-trpa intergenic region:19.0 kd protein in tonb-trpa intergenic region:orf3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1257 b1257 Escherichia coli 562 -11534691 238781 ycie (de:19.0 kd protein in tonb-trpa intergenic region (orf3)) (db:swissprot) YCIE_ECOLI P21363 ESCHERICHIA COLI 562 -11534691 163488 ycie ycie protein:17k:19k protein (db:pir2.dat) (mp:28 min) S07796 S07796 Escherichia coli 562 -11534691 223463 ycie (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #252(28.1-28.4 min.)) (nt:orf_id:o252#15; similar to (pir accession number) (le:13039) (re:13545) (di:complement) D90763 D90763 g1742046 Escherichia coli 562 -11534691 5000692092 (db:genpept-bct1) (de:e. coli dna for intervening region between trp operon and tonbgene.) (nt:orf3 protein (aa 1-168)) (le:867) (re:1373) (di:direct) ECTRTOI X13583 g43210 Escherichia coli 562 -11534691 238787 ycie unknown (db:genpept-bct1) (de:escherichia coli k12 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4576) (re:5082) (di:direct) ECU23489 U23489 g775129 Escherichia coli 562 -11534691 238793 ycie unknown (db:genpept-bct1) (de:escherichia coli ecor 1 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4576) (re:5082) (di:direct) ECU23490 U23490 g775136 Escherichia coli 562 -11534691 238799 ycie unknown (db:genpept-bct1) (de:escherichia coli ecor 4 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4576) (re:5082) (di:direct) ECU23491 U23491 g775143 Escherichia coli 562 -11534691 238952 ycie unknown (db:genpept-bct1) (de:escherichia coli ecor 16 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4576) (re:5082) (di:direct) ECU23492 U23492 g775150 Escherichia coli 562 -11534691 238958 ycie (db:genpept-bct1) (de:escherichia coli ecor 8 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4576) (re:5082) (di:direct) ECU25417 U25417 g924767 Escherichia coli 562 -11534691 238964 ycie (db:genpept-bct1) (de:escherichia coli ecor 15 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4576) (re:5082) (di:direct) ECU25418 U25418 g924774 Escherichia coli 562 -11534691 238970 ycie (db:genpept-bct1) (de:escherichia coli ecor 17 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4576) (re:5082) (di:direct) ECU25419 U25419 g924781 Escherichia coli 562 -11534691 238982 ycie (db:genpept-bct1) (de:escherichia coli ecor 19 anthranilate

238982 ycie (db:genpept-bct1) (de:escherichia coli ecor 19 anthranilate
~~isomerase (trpc), tryptophansynthase beta subunit (trph), tryptophan~~

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501847697	10495	32651	1140	379

Description

6500730834 ycif:b1258 hypothetical 18.6 kd protein in tonb-trpa intergenic region:18.6 kd protein in tonb-trpa intergenic region:orf2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1258 b1258 Escherichia coli 562 -11534692 238780 ycif (de:18.6 kd protein in tonb-trpa intergenic region (orf2)) (db:swissprot) YCIF_ECOLI P21362 ESCHERICHIA COLI 562 -11534692 163463 ycif ycif protein:19k:18.6k protein (db:pir2.dat) (mp:28 min) S07795 S07795 Escherichia coli 562 -11534692 223464 ycif (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #252(28.1-28.4 min.)) (nt:orf_id:o252#16; similar to (pir accession number) (le:13591) (re:14091) (di:complement) D90763 D90763 g1742047 Escherichia coli 562 -11534692 5000692093 (db:genpept-bct1) (de:e. coli dna for intervening region between trp operon and tonbgene.) (nt:orf2 protein (aa 1-166)) (le:321) (re:821) (di:direct) ECTRTOI X13583 g43209 Escherichia coli 562 -11534692 238786 ycif unknown (db:genpept-bct1) (de:escherichia coli k12 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4030) (re:4530) (di:direct) ECU23489 U23489 g775128 Escherichia coli 562 -11534692 238792 ycif unknown (db:genpept-bct1) (de:escherichia coli ecor 1 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4030) (re:4530) (di:direct) ECU23490 U23490 g775135 Escherichia coli 562 -11534692 238798 ycif unknown (db:genpept-bct1) (de:escherichia coli ecor 4 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4030) (re:4530) (di:direct) ECU23491 U23491 g775142 Escherichia coli 562 -11534692 238951 ycif unknown (db:genpept-bct1) (de:escherichia coli ecor 16 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4030) (re:4530) (di:direct) ECU23492 U23492 g775149 Escherichia coli 562 -11534692 238963 ycif (db:genpept-bct1) (de:escherichia coli ecor 8 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4030) (re:4530) (di:direct) ECU25417 U25417 g924766 Escherichia coli 562 -11534692 238969 ycif (db:genpept-bct1) (de:escherichia coli ecor 17 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4030) (re:4530) (di:direct) ECU25419 U25419 g924780 Escherichia coli 562 -11534692 238975 ycif (db:genpept-bct1) (de:escherichia coli ecor 19 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan synthase alpha subunit(trpa), (ycig), (ycif), and (ycie) genes, complete cds.) (le:4030) (re:4530) (di:direct) ECU25420 U25420 g924787 Escherichia coli 562 -11534692 238987 ycif (db:genpept-bct1) (de:escherichia coli ecor 21 anthranilate

238987 ycif (db:genpept-bct1) (de:escherichia coli ecor 21 anthranilate isomerase (trpc), tryptophansynthase beta subunit (trpb), tryptophan

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501847698	10496	32652	207	68

Description

6500730835 ycig:b1259 hypothetical protein in tonb-trpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1259 b1259 Escherichia coli 562 -11534693 7000690984 ycig ycig protein (db:pir2.dat) (mp:28 min) F64873 F64873 Escherichia coli 562 -11534693 7500959849 ycig orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 114 of 400 of the completegenome.) (nt:f78; 100 pct identical to ycig_ecoli sw: p21361 but) (le:2045) (re:2281) (di:complement) AE000224 AE000224 g1787513 Escherichia coli 562 -11534693 5000692094 (de:(ecoli_1219) (pn:hypothetical 6) (gn:ycig) (gtcfc:13.7:14.1) (ec:) (ycig_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1219 ECOLI_1219 Escherichia coli 562 10123245

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501847699	10497	32653	390	129

Description

5000692095 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1266 b1266 Escherichia coli 562 -11534694 7500921840 yciv (de:hypothetical 32.6 kd protein in trpl-btur intergenic region) (db:swissprot) YCIV_ECOLI P77766 ESCHERICHIA COLI 562 -11534694 7000691217 yciv probable metal-dependent phosphoesterase yciv (cl:hypothetical protein hi1400) (db:pir2.dat) E64874 E64874 Escherichia coli 562 -11534694 223474 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #253(28.4-28.7 min..)) (nt:orf_id:o253#3; similar to (swissprot accession) (le:5840) (re:6721) (di:direct) D90764 D90764 g1742058 Escherichia coli 562 -11534694 300277 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min..)) (nt:orf_id:o253#3; similar to (swissprot accession) (le:3346) (re:4227) (di:direct) D90765 D90765 g1742074 Escherichia coli 562 -11534694 300292 yciv putative enzymes (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 114 of 400 of the completegenome.) (nt:o293; this 293 aa orf is 50 pct identical (3 gaps)) (le:9409) (re:10290) (di:direct) AE000224 AE000224 g1787520 Escherichia coli 562 -11534694 223489 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #253(28.4-28.7 min..)) (nt:orf_id:o253#3; similar to (swissprot accession) (le:5840) (re:6721) (di:direct) D90764 D90764 g1742058 Escherichia coli 562 -11534694 6500730836 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1266 b1266 Escherichia coli 562 -11534694

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847700	10498	32654	549	182

Description

6500730837 ycio:b1267 hypothetical 24.5 kd protein in trpl-btur intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1267 b1267 Escherichia coli 562 -11534695 7000687474 ycio probable translation factor ycio (cl:hypothetical protein hi1198) (db:pir2.dat) F64874 F64874 Escherichia coli 562 -11534695 223475 ycio (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #253(28.4-28.7 min.)) (nt:orf_id:o253#4; similar to (swissprot accession) (le:6682) (re:7338) (di:direct) D90764 D90764 g1742059 Escherichia coli 562 -11534695 300293 ycio (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf_id:o253#4; similar to (swissprot accession) (le:4188) (re:4844) (di:direct) D90765 D90765 g1742075 Escherichia coli 562 -11534695 300278 ycio orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 114 of 400 of the completegenome.) (nt:o218; 100 pct identical to ycio_ecoli sw:) (le:10251) (re:10907) (di:direct) AE000224 AE000224 g1787521 Escherichia coli 562 -11534695 110824 ycio (de:hypothetical 24.5 kd protein in trpl-btur intergenic region) (db:swissprot) YCIO_ECOLI P45847 ESCHERICHIA COLI 562 -11534695 223490 ycio (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf_id:o253#4; similar to (swissprot accession) (le:4188) (re:4844) (di:direct) D90765 D90765 g1742075 Escherichia coli 562 -11534695 5000692096 (de:(ecoli_1227) (pn:hypothetical 24) (gn:ycio) (gtcfc:13.7:14.1) (ec:) (ycio_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1227 ECOLI_1227 Escherichia coli 562 10052554

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847703	10499	32655	207	68

Description

6500730838 yciq:ycip:b1268 hypothetical protein in trpl-btur intergenic region:hypothetical 71.3 kd protein in trpl-btur intergenic region:orf2/3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1268 b1268 Escherichia coli 562 -11534696 110826 yciq (de:hypothetical 71.3 kd protein in trpl-btur intergenic region (orf2/3)) (db:swissprot) YCIQ_ECOLI P45848 ESCHERICHIA COLI 562 -11534696 7000687475 yciq probable membrane protein yciq (db:pir2.dat) G64874 G64874 Escherichia coli 562 -11534696 7500921832 yciq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 114 of 400 of the completegenome.) (nt:ycip_ecoli sw: p45848 which has an additional) (le:10935) (re:12830) (di:direct) AE000224 AE000224 g1787522 Escherichia coli 562 -11534696 5000692097 (de:(ecoli_1228) (pn:hypothetical 39) (gn:yciq) (gtcfc:13.7:14.1) (ec:) (yciq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1228 ECOLI_1228 Escherichia coli 562 10123248

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847705	10500	32656	606	202

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847718	10501	32657	3309	1102

Description

6500730839 ycil:b1269 hypothetical 32.7 kd protein in trp1-btur intergenic region:orf4 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1269 b1269 Escherichia coli 562 -11534697 110819 ycil (de:hypothetical 32.7 kd protein in trp1-btur intergenic region (orf4)) (db:swissprot) YCIL_ECOLI P37765 ESCHERICHIA COLI 562 -11534697 7000687471 ycil probable pseudouridylate synthase ycil (cl:conserved hypothetical protein h1243) (db:pir2.dat) H64874 H64874 Escherichia coli 562 -11534697 223480 ycil (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #253(28.4-28.7 min.)) (nt:orf_id:o253#9; similar to (swissprot accession) (le:9472) (re:10347) (di:direct) D90764 D90764 g1742064 Escherichia coli 562 -11534697 300298 ycil (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf_id:o253#9; similar to (swissprot accession) (le:6978) (re:7853) (di:direct) D90765 D90765 g1742080 Escherichia coli 562 -11534697 300283 ycil orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 115 of 400 of the completgenome.) (nt:o291; 100 pct identical to ycil_ecoli sw:) (le:136) (re:1011) (di:direct) AE000225 AE000225 g1787524 Escherichia coli 562 -11534697 223495 ycil (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf_id:o253#9; similar to (swissprot accession) (le:6978) (re:7853) (di:direct) D90765 D90765 g1742080 Escherichia coli 562 -11534697 5000692098 (de:(ecoli_1229) (pn:hypothetical 32) (gn:ycil) (gtcfc:13.7:14.1) (ec:) (ycil_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1229 ECOLI_1229 Escherichia coli 562 10052549

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847736	10502	32658	738	246
<u>Description</u>				
6500730840 ycik:b1271 hypothetical oxidoreductase in btur-sohb intergenic region (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1271 b1271 Escherichia coli 562 -11534698 110817 ycik (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YCIK_ECOLI P31808 ESCHERICHIA COLI 562 -11534698 7000687470 ycik probable dehydrogenase:ycik (cl:short-chain alcohol dehydrogenase homology) (ec:1.1.1.-) (db:pir2.dat) B64875 B64875 Escherichia coli 562 -11534698 223482 ycik internalin b (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #253(28.4-28.7 min.)) (nt:orf_id:o253#11; similar to (pir accession number) (le:10974) (re:11732) (di:complement) D90764 D90764 g1742066 Escherichia coli 562 -11534698 300300 ycik internalin b (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf_id:o253#11; similar to (pir accession number) (le:8480) (re:9238) (di:complement) D90765 D90765 g1742082 Escherichia coli 562 -11534698 300285 ycik putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 115 of 400 of the completegenome.) (nt:f252; 98 pct identical to ycik_ecoli sw: p31808) (le:1638) (re:2396) (di:complement) AE000225 AE000225 g1787526 Escherichia coli 562 -11534698 223497 ycik internalin b (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf_id:o253#11; similar to (pir accession number) (le:8480) (re:9238) (di:complement) D90765 D90765 g1742082 Escherichia coli 562 -11534698 5000692099 (de:(ecoli_1231) (pn:hypothetical oxidoreductase in btur-sohb intergenic region) (gn:ycik) (gtcfc:13.7:14.1) (ec:1.-.-.-) (ycik_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1231 ECOLI_1231 Escherichia coli 562 10119493				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847746	10503	32659	750	249

Description

5000692101 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1279 b1279 Escherichia coli 562 -11534699
7500921833 ycis (de:hypothetical 11.4 kd protein in pgpb-pyrf intergenic region) (db:swissprot) YCIS_ECOLI P77614 ESCHERICHIA COLI 562 -11534699
7000691218 ycis probable membrane protein ycis (cl:hypothetical protein hi1222) (db:pir2.dat) B64876 B64876 Escherichia coli 562 -11534699 223507 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)) (nt:orf_id:o255#4; similar to (swissprot accession) (le:2508) (re:2816) (di:direct) D90766 D90766 g1742093 Escherichia coli 562 -11534699
7500921835 ycis orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 116 of 400 of the completegenome.) (nt:o102; this 102 aa orf is 35 pct identical (0 gaps)) (le:1735) (re:2043) (di:direct) AE000226 AE000226 g1787535 Escherichia coli 562 -11534699 300310 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)) (nt:orf_id:o255#4; similar to (swissprot accession) (le:2508) (re:2816) (di:direct) D90766 D90766 g1742093 Escherichia coli 562 -11534699 6500730841 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1279 b1279 Escherichia coli 562 -11534699

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847747	10504	32660	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847752	10505	32661	507	168

Description

6500730842 ycim:b1280 hypothetical protein in pyrF 5 region:hypothetical 44.5 kd protein in pgpb-pyrF intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1280 b1280 Escherichia coli 562 -11534700 110821 ycim (de:hypothetical 44.5 kd protein in pgpb-pyrF intergenic region precursor) (db:swissprot) YCIM_ECOLI P45576 ESCHERICHIA COLI 562 -11534700 7000687472 ycim ycim protein precursor (cl:hypothetical protein h1223:tetratricopeptide repeat homology) (db:pir2.dat) C64876 C64876 Escherichia coli 562 -11534700 223508 ycim (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)) (nt:orf_id:o255#5; similar to (swissprot accession) (le:2823) (re:3992) (di:direct) D90766 D90766 g1742094 Escherichia coli 562 -11534700 300311 ycim putative heat shock protein (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 116 of 400 of the completengenome.) (nt:o389; 98 pct identical to 82 aa fragment) (le:2050) (re:3219) (di:direct) AE000226 AE000226 g2367116 Escherichia coli 562 -11534700

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847753	10506	32662	432	144

Description

6500730843 ycih:b1282 hypothetical 11.4 kd protein in pyrF-osmb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1282 b1282 Escherichia coli 562 -11534701 7000688991 ycih probable translation initiation factor ycih (cl:pyrF operon conserved hypothetical 11.4k protein) (db:pir1.dat) (mp:28 min) Q3ECPF E64876 Escherichia coli 562 -11534701 7500953693 ycih orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 116 of 400 of the completengenome.) (nt:o109; 100 pct identical to ycih_ecoli sw:) (le:4147) (re:4476) (di:direct) AE000226 AE000226 g1787538 Escherichia coli 562 -11534701 5000692103 (de:(ecoli_1242) (pn:hypothetical 11) (gn:ycih) (gtcfc:13.7:14.1) (ec:) (ycih_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1242 ECOLI_1242 Escherichia coli 562 10123251

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847758	10507	32663	396	131

Description

5000692104 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1284 b1284 Escherichia coli 562 -11534702
7500921837 ycit (de:hypothetical transcriptional regulator in osmb-rnb intergenic region) (db:swissprot) YCIT_ECOLI P76034 ESCHERICHIA COLI 562 -11534702 7000691219 hypothetical protein b1284 (db:pir2.dat) G64876 G64876 Escherichia coli 562 -11534702 7500921839 b1284 putative deor-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 116 of 400 of the completegenome.) (nt:f249; this 249 aa orf is 32 pct identical (8 gaps)) (le:5089) (re:5838) (di:complement) AE000226 AE000226 g1787540 Escherichia coli 562 -11534702 6500730844 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1284 b1284 Escherichia coli 562 -11534702

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847761	10508	32664	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847765	10509	32665	276	91

Description

6500730845 ycir:b1285 hypothetical protein:hypothetical 74.7 kd protein in osmb-rnb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1285 b1285 Escherichia coli 562 -11534703
500684970 ycir (de:hypothetical 74.7 kd protein in osmb-rnb intergenic region) (db:swissprot) YCIR_ECOLI P77334 ESCHERICHIA COLI 562 -11534703
7000687476 ycir probable membrane protein ycir (db:pir2.dat) H64876 H64876 Escherichia coli 562 -11534703 223513 mtcy02b10.18c (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)) (nt:orf_id:o255#12; similar to (swissprot accession) (le:7026) (re:9011) (di:complement) D90766 D90766 g1742099 Escherichia coli 562 -11534703 223521 mtcy02b10.18c (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #256(29.0-29.4 min.)) (nt:orf_id:o255#12; similar to (swissprot accession) (le:421) (re:2406) (di:complement) D90767 D90767 g1742108 Escherichia coli 562 -11534703 300316 ycir orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 116 of 400 of the completegenome.) (nt:f661; this 661 aa orf is 30 pct identical (15 gaps)) (le:6249) (re:8234) (di:complement) AE000226 AE000226 g1787541 Escherichia coli 562 -11534703 5000692105 (de:(ecoli_1245) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1245 ECOLI_1245 Escherichia coli 562 10061004

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847775	10510	32666	435	144

Description

5000692106 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1287 b1287 Escherichia coli 562 -11534704
7500921843 yciw (de:hypothetical 45.1 kd protein in rnb-fabi intergenic region) (db:swissprot) YCIW_ECOLI P76035 ESCHERICHIA COLI 562 -11534704
7000691220 yciw probable membrane protein yciw (db:pir2.dat) B64877 B64877 Escherichia coli 562 -11534704 7500921845 yciw putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 117 of 400 of the completegenome.) (nt:f401; this 401 aa orf is 25 pct identical (7 gaps)) (le:64) (re:1269) (di:complement) AE000227 AE000227 g1787544 Escherichia coli 562 -11534704 6500730846 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1287 b1287 Escherichia coli 562 -11534704

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847778	10511	32667	213	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847788	10512	32668	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847790	10513	32669	531	176

Description

GTC ORF with score 100 to: (fn:integrin analogue) (sr:saccharomyces cerevisiae (library: lambda gt11) dna) (db:genpept-pln1) (de:saccharomyces cerevisiae integrin analogue gene, complete cds.) (nt:putative) (le:1) (re:3049) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847791	10514	32670	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847792	10515	32671	570	190

Description

GTC ORF with score 98 to: (or:Plasmodium chabaudi) (sr:plasmodium chabaudi (strain as, sub_strain chabaudi) dna) (db:genpept-inv) (de:plasmodium chabaudi chabaudi merozoite surface protein-1 gene, complete cds.) (nt:precursor) (le:1) (re:5301) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847813	10516	32672	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847817	10517	32673	624	208

Description

6500730847 ycj d:b1289 hypothetical 14.0 kd protein in envm-sapf intergenic region:hypothetical 14.0 kd protein in fabi-sapf intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1289 b1289 Escherichia coli 562 -11534705 110829 ycj d (de:hypothetical 14.0 kd protein in fabi-sapf intergenic region) (db:swissprot) YCJD_ECOLI P45736 ESCHERICHIA COLI 562 -11534705 7000687478 ycj d ycj d protein (cl:hypothetical protein hi0925) (db:pir2.dat) D64877 D64877 Escherichia coli 562 -11534705 223516 ycj d (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #255(28.8-29.2 min.)) (nt:orf_id:o255#17; similar to (swissprot accession) (le:13675) (re:14028) (di:complement) D90766 D90766 g1742102 Escherichia coli 562 -11534705 223524 ycj d (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #256(29.0-29.4 min.)) (nt:orf_id:o255#17; similar to (swissprot accession) (le:7070) (re:7423) (di:complement) D90767 D90767 g1742111 Escherichia coli 562 -11534705 300319 ycj d orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 117 of 400 of the completegenome.) (nt:f117; 100 pct identical to ycj d_ecoli sw: p45736) (le:2491) (re:2844) (di:complement) AE000227 AE000227 g1787546 Escherichia coli 562 -11534705 5000692107 (de:(ecoli_1249) (pn:hypothetical 14) (gn:ycj d) (gtcfc:13.7:14.1) (ec:) (ycj d_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1249 ECOLI_1249 Escherichia coli 562 10052559

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847846	10518	32674	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847847	10519	32675	1170	389

Description

GTC ORF with score 201 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f26p21 (essaiiproject).) (nt:contains est gb:t13833, t46155) (le:75664:76120:76307) (re:76029:76221:76537) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847868	10520	32676	459	152

Description

5000692112 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1295 b1295 Escherichia coli 562 -11534706
 7500951398 ymja (de:hypothetical 9.3 kd protein in sapa-aldh intergenic region) (db:swissprot) YMJA_ECOLI P76036 ESCHERICHIA COLI 562 -11534706
 7000691221 ymja ymja protein (db:pir2.dat) B64878 B64878 Escherichia coli 562 -11534706 7500951400 ymja orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 117 of 400 of the completegenome.) (nt:f81; this 81 aa orf is 31 pct identical (2 gaps)) (le:8507) (re:8752) (di:complement) AE000227 AE000227 g1787552 Escherichia coli 562 -11534706 6500730848 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1295 b1295 Escherichia coli 562 -11534706

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847873	10521	32677	630	209

Description

5000692113 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1296 b1296 Escherichia coli 562 -11534707
 7000691222 ymjj probable amino acid permease ycjj (db:pir2.dat) C64878 C64878 Escherichia coli 562 -11534707 7500921850 ycjj putative amino acid/amine transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 117 of 400 of the completegenome.) (nt:f479; this 479 aa orf is 63 pct identical (1 gap)) (le:8886) (re:10325) (di:complement) AE000227 AE000227 g1787553 Escherichia coli 562 -11534707 7500921848 ycjj (de:hypothetical 49.8 kd transport protein in sapa-aldh intergenic region) (db:swissprot) YCJJ_ECOLI P76037 ESCHERICHIA COLI 562 -11534707 6500730849 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1296 b1296 Escherichia coli 562 -11534707

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847876	10522	32678	555	185

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847881	10523	32679	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847882	10524	32680	885	294

Description

5000692114 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1297 b1297 Escherichia coli 562 -11534708
 7500921851 ycjk (ec:6.3.1.2) (de:ligase)) (db:swissprot) YCJK_ECOLI P78061 ESCHERICHIA COLI 562 -11534708 7000691223 probable glutamate--ammonia ligase::probable glutamine synthetase (ec:6.3.1.2) (db:pir2.dat) D64878 D64878 Escherichia coli 562 -11534708 7500921853 b1297 putative glutamine synthetase ec 6.3.1.2 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 118 of 400 of the completegenome.) (nt:f498; this 498 aa orf is 31 pct identical (29 gaps)) (le:155) (re:1651) (di:complement) AE000228 AE000228 g1787555 Escherichia coli 562 -11534708
 6500730850 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1297 b1297 Escherichia coli 562 -11534708

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847891	10525	32681	375	124

Description

5000692115 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1298 b1298 Escherichia coli 562 -11534709
 7000691224 ycjl protein:conserved hypothetical protein b1298 (db:pir2.dat) E64878 E64878 Escherichia coli 562 -11534709 7500921856 ycjl probable amidotransferase subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 118 of 400 of the completegenome.) (nt:o258; this 258 aa orf is 35 pct identical (9 gaps)) (le:1773) (re:2549) (di:direct) AE000228 AE000228 g1787556 Escherichia coli 562 -11534709 7500921854 ycjl (de:hypothetical 28.5 kd protein in sapa-aldh intergenic region) (db:swissprot) YCJL_ECOLI P76038 ESCHERICHIA COLI 562 -11534709 6500730851 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1298 b1298 Escherichia coli 562 -11534709

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847892	10526	32682	255	84

Description

6500730852 pspf:b1303 hypothetical protein in pspa 5 region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1303 b1303 Escherichia coli 562 -11534710 7000691924 pspf transcription activator pspf (cl:pseudomonas syringae hrps protein:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) B64879 B64879 Escherichia coli 562 -11534710 7500960471 pspf psp operon transcriptional activator (fn:regulator; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 118 of 400 of the completegenome.) (nt:f330; 100 pct identical to 110 aa) (le:7600) (re:8592) (di:complement) AE000228 AE000228 g1787561 Escherichia coli 562 -11534710 5000692118 (de:(ecoli_1263) (pn:psp operon transcriptional activator) (gn:pspf) (gtcfc:13.7:14.1) (ec:) (pspf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1263 ECOLI_1263 Escherichia coli 562 10123258

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847893	10527	32683	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847917	10528	32684	957	318

Description

5000692124 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1309 b1309 Escherichia coli 562 -11534711 7000691225 probable membrane protein b1309 (db:pir2.dat) H64879 H64879 Escherichia coli 562 -11534711 7500959974 ycjn putative polysaccharide hydrolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o568; this 568 aa orf is 33 pct identical (43 gaps)) (le:568) (re:2274) (di:direct) AE000229 AE000229 g1787568 Escherichia coli 562 -11534711 6500730853 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1309 b1309 Escherichia coli 562 -11534711

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847921	10529	32685	237	78

Description

GTC ORF with score 134 to: (fn:membrane protein mediating transport of) (db:genpept-pln1) (de:candida albicans oligopeptide transporter (opt1) gene, completecds.) (nt:oligopeptide transporter) (le:482:2166) (re:2107:2891) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847922	10530	32686	288	95

Description

5000692125 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1310 b1310 Escherichia coli 562 -11534712
7000691226 probable multiple sugar-binding protein b1310 precursor (db:pir2.dat) A64880 A64880 Escherichia coli 562 -11534712 7500959975 b1310 putative transport periplasmic protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o430; this 430 aa orf is 27 pct identical (35 gaps)) (le:2288) (re:3580) (di:direct) AE000229 AE000229 g1787569 Escherichia coli 562 -11534712 6500730854 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1310 b1310 Escherichia coli 562 -11534712

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847923	10531	32687	390	129

Description

GTC ORF with score 230 to: (fn:membrane protein mediating transport of) (db:genpept-pln1) (de:candida albicans oligopeptide transporter (opt1) gene, completecds.) (nt:oligopeptide transporter) (le:482:2166) (re:2107:2891) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847924	10532	32688	240	79

Description

5000692126 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1311 b1311 Escherichia coli 562 -11534713
7500921857 ycjo (de:hypothetical abc transporter permease protein ycjo) (db:swissprot) YCJO_ECOLI P77653 ESCHERICHIA COLI 562 -11534713 7000691227 probable multiple sugar transport protein b1311 precursor:probable multiple sugar permease b1311 (db:pir2.dat) B64880 B64880 Escherichia coli 562 -11534713 223560 sn-glycerol-3-phosphate transport system (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o258#3; similar to (swissprot accession) (le:6596) (re:7477) (di:direct) D90769 D90769 g1742149 Escherichia coli 562 -11534713
7500921859 ycjo putative binding-protein dependent transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o293; this 293 aa orf is 29 pct identical (18 gaps)) (le:3601) (re:4482) (di:direct) AE000229 AE000229 g1787570 Escherichia coli 562 -11534713 300350 sn-glycerol-3-phosphate transport system (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o258#3; similar to (swissprot accession) (le:6596) (re:7477) (di:direct) D90769 D90769 g1742149 Escherichia coli 562 -11534713 6500730855 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1311 b1311 Escherichia coli 562 -11534713

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847925	10533	32689	333	110

Description

5000692127 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1312 b1312 Escherichia coli 562 -11534714

7500921860 ycjp (de:hypothetical abc transporter permease protein ycjp) (db:swissprot) YCJP_ECOLI P77716 ESCHERICHIA COLI 562 -11534714 7000691228 probable multiple sugar transport protein b1312 precursor:probable multiple sugar permease b1312 (cl:maltose transport protein malg) (db:pir2.dat) C64880 C64880 Escherichia coli 562 -11534714 223561 maltose transport system permease protein malg. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o258#4; similar to (swissprot accession) (le:7464) (re:8306) (di:direct) D90769 D90769 g1742150 Escherichia coli 562 -11534714 300351 maltose transport system permease protein malg. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #259(29.6-30.0 min.)) (nt:orf_id:o258#4; similar to (swissprot accession) (le:674) (re:1516) (di:direct) D90770 D90770 g1742158 Escherichia coli 562 -11534714 7500921862 ycjp putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o280; this 280 aa orf is 32 pct identical (13 gaps)) (le:4469) (re:5311) (di:direct) AE000229 AE000229 g1787571 Escherichia coli 562 -11534714 223568 maltose transport system permease protein malg. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o258#4; similar to (swissprot accession) (le:7464) (re:8306) (di:direct) D90769 D90769 g1742150 Escherichia coli 562 -11534714 6500730856 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1312 b1312 Escherichia coli 562 -11534714

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847952	10534	32690	441	146

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847960	10535	32691	1131	376

Description

5000692128 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1313 b1313 Escherichia coli 562 -11534715
7500921863 ycjq (de:intergenic region) (db:swissprot) YCJQ_ECOLI P76043
ESCHERICHIA COLI 562 -11534715 7000691229 ycjq probable oxidoreductase:ycjq (ec:1.1.1.1.-) (db:pir2.dat) D64880 D64880 Escherichia coli 562 -11534715
7500921865 ycjq putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o350; this 350 aa orf is 35 pct identical (2 gaps)) (le:5342) (re:6394) (di:direct) AE000229 AE000229 g1787572
Escherichia coli 562 -11534715 6500730857 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1313 b1313
Escherichia coli 562 -11534715

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501847961	10536	32692	633	210

Description

5000692129 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1314 b1314 Escherichia coli 562 -11534716
7000691230 hypothetical protein b1314 (db:pir2.dat) E64880 E64880
Escherichia coli 562 -11534716 7500959976 b1314 putative transient receptor potential locus (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o265; this 265 aa orf is 25 pct identical (20 gaps)) (le:6404) (re:7201) (di:direct) AE000229 AE000229 g1787573 Escherichia coli 562 -11534716
6500730858 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1314 b1314 Escherichia coli 562 -11534716

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847964	10537	32693	531	176

Description

5000692130 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1315 b1315 Escherichia coli 562 -11534717

7500921866 ycjs (de:hypothetical 38.7 kd protein in pspe-ompg intergenic region) (db:swissprot) YCJS_ECOLI P77503 ESCHERICHIA COLI 562 -11534717

7000691231 ycjs ycjs protein (db:pir2.dat) F64880 F64880 Escherichia coli 562 -11534717 223563 rhizopine catabolism protein moca. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.).) (nt:orf_id:o258#7; similar to (swissprot accession) (le:10203) (re:11258) (di:direct) D90769 D90769 g1742152 Escherichia coli 562 -11534717 300353 rhizopine catabolism protein moca. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #259(29.6-30.0 min.).) (nt:orf_id:o258#7; similar to (swissprot accession) (le:3413) (re:4468) (di:direct) D90770 D90770 g1742160 Escherichia coli 562 -11534717 7500921868 ycjs putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o351; this 351 aa orf is 27 pct identical (10 gaps)) (le:7211) (re:8266) (di:direct) AE000229 AE000229 g1787574 Escherichia coli 562 -11534717 223570 rhizopine catabolism protein moca. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.).) (nt:orf_id:o258#7; similar to (swissprot accession) (le:10203) (re:11258) (di:direct) D90769 D90769 g1742152 Escherichia coli 562 -11534717 6500730859 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1315 b1315 Escherichia coli 562 -11534717

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847987	10538	32694	1137	378

Description

5000692131 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1316 b1316 Escherichia coli 562 -11534718
7500921869 ycjt (de:hypothetical 84.9 kd protein in pspe-ompg intergenic region) (db:swissprot) YCJT_ECOLI P77154 ESCHERICHIA COLI 562 -11534718
7000691232 ycjt ycjt protein (db:pir2.dat) G64880 G64880 Escherichia coli 562 -11534718 223564 ath1 protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o258#8; similar to (swissprot accession) (le:11255) (re:13522) (di:direct) D90769 D90769 g1742153 Escherichia coli 562 -11534718 300354 ath1 protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #259(29.6-30.0 min.)) (nt:orf_id:o258#8; similar to (swissprot accession) (le:4465) (re:6732) (di:direct) D90770 D90770 g1742161 Escherichia coli 562 -11534718
7500921871 ycjt orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o755; this 755 aa orf is 24 pct identical (24 gaps)) (le:8263) (re:10530) (di:direct) AE000229 AE000229 g1787575 Escherichia coli 562 -11534718 223571 ath1 protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o258#8; similar to (swissprot accession) (le:11255) (re:13522) (di:direct) D90769 D90769 g1742153 Escherichia coli 562 -11534718 6500730860 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1316 b1316 Escherichia coli 562 -11534718

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847990	10539	32695	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847995	10540	32696	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501847999	10541	32697	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848015	10542	32698	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848016	10543	32699	735	244

Description

5000692132 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1317 b1317 Escherichia coli 562 -11534719
7500887970 ycju (ec:5.4.2.6) (de:putative beta-phosphoglucomutase, (beta-pgm)) (db:swissprot) PGMB_ECOLI P77366 ESCHERICHIA COLI 562 -11534719
7000691233 ycju probable beta-phosphoglucomutase:ycju (cl:hypothetical protein b2690) (ec:5.4.2.6) (db:pir2.dat) H64880 H64880 Escherichia coli 562 -11534719 223565 phosphoglycolate phosphatase ec 3.1.3.18 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o258#9; similar to (swissprot accession) (le:13519) (re:14178) (di:direct) D90769 D90769 g1742154 Escherichia coli 562 -11534719 300355 phosphoglycolate phosphatase ec 3.1.3.18 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #259(29.6-30.0 min.)) (nt:orf_id:o258#9; similar to (swissprot accession) (le:6729) (re:7388) (di:direct) D90770 D90770 g1742162 Escherichia coli 562 -11534719 7500887972 ycju putative beta-phosphoglucomutase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o219; this 219 aa orf is 28 pct identical (8 gaps)) (le:10527) (re:11186) (di:direct) AE000229 AE000229 g1787576 Escherichia coli 562 -11534719 223572 phosphoglycolate phosphatase ec 3.1.3.18 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o258#9; similar to (swissprot accession) (le:13519) (re:14178) (di:direct) D90769 D90769 g1742154 Escherichia coli 562 -11534719 6500730861 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1317 b1317 Escherichia coli 562 -11534719

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848037	10544	32700	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848077	10545	32701	456	151

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848078	10546	32702	882	293

Description

5000692133 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1318 b1318 Escherichia coli 562 -11534720
7500921872 ycjv (de:hypothetical abc transporter atp-binding protein ycjv) (db:swissprot) YCJV_ECOLI P77481 ESCHERICHIA COLI 562 -11534720 7000691234 probable abc-type transport protein b1318:probable sugar transport atp-binding protein (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) A64881 A64881 Escherichia coli 562 -11534720 223566 nucleotide-binding protein ugpc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o258#10; similar to (pir accession number) (le:14192) (re:15160) (di:direct) D90769 D90769 g1742155 Escherichia coli 562 -11534720 300356 nucleotide-binding protein ugpc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #259(29.6-30.0 min.)) (nt:orf_id:o258#10; similar to (pir accession number) (le:7402) (re:8370) (di:direct) D90770 D90770 g1742163 Escherichia coli 562 -11534720 7500921874 ycjv putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o322; this 322 aa orf is 62 pct identical (17 gaps)) (le:11200) (re:12168) (di:direct) AE000229 AE000229 g1787577 Escherichia coli 562 -11534720 223573 nucleotide-binding protein ugpc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o258#10; similar to (pir accession number) (le:14192) (re:15160) (di:direct) D90769 D90769 g1742155 Escherichia coli 562 -11534720 6500730862 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1318 b1318 Escherichia coli 562 -11534720

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848090	10547	32703	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848096	10548	32704	384	127

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848099	10549	32705	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848100	10550	32706	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848119	10551	32707	1890	629

Description

6500730863 ompg:b1319 hypothetical protein:outer membrane protein g precursor (gtcfc:11.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1319 b1319 Escherichia coli 562 -11534721 1500686811 ompg (de:outer membrane protein g precursor) (db:swissprot) OMPG_ECOLI P76045 ESCHERICHIA COLI 562 -11534721 7000686039 ompg probable outer membrane protein ompg precursor (db:pir2.dat) B64881 B64881 Escherichia coli 562 -11534721 239633 ompg outer membrane protein (fn:membrane; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 120 of 400 of the completegenome.) (nt:o301; this 301 aa orf is 23 pct identical (3 gaps)) (le:109) (re:1014) (di:direct) AE000230 AE000230 g1787579 Escherichia coli 562 -11534721 294891 ompg porin (db:genpept-bct2) (de:escherichia coli porin (ompg) gene, complete cds.) (le:1473) (re:2378) (di:direct) ECU49400 U49400 g1806593 Escherichia coli 562 -11534721 5000692134 (de:(ecoli_1279) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1279 ECOLI_1279 Escherichia coli 562 10062686

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848141	10552	32708	1680	559

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848146	10553	32709	222	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848157	10554	32710	2595	865

Description

5000692135 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1320 b1320 Escherichia coli 562 -11534722
7500921875 ycjw (de:hypothetical transcriptional regulator in ompg-tyrr intergenic region) (db:swissprot) YCJW_ECOLI P77615 ESCHERICHIA COLI 562 -11534722 7000691235 ycjw probable transcription regulator ycjw (cl:lac repressor) (db:pir2.dat) C64881 C64881 Escherichia coli 562 -11534722
223574 glucose-resistance amylase regulator catabolite (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #259(29.6-30.0 min.)) (nt:orf_id:o260#2; similar to (swissprot accession) (le:9544) (re:10542) (di:complement) D90770 D90770 g1742164 Escherichia coli 562 -11534722
300358 glucose-resistance amylase regulator catabolite (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #260(29.8-30.2 min.)) (nt:orf_id:o260#2; similar to (swissprot accession) (le:1437) (re:2435) (di:complement) D90771 D90771 g1742176 Escherichia coli 562 -11534722
7500921877 ycjw putative lacI-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 120 of 400 of the completegenome.) (nt:f332; this 332 aa orf is 31 pct identical (9 gaps)) (le:1125) (re:2123) (di:complement) AE000230 AE000230 g1787580 Escherichia coli 562 -11534722 223585 glucose-resistance amylase regulator catabolite (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #259(29.6-30.0 min.)) (nt:orf_id:o260#2; similar to (swissprot accession) (le:9544) (re:10542) (di:complement) D90770 D90770 g1742164 Escherichia coli 562 -11534722 6500730864 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1320 b1320 Escherichia coli 562 -11534722

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848167	10555	32711	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848176	10556	32712	1575	524

Description

5000692136 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1321 b1321 Escherichia coli 562 -11534723
7500921878 ycjx (de:hypothetical 52.6 kd protein in ompg-tyrr intergenic region) (db:swissprot) YCJX_ECOLI P76046 ESCHERICHIA COLI 562 -11534723
7000691236 ycjx ycjx protein (db:pir2.dat) D64881 D64881 Escherichia coli 562 -11534723 7500921880 ycjx putative ec 2.1 enzymes (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 120 of 400 of the completegenome.) (nt:o465; this 465 aa orf is 50 pct identical (6 gaps)) (le:2279) (re:3676) (di:direct) AE000230 AE000230 g1787581 Escherichia coli 562 -11534723 6500730865 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1321 b1321 Escherichia coli 562 -11534723

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848177	10557	32713	294	97

Description

6500730866 ycjf:b1322 hypothetical protein in pspe-tyrr intergenic region:hypothetical 39.4 kd protein in pspe-tyrr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1322 b1322 Escherichia coli 562 -11534724 110832 ycjf (de:hypothetical 39.4 kd protein in pspe-tyrr intergenic region) (db:swissprot) YCJF_ECOLI P45525 ESCHERICHIA COLI 562 -11534724 7000687479 ycjf membrane protein ycjf (cl:hypothetical protein hi0043) (db:pir2.dat) E64881 E64881 Escherichia coli 562 -11534724 223576 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #259(29.6-30.0 min.)) (nt:orf_id:o260#4; similar to (swissprot accession) (le:12091) (re:13152) (di:direct) D90770 D90770 g1742166 Escherichia coli 562 -11534724 223587 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #260(29.8-30.2 min.)) (nt:orf_id:o260#4; similar to (swissprot accession) (le:3984) (re:5045) (di:direct) D90771 D90771 g1742178 Escherichia coli 562 -11534724 300360 ycjf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 120 of 400 of the completegenome.) (nt:o353; 100 pct identical to 52 aa of 102 aa) (le:3673) (re:4734) (di:direct) AE000230 AE000230 g1787582 Escherichia coli 562 -11534724 5000692137 (de:(ecoli_1282) (pn:hypothetical protein in pspe-tyrr intergenic region:fragment) (gn:ycjf) (gtcfc:13.7:14.1) (ec:) (ycjf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1282 ECOLI_1282 Escherichia coli 562 10119527

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848196	10558	32714	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848206	10559	32715	1614	537

Description

5000692139 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1325 b1325 Escherichia coli 562 -11534725
7000691237 hypothetical protein b1325 (db:pir2.dat) H64881 H64881
Escherichia coli 562 -11534725 7500959977 ycjg putative muconate cycloisomerase i ec 5.5.-- (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 120 of 400 of the completegenome.) (nt:o335; this 335 aa orf is 29 pct identical (27 gaps)) (le:7050) (re:8057) (di:direct) AE000230 AE000230 g1787585 Escherichia coli 562 -11534725 6500730867 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1325 b1325 Escherichia coli 562 -11534725

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848214	10560	32716	1188	395

Description

6500730868 ycji:b1326 hypothetical protein:hypothetical 28.8 kd protein in tpx-fnr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1326 b1326 Escherichia coli 562 -11534726 110836 ycji (de:hypothetical 28.8 kd protein in tpx-fnr intergenic region) (db:swissprot) YCJI_ECOLI P51983 ESCHERICHIA COLI 562 -11534726 7000687480 ycji ycji protein (db:pir2.dat) A64882 A64882 Escherichia coli 562 -11534726 223581 ycji (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #259(29.6-30.0 min.)) (nt:orf_id:o260#9; similar to (swissprot accession) (le:16450) (re:17238) (di:complement) D90770 D90770 g1742171 Escherichia coli 562 -11534726 223592 ycji (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #260(29.8-30.2 min.)) (nt:orf_id:o260#9; similar to (swissprot accession) (le:8343) (re:9131) (di:complement) D90771 D90771 g1742183 Escherichia coli 562 -11534726 300365 ycji putative carboxypeptidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 120 of 400 of the completegenome.) (nt:f262; this 262 aa orf is 40 pct identical (6 gaps)) (le:8032) (re:8820) (di:complement) AE000230 AE000230 g1787586 Escherichia coli 562 -11534726 5000692140 (de:(ecoli_1286) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1286 ECOLI_1286 Escherichia coli 562 10119531

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848230	10561	32717	288	95

Description

5000692141 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1327 b1327 Escherichia coli 562 -11534727
7500921882 ycjy (de:hypothetical 34.1 kd protein in tpx-fnr intergenic region) (db:swissprot) YCJY_ECOLI P76049 ESCHERICHIA COLI 562 -11534727
7000691238 conserved hypothetical protein b1327 (db:pir2.dat) B64882 B64882 Escherichia coli 562 -11534727 7500921884 b1327 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 120 of 400 of the completegenome.) (nt:f310; this 310 aa orf is 35 pct identical (12 gaps)) (le:9095) (re:10027) (di:complement) AE000230 AE000230 g1787587 Escherichia coli 562 -11534727 6500730869 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1327 b1327 Escherichia coli 562 -11534727

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848231	10562	32718	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848233	10563	32719	234	77

Description

6500730870 ycjz:b1328 hypothetical protein:hypothetical transcriptional regulator in tpx-fnr intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1328 b1328 Escherichia coli 562 -11534728 5500686500 ycjz (de:hypothetical transcriptional regulator in tpx-fnr intergenic region) (db:swissprot) YCJZ_ECOLI P77333 ESCHERICHIA COLI 562 -11534728 7000687481 ycjz probable transcription regulator ycjz (cl:hypothetical protein b1328) (db:pir2.dat) C64882 C64882 Escherichia coli 562 -11534728 223594 xanthosine operon regulatory protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #260(29.8-30.2 min.).) (nt:orf_id:o260#12; similar to (swissprot accession) (le:10464) (re:11363) (di:direct) D90771 D90771 g1742185 Escherichia coli 562 -11534728 300377 xanthosine operon regulatory protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.).) (nt:orf_id:o260#12; similar to (swissprot accession) (le:529) (re:1428) (di:direct) D90772 D90772 g1742196 Escherichia coli 562 -11534728 300367 ycjz putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 121 of 400 of the completegenome.) (nt:o299; this 299 aa orf is 47 pct identical (0 gaps)) (le:93) (re:992) (di:direct) AE000231 AE000231 g1787589 Escherichia coli 562 -11534728 223604 xanthosine operon regulatory protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.).) (nt:orf_id:o260#12; similar to (swissprot accession) (le:529) (re:1428) (di:direct) D90772 D90772 g1742196 Escherichia coli 562 -11534728 5000692142 (de:(ecoli_1288) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1288 ECOLI_1288 Escherichia coli 562 10119535

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848234	10564	32720	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848237	10565	32721	423	140

Description

5000692143 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1329 b1329 Escherichia coli 562 -11534729
7000691239 periplasmic oligopeptide-binding protein precursor (cl:dipeptide transport protein) (db:pir2.dat) D64882 D64882 Escherichia coli 562 -11534729 223595 periplasmic oligopeptide-binding protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #260(29.8-30.2 min.).) (nt:orf_id:o260#13; similar to (swissprot accession) (le:11679) (re:13313) (di:direct) D90771 D90771 g1742186 Escherichia coli 562 -11534729 300378 periplasmic oligopeptide-binding protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.).) (nt:orf_id:o260#13; similar to (swissprot accession) (le:1744) (re:3378) (di:direct) D90772 D90772 g1742197 Escherichia coli 562 -11534729 300368 b1329 putative transport periplasmic protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 121 of 400 of the completegenome.) (nt:o544; this 544 aa orf is 48 pct identical (4 gaps)) (le:1308) (re:2942) (di:direct) AE000231 AE000231 g1787590 Escherichia coli 562 -11534729 223605 periplasmic oligopeptide-binding protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.).) (nt:orf_id:o260#13; similar to (swissprot accession) (le:1744) (re:3378) (di:direct) D90772 D90772 g1742197 Escherichia coli 562 -11534729 6500730871 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1329 b1329 Escherichia coli 562 -11534729

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848242	10566	32722	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848263	10567	32723	1638	546

Description

5000692144 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1330 b1330 Escherichia coli 562 -11534730
7000691240 probable membrane protein b1330 precursor:conserved hypothetical protein b1330 (db:pir2.dat) E64882 E64882 Escherichia coli 562 -11534730
223596 yggB (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #260(29.8-30.2 min.)) (nt:orf_id:o260#14; similar to (swissprot accession) (le:13364) (re:14395) (di:complement) D90771 D90771 g1742187 Escherichia coli 562 -11534730 300379 yggB (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.)) (nt:orf_id:o260#14; similar to (swissprot accession) (le:3429) (re:4460) (di:complement) D90772 D90772 g1742198 Escherichia coli 562 -11534730 300369 b1330 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 121 of 400 of the completegenome.) (nt:f343) (le:2993) (re:4024) (di:complement) AE000231 AE000231 g1787591 Escherichia coli 562 -11534730
223606 yggB (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.)) (nt:orf_id:o260#14; similar to (swissprot accession) (le:3429) (re:4460) (di:complement) D90772 D90772 g1742198 Escherichia coli 562 -11534730 6500730872 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1330 b1330 Escherichia coli 562 -11534730

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848265	10568	32724	1302	433

Description

5000692145 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1332 b1332 Escherichia coli 562 -11534731
7500951711 ynaJ (de:hypothetical 9.3 kd protein in tpx-fnr intergenic region) (db:swissprot) YNAJ_ECOLI P76050 ESCHERICHIA COLI 562 -11534731
7000691241 membrane protein ynaJ precursor:conserved hypothetical protein b1332 (db:pir2.dat) G64882 G64882 Escherichia coli 562 -11534731 7500951713 ynaJ orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 121 of 400 of the completegenome.) (nt:o85; this 85 aa orf is 32 pct identical (0 gaps)) (le:5467) (re:5724) (di:direct) AE000231 AE000231 g1787593 Escherichia coli 562 -11534731
6500730873 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1332 b1332 Escherichia coli 562 -11534731

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848267	10569	32725	501	166

Description

6500730874 ydah:b1336 hypothetical protein in ogt 5region:hypothetical 55.1 kd protein in ogt-dbpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1336 b1336 Escherichia coli 562 -11534732 111217 ydah (de:hypothetical 55.1 kd protein in ogt-dbpa intergenic region) (db:swissprot) YDAH_ECOLI P46133 ESCHERICHIA COLI 562 -11534732 7000687511 ydah membrane protein ydah (db:pir2.dat) C64883 C64883 Escherichia coli 562 -11534732 7500922145 ydah putative pump protein transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 121 of 400 of the completegenome.) (nt:f510; 98 pct identical to 57 aa fragment) (le:8349) (re:9881) (di:complement) AE000231 AE000231 g1787597 Escherichia coli 562 -11534732 5000692147 (de:(ecoli_1296) (pn:hypothetical protein in ogt 5"region:fragment) (gn:ydah) (gtcfc:13.7:14.1) (ec:) (ydah_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1296 ECOLI_1296 Escherichia coli 562 10123269

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848275	10570	32726	615	204

Description

GTC ORF with score 111 to: (db:genpept-bct1) (de:streptococcus pyogenes 42 kd protein (orf1) gene and 67 kdmyosin-crossreactive streptococcal antigen gene, complete cds.) (nt:orf1, putative 42 kda protein) (le:237) (re:1418) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848279	10571	32727	1404	467

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848287	10572	32728	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501848304	10573	32729	1032	343

Description

5000692148 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1337 b1337 Escherichia coli 562 -11534733
 7000691242 hypothetical protein b1337 (db:pir2.dat) D64883 D64883
 Escherichia coli 562 -11534733 7500959978 b1337 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 121 of 400 of the completegenome.) (nt:f481; this 481 aa orf is 27 pct identical (14 gaps)) (le:9912) (re:11357) (di:complement) AE000231 AE000231 g1787598 Escherichia coli 562 -11534733 6500730875 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1337 b1337 Escherichia coli 562 -11534733

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501848311	10574	32730	1092	363

Description

6500730876 ydaj:b1338 hypothetical protein:hypothetical 47.1 kd protein in ogt-dbpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1338 b1338 Escherichia coli 562 -11534734
 1500685831 ydaj (de:hypothetical 47.1 kd protein in ogt-dbpa intergenic region) (db:swissprot) YDAJ_ECOLI P77357 ESCHERICHIA COLI 562 -11534734
 7000687512 ydaj probable amidohydrolase:ydaj (cl:hypothetical protein hi0584) (ec:3.5.-.-) (db:pir2.dat) E64883 E64883 Escherichia coli 562 -11534734 223613 thermostable carboxypeptidase ec 3.4.17.-. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.).) (nt:orf_id:o261#10; similar to (swissprot accession) (le:11793) (re:13118) (di:complement) D90772 D90772 g1742205 Escherichia coli 562 -11534734
 300386 ydaj putative aminohydrolase ec 3.5.1.14 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 121 of 400 of the completegenome.) (nt:f441; this 441 aa orf is 40 pct identical (4 gaps)) (le:11357) (re:12682) (di:complement) AE000231 AE000231 g1787599 Escherichia coli 562 -11534734 5000692149 (de:(ecoli_1298) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1298 ECOLI_1298 Escherichia coli 562 10059232

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501848313	10575	32731	237	78

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501848315	10576	32732	1338	445

Description

5000692150 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1339 b1339 Escherichia coli 562 -11534735
7500922147 ydak (de:hypothetical transcriptional regulator in ogt-dbpa intergenic region) (db:swissprot) YDAK_ECOLI P77744 ESCHERICHIA COLI 562 -11534735 7000691243 ydak probable transcription regulator ydak (db:pir2.dat) F64883 F64883 Escherichia coli 562 -11534735 223614 tdcabc operon transcriptional activator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.)) (nt:orf_id:o261#11; similar to (swissprot accession) (le:13279) (re:14187) (di:direct) D90772 D90772 g1742206 Escherichia coli 562 -11534735 300387 tdcabc operon transcriptional activator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #262(30.3-30.5 min.)) (nt:orf_id:o261#11; similar to (swissprot accession) (le:540) (re:1448) (di:direct) D90773 D90773 g1742210 Escherichia coli 562 -11534735 300390 ydak putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 122 of 400 of the completegenome.) (nt:o302; this 302 aa orf is 27 pct identical (2 gaps)) (le:111) (re:1019) (di:direct) AE000232 AE000232 g1787601 Escherichia coli 562 -11534735 223617 tdcabc operon transcriptional activator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.)) (nt:orf_id:o261#11; similar to (swissprot accession) (le:13279) (re:14187) (di:direct) D90772 D90772 g1742206 Escherichia coli 562 -11534735 6500730877 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1339 b1339 Escherichia coli 562 -11534735

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501848318	10577	32733	198	65

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501848335	10578	32734	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848342	10579	32735	342	113

Description

5000692151 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1340 b1340 Escherichia coli 562 -11534736
 7500922151 ydal (de:hypothetical 21.5 kd protein in ogt-dbpa intergenic region) (db:swissprot) YDAL_ECOLI P76053 ESCHERICHIA COLI 562 -11534736
 7000691244 ydal ydal protein (db:pir2.dat) G64883 G64883 Escherichia coli 562 -11534736 7500922153 ydal orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 122 of 400 of the completegenome.) (nt:o187; this 187 aa orf is 22 pct identical (5 gaps)) (le:1349) (re:1912) (di:direct) AE000232 AE000232 g1787602 Escherichia coli 562 -11534736 6500730878 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1340 b1340 Escherichia coli 562 -11534736

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848374	10580	32736	681	226

Description

GTC ORF with score 116 to: (or:Homo sapiens) (sr:homo sapiens male brain cDNA to mRNA, clone_lib:psport) (db:genpept-pri2) (de:homo sapiens mRNA for megf7, partial cds.) (nt:similar to ldl receptor-like protein; tsxv motif) (le:<1) (re:4731) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848378	10581	32737	1050	349

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848381	10582	32738	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848396	10583	32739	684	227

Description

5000692152 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1341 b1341 Escherichia coli 562 -11534737
7000691245 conserved hypothetical protein b1341 (db:pir2.dat) H64883 H64883 Escherichia coli 562 -11534737 223618 yhck (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #262(30.3-30.5 min.)) (nt:orf_id:o262#1; similar to (swissprot accession) (le:2362) (re:3654) (di:complement) D90773 D90773 g1742211 Escherichia coli 562 -11534737 300391 b1341 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 122 of 400 of the completegenome.) (nt:f430; this 430 aa orf is 31 pct identical (7 gaps)) (le:1933) (re:3225) (di:complement) AE000232 AE000232 g1787603 Escherichia coli 562 -11534737 6500730879 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1341 b1341 Escherichia coli 562 -11534737

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848397	10584	32740	210	69

Description

5000692153 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1342 b1342 Escherichia coli 562 -11534738
7000691246 probable transport protein b1342 (db:pir2.dat) A64884 A64884 Escherichia coli 562 -11534738 7500959979 b1342 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 122 of 400 of the completegenome.) (nt:o327; this 327 aa orf is 20 pct identical (4 gaps)) (le:3420) (re:4403) (di:direct) AE000232 AE000232 g1787604 Escherichia coli 562 -11534738 6500730880 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1342 b1342 Escherichia coli 562 -11534738

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848398	10585	32741	420	139

Description

6500730881 ydao:b1344 hypothetical protein:hypothetical 35.6 kd protein in dbpa-intr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1344 b1344 Escherichia coli 562 -11534739
5500686518 ydao (de:hypothetical 35.6 kd protein in dbpa-intr intergenic region) (db:swissprot) YDAO_ECOLI P76055 ESCHERICHIA COLI 562 -11534739
7000687513 ydao ydao protein:conserved hypothetical protein b1344 (cl:hypothetical protein hp1182) (db:pir2.dat) C64884 C64884 Escherichia coli 562 -11534739 7500922154 ydao orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 122 of 400 of the completgenome.) (nt:f311; this 311 aa orf is 22 pct identical (13 gaps)) (le:6383) (re:7318) (di:complement) AE000232 AE000232 g1787606 Escherichia coli 562 -11534739 5000692154 (de:(ecoli_1304) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1304 ECOLI_1304 Escherichia coli 562 10123273

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848399	10586	32742	354	117

Description

5000692155 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1345 b1345 Escherichia coli 562 -11534740
7000691247 conserved hypothetical protein b1345 (cl:hypothetical protein b1579) (db:pir2.dat) D64884 D64884 Escherichia coli 562 -11534740
7500959980 b1345 putative transposase (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 122 of 400 of the completgenome.) (nt:f411; this 411 aa orf is 25 pct identical (25 gaps)) (le:7370) (re:8605) (di:complement) AE000232 AE000232 g1787607 Escherichia coli 562 -11534740 6500730882 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1345 b1345 Escherichia coli 562 -11534740

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848400	10587	32743	1017	338

Description

5000692156 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1346 b1346 Escherichia coli 562 -11534741
 7500922156 ydaq (de:hypothetical 9.2 kd protein in intr-lar intergenic region) (db:swissprot) YDAQ_ECOLI P76057 ESCHERICHIA COLI 562 -11534741
 7000691248 ydaq ydaq protein (db:pir2.dat) E64884 E64884 Escherichia coli 562 -11534741 7500922158 ydaq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 122 of 400 of the completegenome.) (nt:f79; this 79 aa orf is 30 pct identical (10 gaps)) (le:8607) (re:8846) (di:complement) AE000232 AE000232 g1787608 Escherichia coli 562 -11534741 6500730883 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1346 b1346 Escherichia coli 562 -11534741

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848411	10588	32744	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848418	10589	32745	759	252

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848419	10590	32746	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848423	10591	32747	699	232

Description

6500730884 ydac:b1347 hypothetical protein in rect 3 region:hypothetical 7.9 kd protein in dbpa-lar intergenic region:orfh (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1347 b1347 Escherichia coli 562 -11534742 111213 ydac (de:hypothetical 7.9 kd protein in intr-lar intergenic region (orfh)) (db:swissprot) YDAC_ECOLI P33230 ESCHERICHIA COLI 562 -11534742 7000687510 ydac ydac protein (db:pir2.dat) F64884 F64884 Escherichia coli 562 -11534742 223620 ydac (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #262(30.3-30.5 min.)) (nt:orf_id:o262#6; similar to (swissprot accession) (le:9330) (re:9539) (di:complement) D90773 D90773 g1742213 Escherichia coli 562 -11534742 300393 ydac orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 122 of 400 of the completegenome.) (nt:f69; 100 pct identical to 62 aa fragment) (le:8901) (re:9110) (di:complement) AE000232 AE000232 g1787609 Escherichia coli 562 -11534742 5000692157 (de:(ecoli_1307) (pn:hypothetical protein in rect:3"region:orfh:fragment) (gn:ydac) (gtcfc:13.7:14.1) (ec:) (ydac_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1307 ECOLI_1307 Escherichia coli 562 10119547

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848424	10592	32748	942	313

Description

6500730885 ydad:b1352 hypothetical protein in sieb-racc intergenic region:hypothetical 8.4 kd protein in sieb-racc intergenic region:orfe (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1352 b1352 Escherichia coli 562 -11534743 7000691841 ydad probable cell division inhibitor ydad (db:pir2.dat) C64885 C64885 Escherichia coli 562 -11534743 327233 ydad orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:f77; 100 pct identical to gb: lamorfef_1) (le:601) (re:834) (di:complement) AE000233 AE000233 g1787615 Escherichia coli 562 -11534743 7500960353 orfe (fn:unknown) (sr:bacteriophage lambda (strain lambda reverse) dna) (db:genpept-phg) (de:lambda reverse orfe protein (orfe) gene, complete cds; orff protein(orff) gene, 5'end.) (nt:putative) (le:369) (re:602) (di:direct) LAMORFEF M96749 g215186 Bacteriophage lambda 10710 -11534743 5000692159 (de:(ecoli_1312) (pn:hypothetical 8) (gn:ydad) (gtcfc:13.7:14.1) (ec:) (ydad_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1312 ECOLI_1312 Escherichia coli 562 10123276

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848428	10593	32749	261	86

Description

5000692161 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1354 b1354 Escherichia coli 562 -11534744
 7000691249 hypothetical protein b1354 (db:pir2.dat) E64885 E64885
 Escherichia coli 562 -11534744 7500959981 b1354 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o58) (le:1761) (re:1937) (di:direct) AE000233 AE000233 g1787617 Escherichia coli 562 -11534744 6500730886 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1354 b1354 Escherichia coli 562 -11534744

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848443	10594	32750	723	240

Description

5000692162 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1355 b1355 Escherichia coli 562 -11534745
 7000691250 hypothetical protein b1355 (db:pir2.dat) F64885 F64885
 Escherichia coli 562 -11534745 7500959982 b1355 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:f59; this 59 aa orf is 34 pct identical (3 gaps)) (le:1915) (re:2094) (di:complement) AE000233 AE000233 g1787618 Escherichia coli 562 -11534745 6500730887 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1355 b1355 Escherichia coli 562 -11534745

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848454	10595	32751	1638	545

Description

5000692163 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1356 b1356 Escherichia coli 562 -11534746
 7500922163 racr (de:rac prophage repressor) (db:swissprot) RACR_ECOLI
 P76062 ESCHERICHIA COLI 562 -11534746 7000691251 ydar ydar protein (db:pir2.dat) G64885 G64885 Escherichia coli 562 -11534746 7500922165 ydar orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:f158; this 158 aa orf is 31 pct identical (17 gaps)) (le:2358) (re:2834) (di:complement) AE000233 AE000233 g1787619 Escherichia coli 562 -11534746 6500730888 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1356 b1356 Escherichia coli 562 -11534746

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848455	10596	32752	390	129

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848473	10597	32753	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848479	10598	32754	411	136

Description

5000692164 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1357 b1357 Escherichia coli 562 -11534747
 7500922166 ydas (de:hypothetical 11.0 kd protein in sieb-trkg intergenic region precursor) (db:swissprot) YDAS_ECOLI P76063 ESCHERICHIA COLI 562 -11534747 7000691252 ydas ydas protein (db:pir2.dat) H64885 H64885 Escherichia coli 562 -11534747 7500922168 ydas orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o98; this 98 aa orf is 39 pct identical (0 gaps)) (le:2958) (re:3254) (di:direct) AE000233 AE000233 g1787620 Escherichia coli 562 -11534747 6500730889 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1357 b1357 Escherichia coli 562 -11534747

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848484	10599	32755	1173	390

Description

5000692165 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1358 b1358 Escherichia coli 562 -11534748
 7500922169 ydat (de:hypothetical 15.7 kd protein in sieb-trkg intergenic region) (db:swissprot) YDAT_ECOLI P76064 ESCHERICHIA COLI 562 -11534748 7000691253 ydat ydat protein (db:pir2.dat) A64886 A64886 Escherichia coli 562 -11534748 7500922171 ydat orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o140) (le:3277) (re:3699) (di:direct) AE000233 AE000233 g1787621 Escherichia coli 562 -11534748 6500730890 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1358 b1358 Escherichia coli 562 -11534748

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848487	10600	32756	1071	356

Description

5000692166 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1359 b1359 Escherichia coli 562 -11534749
7500922172 ydau (de:hypothetical 32.5 kd protein in sieb-trkg intergenic region) (db:swissprot) YDAU_ECOLI P76065 ESCHERICHIA COLI 562 -11534749
7000691254 ydau ydau protein (db:pir2.dat) B64886 B64886 Escherichia coli 562 -11534749 7500922174 ydau orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completengenome.) (nt:o285; this 285 aa orf is 35 pct identical (7 gaps)) (le:3712) (re:4569) (di:direct) AE000233 AE000233 g1787622 Escherichia coli 562 -11534749 6500730891 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1359 b1359 Escherichia coli 562 -11534749

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848491	10601	32757	207	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848496	10602	32758	192	63

Description

5000692167 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1360 b1360 Escherichia coli 562 -11534750
7000691255 dnac protein homolog b1360 (cl:dna replication protein dnac) (db:pir1.dat) C64886 C64886 Escherichia coli 562 -11534750 223631 dna replication protein dnac. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #263(30.5-30.9 min.)) (nt:orf_id:o263#10; similar to (swissprot accession) (le:7895) (re:8641) (di:direct) D90774 D90774 g1742225 Escherichia coli 562 -11534750 300404 b1360 putative dna replication factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completengenome.) (nt:o248; this 248 aa orf is 50 pct identical (3 gaps)) (le:4576) (re:5322) (di:direct) AE000233 AE000233 g1787623 Escherichia coli 562 -11534750 6500730892 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1360 b1360 Escherichia coli 562 -11534750

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848498	10603	32759	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848500	10604	32760	252	83

Description

5000692168 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1361 b1361 Escherichia coli 562 -11534751
 7500922175 ydaw (de:hypothetical 22.1 kd protein in sieb-trkg intergenic region) (db:swissprot) YDAW_ECOLI P76066 ESCHERICHIA COLI 562 -11534751
 7000691256 ydaw membrane protein ydaw (db:pir2.dat) D64886 D64886 Escherichia coli 562 -11534751 7500922177 ydaw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o203; this 203 aa orf is 23 pct identical (3 gaps)) (le:5294) (re:5905) (di:direct) AE000233 AE000233 g1787624 Escherichia coli 562 -11534751 6500730893 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1361 b1361 Escherichia coli 562 -11534751

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848502	10605	32761	873	290

Description

5000692169 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1362 b1362 Escherichia coli 562 -11534752
 7000691257 endopeptidase b1362 (cl:phage pa2 endopeptidase) (ec:3.4.-.-) (db:pir2.dat) E64886 E64886 Escherichia coli 562 -11534752 223632 endopeptidase ec 3.4.-.-. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #263(30.5-30.9 min.)) (nt:orf_id:o263#13; similar to (swissprot accession) (le:9251) (re:9556) (di:direct) D90774 D90774 g1742226 Escherichia coli 562 -11534752 300405 b1362 putative rac prophage endopeptidase (fn:is, phage, tn; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o101; this 101 aa orf is 93 pct identical (0 gaps)) (le:5932) (re:6237) (di:direct) AE000233 AE000233 g1787625 Escherichia coli 562 -11534752 6500730894 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1362 b1362 Escherichia coli 562 -11534752

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848531	10606	32762	2259	752

Description

5000692170 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1364 b1364 Escherichia coli 562 -11534753
 7000691258 probable membrane protein b1364 (db:pir2.dat) G64886 G64886 Escherichia coli 562 -11534753 7500959983 b1364 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o93; 30 pct identical (6 gaps) to 75 residues) (le:7771) (re:8052) (di:direct) AE000233 AE000233 g1787627 Escherichia coli 562 -11534753 6500730895 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1364 b1364 Escherichia coli 562 -11534753

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848538	10607	32763	372	123

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848539	10608	32764	963	320

Description

5000692171 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1365 b1365 Escherichia coli 562 -11534754
 7500951714 ynak (de:hypothetical 9.8 kd protein in trkg-lomr intergenic region) (db:swissprot) YNAK_ECOLI P76068 ESCHERICHIA COLI 562 -11534754
 7000691259 hypothetical protein b1365 (db:pir2.dat) H64886 H64886 Escherichia coli 562 -11534754 7500951716 b1365 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o87; 38 pct identical (4 gaps) to 65 residues) (le:7970) (re:8233) (di:direct) AE000233 AE000233 g1787628 Escherichia coli 562 -11534754 6500730896 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1365 b1365 Escherichia coli 562 -11534754

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848557	10609	32765	222	73

Description

5000692172 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1366 b1366 Escherichia coli 562 -11534755
 7500922178 yday (de:hypothetical 13.5 kd protein in trkg-lomr intergenic region) (db:swissprot) YDAY_ECOLI P76069 ESCHERICHIA COLI 562 -11534755
 7000691260 yday yday protein (db:pir2.dat) A64887 A64887 Escherichia coli 562 -11534755 7500922180 yday orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o119; this 119 aa orf is 23 pct identical (2 gaps)) (le:8214) (re:8573) (di:direct) AE000233 AE000233 g1787629 Escherichia coli 562 -11534755 6500730897 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1366 b1366 Escherichia coli 562 -11534755

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848563	10610	32766	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848564	10611	32767	1167	388

Description

5000692173 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1367 b1367 Escherichia coli 562 -11534756
 7000691261 hypothetical protein b1367 (db:pir2.dat) B64887 B64887 Escherichia coli 562 -11534756 7500959984 b1367 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o77; this 77 aa orf is 31 pct identical (4 gaps)) (le:8648) (re:8881) (di:direct) AE000233 AE000233 g1787630 Escherichia coli 562 -11534756 6500730898 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1367 b1367 Escherichia coli 562 -11534756

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848569	10612	32768	366	121

Description

5000692174 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1368 b1368 Escherichia coli 562 -11534757
7000691262 hypothetical protein b1368 (db:pir2.dat) C64887 C64887
Escherichia coli 562 -11534757 223634 minor tail protein precursor h. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #263(30.5-30.9 min.)) (nt:orf_id:o263#17; similar to (swissprot accession) (le:12366) (re:13394) (di:direct) D90774 D90774 g1742228 Escherichia coli 562 -11534757 300416 minor tail protein precursor h. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1 min.)) (nt:orf_id:o263#17; similar to (swissprot accession) (le:813) (re:1841) (di:direct) D90775 D90775 g1742238 Escherichia coli 562 -11534757 300407 b1368 putative alpha helix protein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o342; this 342 aa orf is 33 pct identical (6 gaps)) (le:9047) (re:10075) (di:direct) AE000233 AE000233 g1787631 Escherichia coli 562 -11534757 223643 minor tail protein precursor h. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1 min.)) (nt:orf_id:o263#17; similar to (swissprot accession) (le:813) (re:1841) (di:direct) D90775 D90775 g1742238 Escherichia coli 562 -11534757 6500730899 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1368 b1368 Escherichia coli 562 -11534757

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848588	10613	32769	471	156

Description

GTC ORF with score 461 to: (sr:baker's yeast) (db:genpept-pln2) (de:saccharomyces cerevisiae putative transmembrane protein humlp(hum1) gene, complete cds.) (nt:novel protein; putative transmembrane protein;) (le:1) (re:1236) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848598	10614	32770	417	138

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848632	10615	32771	273	90

Description

5000692175 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1369 b1369 Escherichia coli 562 -11534758
7000691263 hypothetical protein b1369 (db:pir2.dat) D64887 D64887
Escherichia coli 562 -11534758 223635 outer membrane protein lom precursor orf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #263(30.5-30.9 min.)) (nt:orf_id:o263#18; similar to (swissprot accession) (le:13370) (re:13525) (di:direct) D90774 D90774 g1742229 Escherichia coli 562 -11534758 300417 outer membrane protein lom precursor orf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1 min.)) (nt:orf_id:o263#18; similar to (swissprot accession) (le:1817) (re:1972) (di:direct) D90775 D90775 g1742239 Escherichia coli 562 -11534758 300408 b1369 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o51; this 51 aa orf is 43 pct identical (0 gaps)) (le:10051) (re:10206) (di:direct) AE000233 AE000233 g1787632 Escherichia coli 562 -11534758 223644 outer membrane protein lom precursor orf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1 min.)) (nt:orf_id:o263#18; similar to (swissprot accession) (le:1817) (re:1972) (di:direct) D90775 D90775 g1742239 Escherichia coli 562 -11534758 6500730900 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1369 b1369 Escherichia coli 562 -11534758

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848640	10616	32772	285	94

Description

6500730901 yi52_5:b1370 insertion element is5 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1370 b1370 Escherichia coli 562 -11534759 7000689459 yi52_5 probable transposase:38k (db:pir2.dat) E64887 E64887 Escherichia coli 562 -11534759 7500955734 trs5_5 is5 transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 124 of 400 of the completegenome.) (nt:f326; 97 pct identical to yi52_ecoli sw: p03837 but) (le:97) (re:1077) (di:complement) AE000234 AE000234 g1787634 Escherichia coli 562 -11534759 5000692176 (de:(ecoli_1330) (pn:insertion element is5 hypothetical protein) (gn:yi52_5) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1330 ECOLI_1330 Escherichia coli 562 10123289

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848642	10617	32773	639	212

Description

5000692177 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1371 b1371 Escherichia coli 562 -11534760
7000691264 probable outer membrane protein b1371 (db:pir2.dat) F64887
F64887 Escherichia coli 562 -11534760 223638 outer membrane protein lom precursor orf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #263(30.5-30.9 min.)) (nt:orf_id:o263#21; similar to (swissprot accession) (le:14435) (re:14896) (di:direct) D90774 D90774 g1742232 Escherichia coli 562 -11534760 300420 outer membrane protein lom precursor orf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1 min.)) (nt:orf_id:o263#21; similar to (swissprot accession) (le:2882) (re:3343) (di:direct) D90775 D90775 g1742242 Escherichia coli 562 -11534760 300411 b1371 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 124 of 400 of the completegenome.) (nt:o153; this 153 aa orf is 57 pct identical (0 gaps)) (le:874) (re:1335) (di:direct) AE000234 AE000234 g1787635 Escherichia coli 562 -11534760 223647 outer membrane protein lom precursor orf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1 min.)) (nt:orf_id:o263#21; similar to (swissprot accession) (le:2882) (re:3343) (di:direct) D90775 D90775 g1742242 Escherichia coli 562 -11534760
6500730902 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1371 b1371 Escherichia coli 562 -11534760

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848646	10618	32774	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848659	10619	32775	1203	401

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848664	10620	32776	1035	344
<u>Description</u>				
5000692178 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1372 b1372 Escherichia coli 562 -11534761				
7000691265 conserved hypothetical protein b1372 (db:pir2.dat) G64887 G64887 Escherichia coli 562 -11534761 7500959985 b1372 putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 124 of 400 of the completegenome.) (nt:o1122; this 1122 aa orf is 76 pct identical (1) (le:1394) (re:4762) (di:direct) AE000234 AE000234 g1787636 Escherichia coli 562 -11534761 6500730903 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1372 b1372 Escherichia coli 562 -11534761				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848667	10621	32777	207	68
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848672	10622	32778	630	209
<u>Description</u>				
6500730904 ynac:b1373 hypothetical protein:hypothetical 21.3 kd protein in trkg-hslj intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1373 b1373 Escherichia coli 562 -11534762				
4000708195 ynac (de:hypothetical 21.3 kd protein in trkg-hslj intergenic region) (db:swissprot) YNAC_ECOLI P77163 ESCHERICHIA COLI 562 -11534762				
300424 tail fiber assembly protein g (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1 min.)) (nt:orf_id:o264#1; similar to (pir accession number) (le:6770) (re:7345) (di:direct) D90775 D90775 g1742246 Escherichia coli 562 -11534762 223651 ynac orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 124 of 400 of the completegenome.) (nt:o191; this 191 aa orf is 94 pct identical (0 gaps)) (le:4762) (re:5337) (di:direct) AE000234 AE000234 g1787637 Escherichia coli 562 -11534762 5000692179 (de:(ecoli_1333) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1333 ECOLI_1333 Escherichia coli 562 -11534762 7000688158 h64887 (de:(pn:hypothetical protein b1373) (cl:phage t4 tail fiber assembly protein gp38) (db:pir)) H64887 H64887 Escherichia coli 562 10119564				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848674	10623	32779	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848676	10624	32780	387	129

Description

5000692180 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1374 b1374 Escherichia coli 562 -11534763
7000689430 probable resolvase b1374 (cl:transposase repressor) (db:pir2.dat) A64888 A64888 Escherichia coli 562 -11534763 223652
transposon tn2501 resolvase. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1 min.)) (nt:orf_id:o264#2; similar to (swissprot accession) (le:7443) (re:8033) (di:complement) D90775 D90775 g1742247 Escherichia coli 562 -11534763 300425 b1374 putative transposon resolvase (fn:is, phage, tn; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 124 of 400 of the completegenome.) (nt:f196; this 196 aa orf is 76 pct identical (0 gaps)) (le:5435) (re:6025) (di:complement) AE000234 AE000234 g1787638 Escherichia coli 562 -11534763 6500730905
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1374 b1374 Escherichia coli 562 -11534763

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848678	10625	32781	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848684	10626	32782	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848686	10627	32783	513	170

Description

5000692181 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1375 b1375 Escherichia coli 562 -11534764
 7500951708 ynae (de:hypothetical 10.1 kd protein in lomr-hslj intergenic region) (db:swissprot) YNAE_ECOLI P76073 ESCHERICHIA COLI 562 -11534764
 7000691266 ynae ynae protein (db:pir2.dat) B64888 B64888 Escherichia coli 562 -11534764 7500951710 ynae orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 124 of 400 of the completegenome.) (nt:f88; this 88 aa orf is 32 pct identical (4 gaps)) (le:6342) (re:6608) (di:complement) AE000234 AE000234 g1787639 Escherichia coli 562 -11534764 6500730906 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1375 b1375 Escherichia coli 562 -11534764

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848687	10628	32784	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848698	10629	32785	447	148

Description

5000692182 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1376 b1376 Escherichia coli 562 -11534765
 7000689500 conserved hypothetical protein b1376 (cl:escherichia coli ybdq protein) (db:pir2.dat) C64888 C64888 Escherichia coli 562 -11534765
 7500955801 ynaf putative filament protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 124 of 400 of the completegenome.) (nt:f168; this 168 aa orf is 31 pct identical (6 gaps)) (le:7536) (re:8042) (di:complement) AE000234 AE000234 g1787640 Escherichia coli 562 -11534765 6500730907 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1376 b1376 Escherichia coli 562 -11534765

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848708	10630	32786	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848715	10631	32787	411	136

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848720	10632	32788	630	209

Description

5000692183 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1377 b1377 Escherichia coli 562 -11534766
7502852244 ompn (de:outer membrane protein n precursor (porin ompn)) (db:swissprot) OMPN_ECOLI P77747 ESCHERICHIA COLI 562 -11534766 7000691267 outer membrane porin b1377 precursor (cl:outer membrane protein phoe) (db:pir2.dat) D64888 D64888 Escherichia coli 562 -11534766 223654 outer membrane protein f precursor outer (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1 min.)) (nt:orf_id:o264#4; similar to (swissprot accession) (le:10119) (re:11252) (di:complement) D90775 D90775 g1742249 Escherichia coli 562 -11534766 300427 b1377 putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 124 of 400 of the completegenome.) (nt:f377; this 377 aa orf is 69 pct identical (21 gaps)) (le:8111) (re:9244) (di:complement) AE000234 AE000234 g1787641 Escherichia coli 562 -11534766
6500730908 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1377 b1377 Escherichia coli 562 -11534766

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848726	10633	32789	531	176

Description

6500730909 ydbk:b1378 hypothetical protein:probable pyruvate-flavodoxin oxidoreductase (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1378 b1378 Escherichia coli 562 -11534767 111243 ydbk (ec:1.-.-.-) (de:probable pyruvate-flavodoxin oxidoreductase,) (db:swissprot) NIFJ_ECOLI P52647 ESCHERICHIA COLI 562 -11534767 7000685965 ydbk probable pyruvate flavodoxin dehydrogenase:ydbk (cl:pyruvate (flavodoxin) dehydrogenase:ferredoxin 2(4fe-4s) homology) (ec:1.2.99.-) (db:pir2.dat) E64888 E64888 Escherichia coli 562 -11534767 223655 pyruvate-flavodoxin oxidoreductase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1 min.)) (nt:orf_id:o264#5; similar to (swissprot accession) (le:11619) (re:15143) (di:complement) D90775 D90775 g1742250 Escherichia coli 562 -11534767 300433 pyruvate-flavodoxin oxidoreductase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #265(30.9-31.2 min.)) (nt:orf_id:o264#5; similar to (swissprot accession) (le:1337) (re:4861) (di:complement) D90776 D90776 g1742256 Escherichia coli 562 -11534767 300428 ydbk putative oxidoreductase:fe-s subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 124 of 400 of the completegenome.) (nt:f1174; this 1174 aa orf is 55 pct identical) (le:9611) (re:13135) (di:complement) AE000234 AE000234 g1787642 Escherichia coli 562 -11534767 223660 pyruvate-flavodoxin oxidoreductase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #265(30.9-31.2 min.)) (nt:orf_id:o264#5; similar to (swissprot accession) (le:1337) (re:4861) (di:complement) D90776 D90776 g1742256 Escherichia coli 562 -11534767 5000692184 (de:(ecoli_1338) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1338 ECOLI_1338 Escherichia coli 562 10119568

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848727	10634	32790	570	189

Description

6500730910 ydbh:b1381 hypothetical protein:hypothetical 96.8 kd protein in ldha-tyna intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1381 b1381 Escherichia coli 562 -11534768 111238 ydbh (de:hypothetical 96.8 kd protein in ldha-tyna intergenic region) (db:swissprot) YDBH_ECOLI P52645 ESCHERICHIA COLI 562 -11534768 7000687514 ydbh membrane protein ydbh (db:pir2.dat) H64888 H64888 Escherichia coli 562 -11534768 223664 ydbh (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #265(30.9-31.2 min.)) (nt:orf_id:o265#2; similar to (swissprot accession) (le:7128) (re:9767) (di:direct) D90776 D90776 g1742260 Escherichia coli 562 -11534768 300437 ydbh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 125 of 400 of the completegenome.) (nt:o879; this 879 aa orf is 23 pct identical (22 gaps)) (le:2029) (re:4668) (di:direct) AE000235 AE000235 g1787646 Escherichia coli 562 -11534768 5000692186 (de:(ecoli_1341) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1341 ECOLI_1341 Escherichia coli 562 10119571

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848728	10635	32791	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848729	10636	32792	432	143

Description

5000692187 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1382 b1382 Escherichia coli 562 -11534769 7500951733 ynbe (de:hypothetical 6.8 kd protein in ldha-fear intergenic region) (db:swissprot) YNBE_ECOLI P76075 ESCHERICHIA COLI 562 -11534769 7000691268 ynbe ynbe protein precursor (db:pir2.dat) A64889 A64889 Escherichia coli 562 -11534769 7500951735 ynbe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 125 of 400 of the completegenome.) (nt:o61; residues 8-41 are 35 pct identical to aa) (le:4665) (re:4850) (di:direct) AE000235 AE000235 g1787647 Escherichia coli 562 -11534769 6500730911 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1382 b1382 Escherichia coli 562 -11534769

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848730	10637	32793	438	145

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848734	10638	32794	639	212

Description

5000692188 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1383 b1383 Escherichia coli 562 -11534770
7000691269 ydb1 ydb1 protein precursor (db:pir2.dat) B64889 B64889 Escherichia coli 562 -11534770 7500922188 ydb1 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 125 of 400 of the completegenome.) (nt:ol10) (le:4852) (re:5184) (di:direct) AE000235 AE000235 g1787648 Escherichia coli 562 -11534770 7500922186 ydb1 (de:hypothetical 12.1 kd protein in ldha-fear intergenic region precursor) (db:swissprot) YDBL_ECOLI P76076 ESCHERICHIA COLI 562 -11534770 6500730912 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1383 b1383 Escherichia coli 562 -11534770

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848759	10639	32795	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848778	10640	32796	417	138

Description

6500730913 fear:maor:maob:b1384 hypothetical protein:transcriptional activator fear (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1384 b1384 Escherichia coli 562 -11534771 306939 fear:maor:maob (de:transcriptional activator fear) (db:swissprot) FEAR_ECOLI Q47129 ESCHERICHIA COLI 562 -11534771 7000685223 fear probable transcription activator fear (db:pir2.dat) C64889 C64889 Escherichia coli 562 -11534771 222768 maob maob (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli maob gene for maob, complete cds.) (le:150) (re:1055) (di:direct) D67041 D67041 g1480003 Escherichia coli 562 -11534771 5000692189 fear positive acting regulator protein (db:genpept-bct1) (de:e.coli fear & feab genes.) (le:267) (re:1172) (di:complement) ECFEA X99402 g1531767 Escherichia coli 562 -11534771 232843 fear regulatory protein for 2-phenylethylamine (fn:regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 125 of 400 of the completegenome.) (nt:f301; this 301 aa orf is 25 pct identical (9 gaps)) (le:5356) (re:6261) (di:complement) AE000235 AE000235 g1787649 Escherichia coli 562 -11534771 118635 fear:maor:maob (de:transcriptional activator fear) (db:swissprot) FEAR_ECOLI Q47129 ESCHERICHIA COLI 562 -11534771

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848784	10641	32797	414	137

Description

6500730914 maoc:b1387 hypothetical protein:maoc protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1387 b1387 Escherichia coli 562 -11534772 1500685996 maoc:paaz (de:maoc protein (phenylacetic acid degradation protein paaz)) (db:swissprot) MAOC_ECOLI P77455 ESCHERICHIA COLI 562 -11534772 7000685789 membrane protein maoc (db:pir2.dat) F64889 F64889 Escherichia coli 562 -11534772 223670 maoc protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #266(31.1-31.5 min.)) (nt:orf_id:o266#2; similar to (swissprot accession) (le:7815) (re:9860) (di:complement) D90777 D90777 g1742267 Escherichia coli 562 -11534772 300443 maoc putative aldehyde dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the completegenome.) (nt:f681; residues 334-644 are 84 pct identical to) (le:154) (re:2199) (di:complement) AE000236 AE000236 g1787653 Escherichia coli 562 -11534772 5000692191 (de:(ecoli_1347) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1347 ECOLI_1347 Escherichia coli 562 10060014

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848792	10642	32798	1047	348

Description

5000692192 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1388 b1388 Escherichia coli 562 -11534773
 7500887562 paaa (de:phenylacetic acid degradation protein paaa) (db:swissprot) PAAA_ECOLI P76077 ESCHERICHIA COLI 562 -11534773 7000691271 ydbo ydbo protein (db:pir2.dat) G64889 G64889 Escherichia coli 562 -11534773
 7500887564 ydbo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the completegenome.) (nt:o309; this 309 aa orf is 26 pct identical (16 gaps)) (le:2484) (re:3413) (di:direct) AE000236 AE000236 gl787654 Escherichia coli 562 -11534773 6500730915 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1388 b1388 Escherichia coli 562 -11534773

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848803	10643	32799	555	184

Description

5000692193 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1389 b1389 Escherichia coli 562 -11534774
 7500887565 paab (de:phenylacetic acid degradation protein paab) (db:swissprot) PAAB_ECOLI P76078 ESCHERICHIA COLI 562 -11534774 7000691272 ynbf ynbf protein (db:pir2.dat) H64889 H64889 Escherichia coli 562 -11534774
 7000691273 paab (db:genpept-bct1) (de:e.coli paa cluster for phenylacetic acid degradation.) (le:3697) (re:3984) (di:direct) ECPAA X97452 g2764824 Escherichia coli 562 -11534774 7500887567 ynbf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the completegenome.) (nt:o95; this 95 aa orf is 35 pct identical (7 gaps)) (le:3425) (re:3712) (di:direct) AE000236 AE000236 gl787655 Escherichia coli 562 -11534774 6500730916 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1389 b1389 Escherichia coli 562 -11534774

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848804	10644	32800	441	146

Description

GTC ORF with score 252 to: (sr:fruit fly) (db:genpept-inv) (de:drosophila melanogaster cosmid 62d9, complete sequence.) (nt:predicted using genefinder; preliminary prediction) (le:35237:35475:35738:37377) (re:35340:35575:36510:37441) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848805	10645	32801	1611	536

Description

5000692194 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1390 b1390 Escherichia coli 562 -11534775
7500887569 paac (de:phenylacetic acid degradation protein paac) (db:swissprot) PAAC_ECOLI P76079 ESCHERICHIA COLI 562 -11534775 7000691274 ydbp ydbp protein (db:pir2.dat) A64890 A64890 Escherichia coli 562 -11534775
7500887571 ydbp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the completegenome.) (nt:o248; 34 pct identical (13 gaps) to 111 residues) (le:3721) (re:4467) (di:direct) AE000236 AE000236 g1787656 Escherichia coli 562 -11534775 6500730917 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1390 b1390 Escherichia coli 562 -11534775

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848814	10646	32802	300	99

Description

5000692195 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1391 b1391 Escherichia coli 562 -11534776
7500887572 paad (de:phenylacetic acid degradation protein paad) (db:swissprot) PAAD_ECOLI P76080 ESCHERICHIA COLI 562 -11534776 7000691275 hypothetical protein b1391 (db:pir2.dat) B64890 B64890 Escherichia coli 562 -11534776 7500887574 b1391 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the completegenome.) (nt:o167; 25 pct identical (13 gaps) to 114 residues of) (le:4476) (re:4979) (di:direct) AE000236 AE000236 g1787657 Escherichia coli 562 -11534776 6500730918 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1391 b1391 Escherichia coli 562 -11534776

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848822	10647	32803	1095	364

Description

5000692196 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1392 b1392 Escherichia coli 562 -11534777
7000691276 probable electron transfer protein (db:pir2.dat) C64890 C64890 Escherichia coli 562 -11534777 7500959986 b1392 putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the completegenome.) (nt:o356; 26 pct identical (20 gaps) to 295 residues) (le:4987) (re:6057) (di:direct) AE000236 AE000236 g1787658 Escherichia coli 562 -11534777 6500730919 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1392 b1392 Escherichia coli 562 -11534777

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848826	10648	32804	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848831	10649	32805	492	163

Description

5000692198 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1394 b1394 Escherichia coli 562 -11534778
7500887576 paag (ec:4.2.1.17) (de:probable enoyl-coa hydratase paag,) (db:swissprot) PAAG_ECOLI P77467 ESCHERICHIA COLI 562 -11534778 7000691277 probable membrane protein b1394 (cl:naphthoate synthase:enoyl-coa hydratase homology) (db:pir2.dat) E64890 E64890 Escherichia coli 562 -11534778 223673 enoyl-coa hydratase homolog orf257 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #266(31.1-31.5 min.).) (nt:orf_id:o266#9; similar to (swissprot accession) (le:14483) (re:15271) (di:direct) D90777 D90777 g1742270 Escherichia coli 562 -11534778 300446 enoyl-coa hydratase homolog orf257 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #267(31.4-31.7 min.).) (nt:orf_id:o266#9; similar to (swissprot accession) (le:2264) (re:3052) (di:direct) D90778 D90778 g1742276 Escherichia coli 562 -11534778 300451 b1394 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the completegenome.) (nt:o262; 44 pct identical (6 gaps) to 254 residues) (le:6821) (re:7609) (di:direct) AE000236 AE000236 g1787660 Escherichia coli 562 -11534778 223678 enoyl-coa hydratase homolog orf257 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #266(31.1-31.5 min.).) (nt:orf_id:o266#9; similar to (swissprot accession) (le:14483) (re:15271) (di:direct) D90777 D90777 g1742270 Escherichia coli 562 -11534778 6500730920 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1394 b1394 Escherichia coli 562 -11534778

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848833	10650	32806	621	206

Description

GTC ORF with score 285 to: (fn:pentose phosphate pathway protein) (sr:mus musculus (strain balb/c, sub_species domesticus) cdna to mrna) (db:genpept-rod) (de:mus musculus ribose 5-phosphate isomerase (rpi) mrna exons 1-6,complete cds.) (le:208) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848834	10651	32807	390	130

Description

5000692200 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1396 b1396 Escherichia coli 562 -11534779
7500887578 paai (de:phenylacetic acid degradation protein paai)
(db:swissprot) PAAI_ECOLI P76084 ESCHERICHIA COLI 562 -11534779 7000691278
conserved hypothetical protein b1396 (cl:hypothetical protein b139)
(db:pir2.dat) G64890 G64890 Escherichia coli 562 -11534779 7000691279 paai
(db:genpept-bct1) (de:e.coli paa cluster for phenylacetic acid degradation.)
(le:9300) (re:9722) (di:direct) ECPAA X97452 g2764831 Escherichia coli 562
-11534779 7500887580 b1396 orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the
completegenome.) (nt:o140; 28 pct identical (5 gaps) to 120 residues)
(le:9028) (re:9450) (di:direct) AE000236 AE000236 g1787662 Escherichia coli
562 -11534779 6500730921 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b1396 b1396 Escherichia coli 562
-11534779

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848852	10652	32808	330	109

Description

5000692201 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1397 b1397 Escherichia coli 562 -11534780
7000691280 probable acetyl-coa c-acyltransferase (cl:acetyl-coa acetyltransferase) (ec:2.3.1.16) (db:pir2.dat) H64890 H64890 Escherichia coli 562 -11534780 223675 3-ketoacyl-coa thiolase ec 2.3.1.16 fatty (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #266(31.1-31.5 min.)) (nt:orf_id:o266#12; similar to (swissprot accession) (le:17112) (re:18317) (di:direct) D90777 D90777 g1742272 Escherichia coli 562 -11534780 300453 3-ketoacyl-coa thiolase ec 2.3.1.16 fatty (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #267(31.4-31.7 min.)) (nt:orf_id:o266#12; similar to (swissprot accession) (le:4893) (re:6098) (di:direct) D90778 D90778 g1742278 Escherichia coli 562 -11534780 300448 b1397 putative acyltransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 126 of 400 of the completegenome.) (nt:o401; this 401 aa orf is 45 pct identical (9 gaps)) (le:9450) (re:10655) (di:direct) AE000236 AE000236 g1787663 Escherichia coli 562 -11534780 223680 3-ketoacyl-coa thiolase ec 2.3.1.16 fatty (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #267(31.4-31.7 min.)) (nt:orf_id:o266#12; similar to (swissprot accession) (le:4893) (re:6098) (di:direct) D90778 D90778 g1742278 Escherichia coli 562 -11534780 6500730922 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1397 b1397 Escherichia coli 562 -11534780

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848853	10653	32809	345	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848857	10654	32810	447	148

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848878	10655	32811	330	109

Description

5000692202 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1398 b1398 Escherichia coli 562 -11534781
7000691281 coenzyme f390 synthetase homolog (cl:coenzyme f390 synthetase ii) (db:pir2.dat) A64891 A64891 Escherichia coli 562 -11534781 7500959987 b1398 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 126 of 400 of the completegenome.) (nt:o437; 22 pct identical (2 gaps) to 106 residues) (le:10682) (re:11995) (di:direct) AE000236 AE000236 g1787664 Escherichia coli 562 -11534781
6500730923 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1398 b1398 Escherichia coli 562 -11534781

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848882	10656	32812	441	146

Description

5000692203 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1399 b1399 Escherichia coli 562 -11534782
7500887582 paax (de:phenylacetic acid degradation protein paax) (db:swissprot) PAAX_ECOLI P76086 ESCHERICHIA COLI 562 -11534782 7000691282 hypothetical protein b1399 (db:pir2.dat) B64891 B64891 Escherichia coli 562 -11534782 7500887584 b1399 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 127 of 400 of the completegenome.) (nt:o316; this 316 aa orf is 24 pct identical (8 gaps)) (le:81) (re:1031) (di:direct) AE000237 AE000237 g1787666 Escherichia coli 562 -11534782 6500730924 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1399 b1399 Escherichia coli 562 -11534782

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848884	10657	32813	618	205

Description

5000692204 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1400 b1400 Escherichia coli 562 -11534783
7000691283 ferripyochelin-binding protein homolog b1400 (cl:ferripyochelin binding protein) (db:pir2.dat) C64891 C64891 Escherichia coli 562 -11534783
223681 carnitine operon protein caie. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #267(31.4-31.7 min.)) (nt:orf_id:o267#3; similar to (swissprot accession) (le:8470) (re:9060) (di:direct) D90778 D90778 g1742279 Escherichia coli 562 -11534783 300454 b1400 putative transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 127 of 400 of the completegenome.) (nt:o196; this 196 aa orf is 59 pct identical (0 gaps)) (le:1013) (re:1603) (di:direct) AE000237 AE000237 g1787667 Escherichia coli 562 -11534783 6500730925 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1400 b1400 Escherichia coli 562 -11534783

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848885	10658	32814	732	244

Description

6500730926 ydba_1:b1401 hypothetical protein near replication terminus (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1401 b1401 Escherichia coli 562 -11534784 7500960355 ydba_1 split orf (fn:orf; unknown function) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 127 of 400 of the completegenome.) (nt:o852; 99 pct identical to 376 aa of) (le:1934) (re:4492) (di:direct) AE000237 AE000237 g1787668 Escherichia coli 562 -11534784 7000691845 ydba_1 hypothetical protein near replication terminus interrupted (db:pir) D64891 D64891 Escherichia coli 562 -11534784
5000692205 (de:(ecoli_1361) (pn:hypothetical protein near replication terminus) (gn:ydba_1) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1361 ECOLI_1361 Escherichia coli 562 10123305

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848892	10659	32815	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848893	10660	32816	588	196

Description

6500730927 ydbc:b1406 hypothetical 30.7 kd protein near the replication terminus:hypothetical oxidoreductase in maoc-acpd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1406 b1406 Escherichia coli 562 -11534785 300469 ydbc (de:hypothetical oxidoreductase in maoc-acpd intergenic region) (db:swissprot) YDBC_ECOLI P25906 ESCHERICHIA COLI 562 -11534785 162618 ydbc probable oxidoreductase:ydbc (ec:1.-.-.-) (db:pir2.dat) A48399 A48399 Escherichia coli 562 -11534785 223696 ydbc in2-2 protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #268(31.6-32.0 min..)) (nt:orf_id:o268#2; similar to (swissprot accession) (le:6931) (re:7791) (di:direct) D90779 D90779 g1742295 Escherichia coli 562 -11534785 5000692208 (db:genpept-bct1) (de:e.coli insertion sequences is2 and is30.) (nt:orf) (le:7443) (re:8303) (di:direct) ECIS2IS30 X62680 g41830 Escherichia coli 562 -11534785 233247 ydbc putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 128 of 400 of the completegenome.) (nt:o286; 100 pct identical to ydbc_ecoli sw:) (le:134) (re:994) (di:direct) AE000238 AE000238 g1787674 Escherichia coli 562 -11534785 111232 ydbc (de:hypothetical oxidoreductase in maoc-acpd intergenic region) (db:swissprot) YDBC_ECOLI P25906 ESCHERICHIA COLI 562 -11534785

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848895	10661	32817	1011	336

Description

6500730928 ydbd:b1407 hypothetical protein near replication terminus:hypothetical 86.7 kd protein in maoc-acpd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1407 b1407 Escherichia coli 562 -11534786 7000691846 ydbd ydbd protein (db:pir2.dat) B64892 B64892 Escherichia coli 562 -11534786 7500960356 ydbd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 128 of 400 of the completegenome.) (nt:o770; 100 pct identical to fragment ydbd_ecoli) (le:1051) (re:3363) (di:direct) AE000238 AE000238 g1787675 Escherichia coli 562 -11534786 5000692209 (de:(ecoli_1367) (pn:hypothetical protein near the replication terminus:fragment) (gn:ydbd) (gtcfc:13.7:14.1) (ec:) (ydbd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1367 ECOLI_1367 Escherichia coli 562 10123307

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848901	10662	32818	387	128
<u>Description</u>				
5000692210 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1408 b1408 Escherichia coli 562 -11534787				
7000691284 probable membrane protein b1408 (db:pir2.dat) C64892 C64892 Escherichia coli 562 -11534787 7500959988 b1408 probable enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 128 of 400 of the completegenome.) (nt:o203; this 203 aa orf is 26 pct identical (6 gaps)) (le:3528) (re:4139) (di:direct) AE000238 AE000238 g1787676 Escherichia coli 562 -11534787 6500730929 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1408 b1408 Escherichia coli 562 -11534787				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848904	10663	32819	384	127
<u>Description</u>				
5000692211 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1409 b1409 Escherichia coli 562 -11534788				
7500951729 ynbb (de:hypothetical 33.1 kd protein in maoc-acpd intergenic region) (db:swissprot) YNBB_ECOLI P76091 ESCHERICHIA COLI 562 -11534788				
7000691285 phosphatidate cytidylyltransferase homolog (db:pir2.dat) D64892 D64892 Escherichia coli 562 -11534788 7500951731 b1409 putative phosphatidate cytidiltransferase (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 128 of 400 of the completegenome.) (nt:o298; this 298 aa orf is 33 pct identical (24 gaps)) (le:4139) (re:5035) (di:direct) AE000238 AE000238 g1787677 Escherichia coli 562 -11534788 6500730930 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1409 b1409 Escherichia coli 562 -11534788				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848906	10664	32820	1704	567

Description

5000692212 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1410 b1410 Escherichia coli 562 -11534789
7000691286 probable membrane protein b1410 (db:pir2.dat) E64892 E64892 Escherichia coli 562 -11534789 7000691287 (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:escherichia coli gene, replication terminus region, partial andcomplete cds.) (nt:unnamed protein product) (le:3469) (re:5226) (di:direct) D85081 D85081 g3041757 Escherichia coli 562 -11534789 7500959989 b1410 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 128 of 400 of the completegenome.) (nt:o585; 22 pct identical (19 gaps) to 263 residues) (le:5051) (re:6808) (di:direct) AE000238 AE000238 g1787678 Escherichia coli 562 -11534789 6500730931 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1410 b1410 Escherichia coli 562 -11534789

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848911	10665	32821	1836	611

Description

6500730932 ynbd:b1411 hypothetical protein:hypothetical 49.6 kd protein in maoc-acpd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1411 b1411 Escherichia coli 562 -11534790
4000708196 ynbd (de:hypothetical 49.6 kd protein in maoc-acpd intergenic region) (db:swissprot) YNBD_ECOLI P76093 ESCHERICHIA COLI 562 -11534790
7000688159 ynbd probable membrane protein b1411 (db:pir2.dat) F64892 F64892 Escherichia coli 562 -11534790 7500951732 ynbd putative enzymes (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 128 of 400 of the completegenome.) (nt:o430; 31 pct identical (2 gaps) to 73 residues) (le:6822) (re:8114) (di:direct) AE000238 AE000238 g1787679 Escherichia coli 562 -11534790 5000692213 (de:(ecoli_1371) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1371 ECOLI_1371 Escherichia coli 562 10123311

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848912	10666	32822	186	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848917	10667	32823	585	194

Description

6500730933 ydcf:b1414 hypothetical protein in alda 5 region:hypothetical
29.7 kd protein in hrpa-alda intergenic region (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b1414 b1414 Escherichia coli 562
-11534791 111253 ydcf (de:hypothetical 29.7 kd protein in hrpa-alda
intergenic region) (db:swissprot) YDCF_ECOLI P34209 ESCHERICHIA COLI 562
-11534791 7000687518 ydcf ydcf protein (db:pir2.dat) A64893 A64893
Escherichia coli 562 -11534791 223705 ydcf (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #269(31.8-32.1 min..))
(nt:orf_id:o270#1; similar to (swissprot accession) (le:10087) (re:10887)
(di:direct) D90780 D90780 g1742305 Escherichia coli 562 -11534791 223710
ydcf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #270(32.0-32.3
min..)) (nt:orf_id:o270#1; similar to (swissprot accession) (le:2903)
(re:3703) (di:direct) D90781 D90781 g1742311 Escherichia coli 562 -11534791
300475 ydcf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.)
(nt:o266; 99 pct identical to 193 aa of ydcf_ecoli) (le:166) (re:966)
(di:direct) AE000239 AE000239 g1787683 Escherichia coli 562 -11534791
5000692216 (de:(ecoli_1374) (pn:hypothetical 25) (gn:ydcf)
(gtcfc:13.7:14.1) (ec:) (ydcf_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_1374 ECOLI_1374 Escherichia coli 562
10119591

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848924	10668	32824	861	286

Description

6500730934 ydca:b1419 hypothetical protein:hypothetical 5.9 kd protein in cybb-trg intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1419 b1419 Escherichia coli 562 -11534792 111248 ydca (de:hypothetical 5.9 kd protein in cybb-trg intergenic region precursor) (db:swissprot) YDCA_ECOLI P23864 ESCHERICHIA COLI 562 -11534792 7000687515 ydca ydca protein precursor (db:pir2.dat) F64893 F64893 Escherichia coli 562 -11534792 223715 ydca (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #270(32.0-32.3 min.)) (nt:orf_id:o270#8; similar to (swissprot accession) (le:7348) (re:7521) (di:direct) D90781 D90781 g1742316 Escherichia coli 562 -11534792 300490 ydca (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.)) (nt:orf_id:o270#8; similar to (swissprot accession) (le:87) (re:260) (di:direct) D90782 D90782 g1742327 Escherichia coli 562 -11534792 300480 ydca orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.) (nt:o57; this 57 aa orf is 85 pct identical (1 gap)) (le:4608) (re:4781) (di:direct) AE000239 AE000239 g1787688 Escherichia coli 562 -11534792 223725 ydca (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.)) (nt:orf_id:o270#8; similar to (swissprot accession) (le:87) (re:260) (di:direct) D90782 D90782 g1742327 Escherichia coli 562 -11534792 5000692217 (de:(ecoli_1379) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1379 ECOLI_1379 Escherichia coli 562 10119595

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848926	10669	32825	618	205

Description

5000692218 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1420 b1420 Escherichia coli 562 -11534793 7000691288 hypothetical protein b1420 (db:pir2.dat) G64893 G64893 Escherichia coli 562 -11534793 7500959990 b1420 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.) (nt:f55; this 55 aa orf is 33 pct identical (0 gaps)) (le:4893) (re:5060) (di:complement) AE000239 AE000239 g1787689 Escherichia coli 562 -11534793 6500730935 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1420 b1420 Escherichia coli 562 -11534793

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848929	10670	32826	294	97

Description

5000692219 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1422 b1422 Escherichia coli 562 -11534794
7000691289 probable regulatory protein b1422 (db:pir2.dat) A64894 A64894 Escherichia coli 562 -11534794 223720 pca operon transcriptional activator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #270(32.0-32.3 min.)) (nt:orf_id:o270#13; similar to (swissprot accession) (le:9819) (re:10883) (di:complement) D90781 D90781 g1742321 Escherichia coli 562 -11534794 300495 pca operon transcriptional activator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.)) (nt:orf_id:o270#13; similar to (swissprot accession) (le:2558) (re:3622) (di:complement) D90782 D90782 g1742332 Escherichia coli 562 -11534794 300485 b1422 putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.) (nt:f354; this 354 aa orf is 30 pct identical (9 gaps)) (le:7079) (re:8143) (di:complement) AE000239 AE000239 g1787691 Escherichia coli 562 -11534794 223730 pca operon transcriptional activator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.)) (nt:orf_id:o270#13; similar to (swissprot accession) (le:2558) (re:3622) (di:complement) D90782 D90782 g1742332 Escherichia coli 562 -11534794 6500730936 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1422 b1422 Escherichia coli 562 -11534794

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501848973	10671	32827	1110	370

Description

5000692220 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1423 b1423 Escherichia coli 562 -11534795
7000691290 hypothetical protein b1423 (db:pir2.dat) B64894 B64894 Escherichia coli 562 -11534795 7500959991 b1423 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.) (nt:o447; this 447 aa orf is 29 pct identical (4 gaps)) (le:8219) (re:9562) (di:direct) AE000239 AE000239 g1787692 Escherichia coli 562 -11534795 6500730937 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1423 b1423 Escherichia coli 562 -11534795

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848992	10672	32828	249	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501848994	10673	32829	1197	398

Description

5000692221 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1424 b1424 Escherichia coli 562 -11534796
7000691291 hypothetical protein b1424 (cl:periplasmic glucans biosynthesis protein mdog) (db:pir2.dat) C64894 C64894 Escherichia coli 562 -11534796
7500959992 ydcg putative glycoprotein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.) (nt:o551; this 551 aa orf is 38 pct identical (21 gaps)) (le:9787) (re:11442) (di:direct) AE000239 AE000239 g1787693 Escherichia coli 562 -11534796 6500730938 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1424 b1424 Escherichia coli 562 -11534796

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849000	10674	32830	624	207

Description

5000692222 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1425 b1425 Escherichia coli 562 -11534797
7000691292 hypothetical protein b1425 (db:pir2.dat) D64894 D64894 Escherichia coli 562 -11534797 7500959993 b1425 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 129 of 400 of the completegenome.) (nt:f67; this 67 aa orf is 34 pct identical (3 gaps)) (le:11363) (re:11566) (di:complement) AE000239 AE000239 g1787694 Escherichia coli 562 -11534797 6500730939 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1425 b1425 Escherichia coli 562 -11534797

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849001	10675	32831	564	187

Description

6500730940 ydch:b1426 hypothetical 6.5 kd protein in riml
5region:hypothetical 6.5 kd protein in trg-riml intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1426
b1426 Escherichia coli 562 -11534798 111255 ydch (de:hypothetical 6.5 kd
protein in trg-riml intergenic region) (db:swissprot) YDCH_ECOLI P46135
ESCHERICHIA COLI 562 -11534798 7000687519 ydch ydch protein
(cl:hypothetical protein hp1242) (db:pir2.dat) E64894 E64894 Escherichia
coli 562 -11534798 223722 ydch (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #270(32.0-32.3 min.)) (nt:orf_id:o270#16; similar to
(swissprot accession) (le:14379) (re:14546) (di:direct) D90781 D90781
g1742323 Escherichia coli 562 -11534798 300497 ydch (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.))
(nt:orf_id:o270#16; similar to (swissprot accession) (le:7118) (re:7285)
(di:direct) D90782 D90782 g1742334 Escherichia coli 562 -11534798 300487
ydch orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 130 of 400 of the completegenome.)
(nt:o55; 100 pct identical to ydch_ecoli sw:) (le:67) (re:234) (di:direct)
AE000240 AE000240 g1787696 Escherichia coli 562 -11534798 223732 ydch
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5
min.)) (nt:orf_id:o270#16; similar to (swissprot accession) (le:7118)
(re:7285) (di:direct) D90782 D90782 g1742334 Escherichia coli 562 -11534798
5000692223 (de:(ecoli_1386) (pn:hypothetical 6) (gn:ydch) (gtcfc:13.7:14.1)
(ec:) (ydch_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_1386 ECOLI_1386 Escherichia coli 562 10052985

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849006	10676	32832	846	282

Description

5000692224 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1428 b1428 Escherichia coli 562 -11534799
7000691293 hypothetical protein b1428 (db:pir2.dat) G64894 G64894
Escherichia coli 562 -11534799 7500959994 b1428 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
130 of 400 of the completegenome.) (nt:f326; this 326 aa orf is 19 pct
identical (7 gaps)) (le:828) (re:1808) (di:complement) AE000240 AE000240
g1787698 Escherichia coli 562 -11534799 6500730941 hypothetical protein
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1428
b1428 Escherichia coli 562 -11534799

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849014	10677	32833	384	127

Description

5000692225 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1431 b1431 Escherichia coli 562 -11534800
7000691294 hypothetical protein b1431 (db:pir2.dat) B64895 B64895
Escherichia coli 562 -11534800 7500959995 b1431 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 130 of 400 of the completegenome.) (nt:o222; this 222 aa orf is 21 pct identical (5 gaps)) (le:3816) (re:4484) (di:direct) AE000240 AE000240
g1787701 Escherichia coli 562 -11534800 6500730942 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1431 b1431 Escherichia coli 562 -11534800

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849030	10678	32834	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849031	10679	32835	327	109

Description

GTC ORF with score 215 to: (sr:yeast (s.cerevisiae; dby939) dna) (db:genpept-pln1) (de:yeast (s.cerevisiae) mod5 gene encoding trna isopentenyltransferase, complete cds.) (nt:trna isopentenyl transferase) (le:274:1213) (re:1209:1560) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849043	10680	32836	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849044	10681	32837	633	211

Description

5000692226 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1432 b1432 Escherichia coli 562 -11534801
7000691295 hypothetical protein b1432 (cl:hypothetical protein b1432) (db:pir2.dat) C64895 C64895 Escherichia coli 562 -11534801 7500959996 b1432 putative virulence protein (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 130 of 400 of the completegenome.) (nt:o402; this 402 aa orf is 30 pct identical (9 gaps)) (le:5016) (re:6224) (di:direct) AE000240 AE000240 g1787702 Escherichia coli 562 -11534801 6500730943 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1432 b1432 Escherichia coli 562 -11534801

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849054	10682	32838	882	293

Description

5000692227 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1433 b1433 Escherichia coli 562 -11534802
7000691296 probable membrane protein b1433 (db:pir2.dat) D64895 D64895 Escherichia coli 562 -11534802 7500959997 b1433 putative membrane transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 130 of 400 of the completegenome.) (nt:f478; this 478 aa orf is 38 pct identical (2 gaps)) (le:6264) (re:7700) (di:complement) AE000240 AE000240 g1787703 Escherichia coli 562 -11534802 6500730944 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1433 b1433 Escherichia coli 562 -11534802

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849064	10683	32839	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849088	10684	32840	990	329

Description

5000692228 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1434 b1434 Escherichia coli 562 -11534803
5500686520 ydcn (de:hypothetical 19.7 kd protein in tehb-rhse intergenic region) (db:swissprot) YDCN_ECOLI P77626 ESCHERICHIA COLI 562 -11534803
7000687520 ydcn ydcn protein (db:pir2.dat) E64895 E64895 Escherichia coli 562 -11534803 223738 hipb protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #271(32.1-32.5 min.)) (nt:orf_id:o271#7; similar to (swissprot accession) (le:14582) (re:15118) (di:direct) D90782 D90782 g1742340 Escherichia coli 562 -11534803 300508 hipb protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #272(32.4-32.7 min.)) (nt:orf_id:o271#7; similar to (swissprot accession) (le:4552) (re:5088) (di:direct) D90783 D90783 g1742346 Escherichia coli 562 -11534803 300503 ydcn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 130 of 400 of the completegenome.) (nt:o178; residues 15-87 are 31 pct identical to) (le:7531) (re:8067) (di:direct) AE000240 AE000240 g1787704 Escherichia coli 562 -11534803 223743 hipb protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #272(32.4-32.7 min.)) (nt:orf_id:o271#7; similar to (swissprot accession) (le:4552) (re:5088) (di:direct) D90783 D90783 g1742346 Escherichia coli 562 -11534803 6500730945 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1434 b1434 Escherichia coli 562 -11534803

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849089	10685	32841	672	223

Description

5000692229 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1435 b1435 Escherichia coli 562 -11534804
7000691297 hypothetical protein b1435 (db:pir2.dat) F64895 F64895 Escherichia coli 562 -11534804 7500959998 ydcp putative collagenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 130 of 400 of the completegenome.) (nt:o667; this 667 aa orf is 35 pct identical (11 gaps)) (le:8098) (re:10101) (di:direct) AE000240 AE000240 g1787705 Escherichia coli 562 -11534804 6500730946 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1435 b1435 Escherichia coli 562 -11534804

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849102	10686	32842	1497	498

Description

5000692230 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1436 b1436 Escherichia coli 562 -11534805
7500951750 yncj (de:hypothetical 8.7 kd protein in tehb-ansp intergenic region precursor) (db:swissprot) YNCJ_ECOLI P76105 ESCHERICHIA COLI 562 -11534805 7000691298 hypothetical protein b1436 precursor (db:pir2.dat) G64895 G64895 Escherichia coli 562 -11534805 7500951752 b1436 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:f76; this 76 aa orf is 34 pct identical (1 gap)) (le:76) (re:306) (di:complement) AE000241 AE000241 g1787707 Escherichia coli 562 -11534805 6500730947 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1436 b1436 Escherichia coli 562 -11534805

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849103	10687	32843	714	237

Description

5000692231 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1437 b1437 Escherichia coli 562 -11534806
7000691299 hypothetical protein b1437 (db:pir2.dat) H64895 H64895 Escherichia coli 562 -11534806 7500959999 b1437 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:f65; uug start; this 65 aa orf is 31 pct identical) (le:492) (re:689) (di:complement) AE000241 AE000241 g1787708 Escherichia coli 562 -11534806 6500730948 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1437 b1437 Escherichia coli 562 -11534806

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849108	10688	32844	606	201

Description

5000692232 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1438 b1438 Escherichia coli 562 -11534807
7500922194 ydcq (de:hypothetical 16.1 kd protein in tehb-ansp intergenic region) (db:swissprot) YDCQ_ECOLI P76107 ESCHERICHIA COLI 562 -11534807
7000691300 hypothetical protein b1438 (db:pir2.dat) A64896 A64896 Escherichia coli 562 -11534807 7500922196 b1438 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:o145; this 145 aa orf is 30 pct identical (1 gap)) (le:729) (re:1166) (di:direct) AE000241 AE000241 g1787709 Escherichia coli 562 -11534807 6500730949 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1438 b1438 Escherichia coli 562 -11534807

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849114	10689	32845	312	103

Description

5000692233 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1439 b1439 Escherichia coli 562 -11534808
7000689493 hypothetical protein b1439 (cl:hypothetical protein b1439) (db:pir2.dat) B64896 B64896 Escherichia coli 562 -11534808 223745 tyrosine aminotransferase ec 2.6.1.5 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #272(32.4-32.7 min.)) (nt:orf_id:o272#4; similar to (swissprot accession) (le:8383) (re:9789) (di:direct) D90783 D90783 g1742348 Escherichia coli 562 -11534808 300516 tyrosine aminotransferase ec 2.6.1.5 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #273(32.5-32.8 min.)) (nt:orf_id:o272#4; similar to (swissprot accession) (le:2041) (re:3447) (di:direct) D90784 D90784 g1742355 Escherichia coli 562 -11534808 300510 b1439 multi modular:putative transcriptional (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:o468; this 468 aa orf is 35 pct identical (5 gaps)) (le:1245) (re:2651) (di:direct) AE000241 AE000241 g1787710 Escherichia coli 562 -11534808 223751 tyrosine aminotransferase ec 2.6.1.5 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #273(32.5-32.8 min.)) (nt:orf_id:o272#4; similar to (swissprot accession) (le:2041) (re:3447) (di:direct) D90784 D90784 g1742355 Escherichia coli 562 -11534808 6500730950 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1439 b1439 Escherichia coli 562 -11534808

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849126	10690	32846	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849129	10691	32847	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849138	10692	32848	366	121

Description

5000692234 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1440 b1440 Escherichia coli 562 -11534809
7000691301 hypothetical protein b1440 precursor (db:pir2.dat) C64896 C64896 Escherichia coli 562 -11534809 7500960000 b1440 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:o381; this 381 aa orf is 28 pct identical (16 gaps)) (le:2896) (re:4041) (di:direct) AE000241 AE000241 g1787711 Escherichia coli 562 -11534809 6500730951 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1440 b1440 Escherichia coli 562 -11534809

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849150	10693	32849	1422	473

Description

5000692235 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1441 b1441 Escherichia coli 562 -11534810
7500922197 ydct (de:hypothetical abc transporter atp-binding protein ydct) (db:swissprot) YDCT_ECOLI P77795 ESCHERICHIA COLI 562 -11534810 7000691302 probable abc-type transport protein b1441 (cl:atp-binding cassette homology) (db:pir2.dat) D64896 D64896 Escherichia coli 562 -11534810 223746 spermidine/putrescine transport atp-binding (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #272(32.4-32.7 min.).) (nt:orf_id:o272#6; similar to (swissprot accession) (le:11197) (re:12210) (di:direct) D90783 D90783 g1742349 Escherichia coli 562 -11534810 300511 spermidine/putrescine transport atp-binding (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #273(32.5-32.8 min.).) (nt:orf_id:o272#6; similar to (swissprot accession) (le:4855) (re:5868) (di:direct) D90784 D90784 g1742356 Escherichia coli 562 -11534810 300517 b1441 putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:o337; residues 30-234 are 59 pct identical to) (le:4059) (re:5072) (di:direct) AE000241 AE000241 g1787712 Escherichia coli 562 -11534810 223752 spermidine/putrescine transport atp-binding (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #272(32.4-32.7 min.).) (nt:orf_id:o272#6; similar to (swissprot accession) (le:11197) (re:12210) (di:direct) D90783 D90783 g1742349 Escherichia coli 562 -11534810 6500730952 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1441 b1441 Escherichia coli 562 -11534810

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849174	10694	32850	318	105

Description

5000692236 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1442 b1442 Escherichia coli 562 -11534811

7000691303 probable membrane protein b1442 (db:pir2.dat) E64896 E64896 Escherichia coli 562 -11534811 223747 putrescine transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #272(32.4-32.7 min.)) (nt:orf_id:o272#7; similar to (swissprot accession) (le:12211) (re:13152) (di:direct) D90783 D90783 g1742350 Escherichia coli 562 -11534811 300518 putrescine transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #273(32.5-32.8 min.)) (nt:orf_id:o272#7; similar to (swissprot accession) (le:5869) (re:6810) (di:direct) D90784 D90784 g1742357 Escherichia coli 562 -11534811 300512 b1442 putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:o313; this 313 aa orf is 28 pct identical (18 gaps)) (le:5073) (re:6014) (di:direct) AE000241 AE000241 g1787713 Escherichia coli 562 -11534811 223753 putrescine transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #273(32.5-32.8 min.)) (nt:orf_id:o272#7; similar to (swissprot accession) (le:5869) (re:6810) (di:direct) D90784 D90784 g1742357 Escherichia coli 562 -11534811 6500730953 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1442 b1442 Escherichia coli 562 -11534811

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849176	10695	32851	987	328

Description

5000692237 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1443 b1443 Escherichia coli 562 -11534812

7000691304 probable membrane protein b1443 (db:pir2.dat) F64896 F64896 Escherichia coli 562 -11534812 223748 spermidine/putrescine transport system permease (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #272(32.4-32.7 min.)) (nt:orf_id:o272#8; similar to (swissprot accession) (le:13142) (re:13936) (di:direct) D90783 D90783 g1742351 Escherichia coli 562 -11534812 300519 spermidine/putrescine transport system permease (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #273(32.5-32.8 min.)) (nt:orf_id:o272#8; similar to (swissprot accession) (le:6800) (re:7594) (di:direct) D90784 D90784 g1742358 Escherichia coli 562 -11534812 300513 b1443 putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:o264; this 264 aa orf is 33 pct identical (11 gaps)) (le:6004) (re:6798) (di:direct) AE000241 AE000241 g1787714 Escherichia coli 562 -11534812 223754 spermidine/putrescine transport system permease (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #273(32.5-32.8 min.)) (nt:orf_id:o272#8; similar to (swissprot accession) (le:6800) (re:7594) (di:direct) D90784 D90784 g1742358 Escherichia coli 562 -11534812 6500730954 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1443 b1443 Escherichia coli 562 -11534812

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849181	10696	32852	381	127

Description

5000692238 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1444 b1444 Escherichia coli 562 -11534813
7500922199 ydcw (ec:1.2.1.8) (de:putative betaine aldehyde dehydrogenase, (badh)) (db:swissprot) YDCW_ECOLI P77674 ESCHERICHIA COLI 562 -11534813
7000691305 probable aldehyde dehydrogenase (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (ec:1.2.1.-) (db:pir2.dat) G64896 G64896 Escherichia coli 562 -11534813 223749 betaine-aldehyde dehydrogenase precursor ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #272(32.4-32.7 min.)) (nt:orf_id:o272#9; similar to (swissprot accession) (le:13958) (re:15382) (di:direct) D90783 D90783 g1742352 Escherichia coli 562 -11534813 300514 betaine-aldehyde dehydrogenase precursor ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #273(32.5-32.8 min.)) (nt:orf_id:o272#9; similar to (swissprot accession) (le:7616) (re:9040) (di:direct) D90784 D90784 g1742359 Escherichia coli 562 -11534813 300520 b1444 putative aldehyde dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:o474; this 474 aa orf is 40 pct identical (8 gaps)) (le:6820) (re:8244) (di:direct) AE000241 AE000241 g1787715 Escherichia coli 562 -11534813 223755 betaine-aldehyde dehydrogenase precursor ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #272(32.4-32.7 min.)) (nt:orf_id:o272#9; similar to (swissprot accession) (le:13958) (re:15382) (di:direct) D90783 D90783 g1742352 Escherichia coli 562 -11534813 6500730955 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1444 b1444 Escherichia coli 562 -11534813

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849186	10697	32853	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849200	10698	32854	489	162

Description

5000692239 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1445 b1445 Escherichia coli 562 -11534814
7500922201 ydcx (de:hypothetical 9.6 kd protein in teh-anp intergenic region) (db:swissprot) YDCX_ECOLI P76109 ESCHERICHIA COLI 562 -11534814
7000691306 probable membrane protein b1445 (db:pir2.dat) H64896 H64896 Escherichia coli 562 -11534814 7500922203 b1445 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:o82; this 82 aa orf is 33 pct identical (1 gap)) (le:8556) (re:8804) (di:direct) AE000241 AE000241 g1787716 Escherichia coli 562 -11534814 6500730956 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1445 b1445 Escherichia coli 562 -11534814

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849235	10699	32855	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849261	10700	32856	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849263	10701	32857	273	90

Description

5000692240 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1446 b1446 Escherichia coli 562 -11534815
7500922204 ydcy (de:hypothetical 8.8 kd protein in teh-anp intergenic region) (db:swissprot) YDCY_ECOLI P76110 ESCHERICHIA COLI 562 -11534815
7000691307 hypothetical protein b1446 (db:pir2.dat) A64897 A64897 Escherichia coli 562 -11534815 7500922206 b1446 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:o77; this 77 aa orf is 30 pct identical (0 gaps)) (le:8890) (re:9123) (di:direct) AE000241 AE000241 g1787717 Escherichia coli 562 -11534815 6500730957 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1446 b1446 Escherichia coli 562 -11534815

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849269	10702	32858	894	297

Description

5000692241 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1447 b1447 Escherichia coli 562 -11534816
7500922207 ydcz (de:hypothetical 15.9 kd protein in tehb-ansp intergenic region) (db:swissprot) YDCZ_ECOLI P76111 ESCHERICHIA COLI 562 -11534816
7000691308 probable membrane protein b1447 (db:pir2.dat) B64897 B64897 Escherichia coli 562 -11534816 7500922209 b1447 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:f149; this 149 aa orf is 31 pct identical (11 gaps)) (le:9124) (re:9573) (di:complement) AE000241 AE000241 g1787718 Escherichia coli 562 -11534816 6500730958 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1447 b1447 Escherichia coli 562 -11534816

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849270	10703	32859	429	142

Description

5000692242 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1448 b1448 Escherichia coli 562 -11534817
7000691309 probable phosphinothricin n-acetyltransferase (cl:phosphinothricin n-acetyltransferase) (ec:2.3.1.-) (db:pir2.dat) C64897 C64897 Escherichia coli 562 -11534817 7500955853 b1448 putative resistance protein (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 131 of 400 of the completegenome.) (nt:f172; 38 pct identical (3 gaps) to 169 residues of) (le:9570) (re:10088) (di:complement) AE000241 AE000241 g1787719 Escherichia coli 562 -11534817 6500730959 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1448 b1448 Escherichia coli 562 -11534817

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849278	10704	32860	1182	393

Description

5000692243 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1449 b1449 Escherichia coli 562 -11534818
7000691310 probable quinone oxidoreductase (ec:1.6.5.5) (db:pir2.dat) D64897 D64897 Escherichia coli 562 -11534818 7500960001 yncb putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 132 of 400 of the completegenome.) (nt:o376; this 376 aa orf is 27 pct identical (16 gaps)) (le:74) (re:1204) (di:direct) AE000242 AE000242 g1787721 Escherichia coli 562 -11534818 6500730960 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1449 b1449 Escherichia coli 562 -11534818

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849289	10705	32861	1692	563

Description

5000692244 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1450 b1450 Escherichia coli 562 -11534819
7000691311 hypothetical protein b1450 (db:pir2.dat) E64897 E64897
Escherichia coli 562 -11534819 7500960002 b1450 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 132 of 400 of the completegenome.) (nt:o240; this 240 aa orf is 29 pct identical (4 gaps)) (le:1345) (re:2067) (di:direct) AE000242 AE000242
g1787722 Escherichia coli 562 -11534819 6500730961 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1450 b1450 Escherichia coli 562 -11534819

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849302	10706	32862	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849305	10707	32863	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849317	10708	32864	1683	560

Description

5000692245 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1451 b1451 Escherichia coli 562 -11534820
7000691312 hypothetical protein b1451 precursor (cl:tonb-dependent receptor amino-terminal homology) (db:pir2.dat) F64897 F64897 Escherichia coli 562 -11534820 7500960003 b1451 putative outer membrane receptor for iron (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 132 of 400 of the completegenome.) (nt:f700; this 700 aa orf is 26 pct identical (64 gaps)) (le:2103) (re:4205) (di:complement) AE000242 AE000242 g1787723 Escherichia coli 562 -11534820
6500730962 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1451 b1451 Escherichia coli 562 -11534820

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849330	10709	32865	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849331	10710	32866	231	76

Description

5000692246 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1452 b1452 Escherichia coli 562 -11534821
 7000691313 hypothetical protein b1452 (db:pir2.dat) G64897 G64897
 Escherichia coli 562 -11534821 7500960004 b1452 putative receptor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 132 of 400 of the completegenome.) (nt:o353; this 353 aa orf is 22 pct identical (17 gaps)) (le:4447) (re:5508) (di:direct) AE000242 AE000242 g1787724 Escherichia coli 562 -11534821 6500730963 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1452 b1452 Escherichia coli 562 -11534821

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849332	10711	32867	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849344	10712	32868	888	295

Description

GTC ORF with score 124 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone f4d11 (essaiiproject).) (nt:similarity to protein kinase tmk1, arabidopsis) (le:33819:34133:34431) (re:34034:34294:34578) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849359	10713	32869	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849368	10714	32870	2622	873

Description

GTC ORF with score 369 to: (fn:uteroglobin promoter binding protein)
(sr:european rabbit) (db:genpept-mam) (de:oryctolagus cuniculus rush-1beta
mrna, complete cds.) (nt:progesterone-dependent splice variant of) (le:171)
(re:2681) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849384	10715	32871	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849390	10716	32872	789	262

Description

6500730964 ansp:b1453 hypothetical protein:l-asparagine
permease:l-asparagine transport protein (gtcfc:12.1:11.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b1453 b1453 Escherichia coli 562
-11534822 7000684582 ansp amino acid transport protein:amino acid permease
(cl:arginine permease) (db:pir2.dat) H64897 H64897 Escherichia coli 562
-11534822 300527 l-asparagine permease l-asparagine transport
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #274(32.7-33.0
min.)) (nt:orf_id:o274#2; similar to (swissprot accession) (le:6717)
(re:8267) (di:complement) D90785 D90785 g1742367 Escherichia coli 562
-11534822 223762 l-asparagine permease l-asparagine transport
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #275(32.8-33.2
min.)) (nt:orf_id:o274#2; similar to (swissprot accession) (le:785)
(re:2335) (di:complement) D90786 D90786 g1742375 Escherichia coli 562
-11534822 223769 ansp l-asparagine permease (fn:transport; transport of
small molecules: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
section 132 of 400 of the completegenome.) (nt:f516; uug start; this 516 aa
orf is 91 pct) (le:5621) (re:7171) (di:complement) AE000242 AE000242
g1787725 Escherichia coli 562 -11534822 1500685774 ansp_ecoli
(de:l-asparagine permease \ (l-asparagine transport protein\),) P77610 P77610
Escherichia coli 562 -11534822 5000692247 (de:(ecoli_1413) (pn:function not
assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_1413 ECOLI_1413 Escherichia coli 562
10059028

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849419	10717	32873	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849421	10718	32874	228	75

Description

5000692248 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1454 b1454 Escherichia coli 562 -11534823
7000691314 hypothetical protein b1454 (db:pir2.dat) A64898 A64898 Escherichia coli 562 -11534823 7500960007 b1454 putative transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 132 of 400 of the completegenome.) (nt:o205; this 205 aa orf is 25 pct identical (9 gaps)) (le:7387) (re:8004) (di:direct) AE000242 AE000242 g1787726 Escherichia coli 562 -11534823 6500730965 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1454 b1454 Escherichia coli 562 -11534823

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849423	10719	32875	417	138

Description

5000692249 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1455 b1455 Escherichia coli 562 -11534824
7500951747 yncH (de:hypothetical 8.3 kd protein in ansp-rhse intergenic region) (db:swissprot) YNCH_ECOLI P76118 ESCHERICHIA COLI 562 -11534824
7000691315 hypothetical protein b1455 (db:pir2.dat) B64898 B64898 Escherichia coli 562 -11534824 7500951749 b1455 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 132 of 400 of the completegenome.) (nt:o70; residues 3-45 are 23 pct identical to) (le:8080) (re:8292) (di:direct) AE000242 AE000242 g1787727 Escherichia coli 562 -11534824 6500730966 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1455 b1455 Escherichia coli 562 -11534824

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849428	10720	32876	456	151

Description

GTC ORF with score 105 to: (db:genpept-inv) (de:brugia malayi microfilarial sheath protein shp3a (bmshp3a) andmicrofilarial sheath protein shp3 precursor (bmshp3) genes,complete cds.) (nt:structural protein) (le:8295:8691) (re:8357:9296) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849443	10721	32877	1749	582

Description

5000692252 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1458 b1458 Escherichia coli 562 -11534825
7000691316 h repeat-associated protein-like protein b1458 (db:pir2.dat)
E64898 E64898 Escherichia coli 562 -11534825 7500960008 b1458
orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 133 of 400 of the completegenome.) (nt:o248; this 248 aa orf is 59 pct identical (0 gaps)) (le:121) (re:867) (di:direct)
AE000243 AE000243 g1787731 Escherichia coli 562 -11534825 6500730967
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1458 b1458 Escherichia coli 562 -11534825

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849461	10722	32878	804	267

Description

5000692253 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1459 b1459 Escherichia coli 562 -11534826
7000691317 h repeat-associated protein-like protein b1459 (db:pir2.dat)
F64898 F64898 Escherichia coli 562 -11534826 7500960009 b1459
orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 133 of 400 of the completegenome.) (nt:o66; uug start; this 66 aa orf is 57 pct identical) (le:911) (re:1111) (di:direct)
AE000243 AE000243 g1787732 Escherichia coli 562 -11534826 6500730968
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1459 b1459 Escherichia coli 562 -11534826

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849462	10723	32879	405	135

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849465	10724	32880	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849468	10725	32881	885	295

Description

6500730969 ydce:b1461 hypothetical 8.7 kd protein in rhse-narv intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1461 b1461 Escherichia coli 562 -11534827 111252 ydce (de:hypothetical 8.7 kd protein in rhse-narv intergenic region) (db:swissprot) YDCE_ECOLI P31992 ESCHERICHIA COLI 562 -11534827 7000687517 ydce ydce protein (db:pir2.dat) H64898 H64898 Escherichia coli 562 -11534827 300533 ydce (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #274(32.7-33.0 min..)) (nt:orf_id:o274#10; similar to (swissprot accession) (le:15288) (re:15521) (di:direct) D90785 D90785 g1742373 Escherichia coli 562 -11534827 223775 ydce (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #275(32.8-33.2 min..)) (nt:orf_id:o274#10; similar to (swissprot accession) (le:9356) (re:9589) (di:direct) D90786 D90786 g1742381 Escherichia coli 562 -11534827 300539 ydce (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #276(33.0-33.3 min..)) (nt:orf_id:o274#10; similar to (swissprot accession) (le:3282) (re:3515) (di:direct) D90787 D90787 g1742394 Escherichia coli 562 -11534827 299932 (db:genpept-bct1) (de:escherichia coli rhse genetic element; defective rhse core protein,complete cds; complete orf-e2; h-rpt subelement; complete orf-h.) (nt:unknown orf) (le:5162) (re:5395) (di:direct) ECORHSEX L19083 g304948 Escherichia coli 562 -11534827 235831 ydce orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 133 of 400 of the completegenome.) (nt:o77; 100 pct identical to ydce_ecoli sw: p31992;) (le:2587) (re:2820) (di:direct) AE000243 AE000243 g1787734 Escherichia coli 562 -11534827 223768 ydce (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #274(32.7-33.0 min..)) (nt:orf_id:o274#10; similar to (swissprot accession) (le:15288) (re:15521) (di:direct) D90785 D90785 g1742373 Escherichia coli 562 -11534827 223787 ydce (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #276(33.0-33.3 min..)) (nt:orf_id:o274#10; similar to (swissprot accession) (le:3282) (re:3515) (di:direct) D90787 D90787 g1742394 Escherichia coli 562 -11534827 5000692255 (de:(ecoli_1421) (pn:hypothetical 8) (gn:ydce) (gtcfc:13.7:14.1) (ec:) (ydce_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1421 ECOLI_1421 Escherichia coli 562 10052982

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849478	10726	32882	843	280

Description

5000692256 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1462 b1462 Escherichia coli 562 -11534828
7500922212 yddh (de:hypothetical 22.8 kd protein in tehb-ansp intergenic region) (db:swissprot) YDDH_ECOLI P76121 ESCHERICHIA COLI 562 -11534828
7000691318 hypothetical protein b1462 (db:pir2.dat) A64899 A64899 Escherichia coli 562 -11534828 7500922214 b1462 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 133 of 400 of the completegenome.) (nt:f205; uug start; this 205 aa orf is 22 pct) (le:2817) (re:3434) (di:complement) AE000243 AE000243 g1787735 Escherichia coli 562 -11534828 6500730970 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1462 b1462 Escherichia coli 562 -11534828

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849481	10727	32883	663	220

Description

5000692257 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1463 b1463 Escherichia coli 562 -11534829
7000691319 n-hydroxyarylamine o-acetyltransferase (ec:2.3.1.118) (db:pir2.dat) B64899 B64899 Escherichia coli 562 -11534829 223776 n-hydroxyarylamine o-acetyltransferase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #275(32.8-33.2 min.)) (nt:orf_id:o276#2; similar to (swissprot accession) (le:10328) (re:11173) (di:direct) D90786 D90786 g1742382 Escherichia coli 562 -11534829 223788 n-hydroxyarylamine o-acetyltransferase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #276(33.0-33.3 min.)) (nt:orf_id:o276#2; similar to (swissprot accession) (le:4254) (re:5099) (di:direct) D90787 D90787 g1742395 Escherichia coli 562 -11534829 300540 b1463 putative n-hydroxyarylamine o-acetyltransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 133 of 400 of the completegenome.) (nt:o281; 74 pct identical amino acid sequence and) (le:3559) (re:4404) (di:direct) AE000243 AE000243 g1787736 Escherichia coli 562 -11534829 6500730971 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1463 b1463 Escherichia coli 562 -11534829

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849484	10728	32884	366	121

Description

5000692260 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1470 b1470 Escherichia coli 562 -11534830
7500922215 yddj (de:hypothetical 12.9 kd protein in naru-fdng intergenic region) (db:swissprot) YDDJ_ECOLI P76122 ESCHERICHIA COLI 562 -11534830
7000691320 hypothetical protein b1470 (db:pir2.dat) A64900 A64900
Escherichia coli 562 -11534830 7500922217 b1470 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:f111; this 111 aa orf is 27 pct identical (7 gaps)) (le:1783) (re:2118) (di:complement) AE000244 AE000244 g1787744 Escherichia coli 562 -11534830 6500730972 b1470 orf:hypothetical protein (fn:orf; unknown) (db:genpept) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:f111; this 111 aa orf is 27 pct identical (7 gaps)) (le:1783) (re:2118) (di:complement) AE000244 AE000244 g1787744 Escherichia coli 562 -11534830

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849485	10729	32885	477	158

Description

5000692261 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1471 b1471 Escherichia coli 562 -11534831
7500922218 yddk (de:hypothetical 36.2 kd protein in naru-fdng intergenic region) (db:swissprot) YDDK_ECOLI P76123 ESCHERICHIA COLI 562 -11534831
7000691321 hypothetical protein b1471 (db:pir2.dat) B64900 B64900
Escherichia coli 562 -11534831 7500922220 b1471 putative glycoprotein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:f318; this 318 aa orf is 34 pct identical (14 gaps)) (le:2157) (re:3113) (di:complement) AE000244 AE000244 g1787745 Escherichia coli 562 -11534831 6500730973 b1471 putative glycoprotein (fn:putative structure; not classified) (db:genpept) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:f318; this 318 aa orf is 34 pct identical (14 gaps)) (le:2157) (re:3113) (di:complement) AE000244 AE000244 g1787745 Escherichia coli 562 -11534831

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849486	10730	32886	192	63

Description

5000692262 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1472 b1472 Escherichia coli 562 -11534832
7000691322 outer membrane porin homolog b1472 precursor:truncated (db:pir2.dat) C64900 C64900 Escherichia coli 562 -11534832 223797 outer membrane protein c precursor porin . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #277(33.2-33.6 min.)) (nt:orf_id:o277#1; similar to (swissprot accession) (le:3542) (re:3832) (di:complement) D90788 D90788 g1742405 Escherichia coli 562 -11534832 300549 b1472 putative outer membrane porin protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:f96; this 96 aa orf is 59 pct identical (0 gaps)) (le:3137) (re:3427) (di:complement) AE000244 AE000244 g1787746 Escherichia coli 562 -11534832 6500730974 b1472 putative outer membrane porin protein (fn:putative membrane; not classified) (db:genpept) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:f96; this 96 aa orf is 59 pct identical (0 gaps)) (le:3137) (re:3427) (di:complement) AE000244 AE000244 g1787746 Escherichia coli 562 -11534832

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849505	10731	32887	327	108

Description

6500730975 yddm:b1477 hypothetical protein:hypothetical 13.3 kd protein in fdni-sfca intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1477 b1477 Escherichia coli 562 -11534833
4000708198 yddm (de:hypothetical 13.3 kd protein in fdni-adhp intergenic region) (db:swissprot) YDDM_ECOLI P76125 ESCHERICHIA COLI 562 -11534833
7000687524 hypothetical protein b1477 (cl:hypothetical protein b1477) (db:pir2.dat) H64900 H64900 Escherichia coli 562 -11534833 7500922221 yddm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:f120; residues 35-97 are 46 pct identical to aa) (le:9797) (re:10159) (di:complement) AE000244 AE000244 g1787751 Escherichia coli 562 -11534833 5000692264 yddm orf:hypothetical protein (fn:orf; unknown) (db:genpept) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:f120; residues 35-97 are 46 pct identical to aa) (le:9797) (re:10159) (di:complement) AE000244 AE000244 g1787751 Escherichia coli 562 -11534833

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849506	10732	32888	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849507	10733	32889	1047	348
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849509	10734	32890	186	61
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849515	10735	32891	573	190
<u>Description</u>				

5000692265 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1478 b1478 Escherichia coli 562 -11534834
7000689017 alcohol dehydrogenase:b1478 (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.1) (db:pir1.dat) A64901 A64901 Escherichia coli 562 -11534834 7500953163 adhbp alcohol dehydrogenase (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completegenome.) (nt:f346; 79 pct identical to 336 amino acids) (le:64) (re:1104) (di:complement) AE000245 AE000245 g1787753 Escherichia coli 562 -11534834 6500730976 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1478 b1478 Escherichia coli 562 -11534834

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849527	10736	32892	1392	464
<u>Description</u>				

5000692266 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1481 b1481 Escherichia coli 562 -11534835
7500922237 yddx (de:hypothetical 10.4 kd protein in sfca-osmc intergenic region) (db:swissprot) YDDX_ECOLI P76127 ESCHERICHIA COLI 562 -11534835
7000691323 hypothetical protein b1481 (db:pir2.dat) D64901 D64901 Escherichia coli 562 -11534835 7500922239 b1481 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completegenome.) (nt:f92) (le:3301) (re:3579) (di:complement) AE000245 AE000245 g1787756 Escherichia coli 562 -11534835 6500730977 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1481 b1481 Escherichia coli 562 -11534835

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849535	10737	32893	576	191

Description

5000692267 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1483 b1483 Escherichia coli 562 -11534836
7500922222 yddo (de:hypothetical abc transporter atp-binding protein yddo) (db:swissprot) YDDO_ECOLI P77622 ESCHERICHIA COLI 562 -11534836 7000691324 abc-type transport protein b1483 (cl:atp-binding cassette homology) (db:pir2.dat) F64901 F64901 Escherichia coli 562 -11534836 223814 dipeptide transport atp-binding protein dppf. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf_id:o279#1; similar to (swissprot accession) (le:11292) (re:12218) (di:complement) D90789 D90789 g1742423 Escherichia coli 562 -11534836 300561 dipeptide transport atp-binding protein dppf. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #279(33.5-33.9 min.)) (nt:orf_id:o279#1; similar to (swissprot accession) (le:3395) (re:4321) (di:complement) D90790 D90790 g1742434 Escherichia coli 562 -11534836 7500922224 b1483 putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completgenome.) (nt:f308; this 308 aa orf is 46 pct identical (16 gaps)) (le:4348) (re:5274) (di:complement) AE000245 AE000245 g1787758 Escherichia coli 562 -11534836 223824 dipeptide transport atp-binding protein dppf. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf_id:o279#1; similar to (swissprot accession) (le:11292) (re:12218) (di:complement) D90789 D90789 g1742423 Escherichia coli 562 -11534836 6500730978 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1483 b1483 Escherichia coli 562 -11534836

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849539	10738	32894	909	302

Description

5000692268 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1484 b1484 Escherichia coli 562 -11534837
7500922225 yddp (de:hypothetical abc transporter atp-binding protein yddp) (db:swissprot) YDDP_ECOLI P77268 ESCHERICHIA COLI 562 -11534837 7000691325 abc-type transport protein b1484 (cl:atp-binding cassette homology) (db:pir2.dat) G64901 G64901 Escherichia coli 562 -11534837 223815 dipeptide transport atp-binding protein dppd. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf_id:o279#2; similar to (swissprot accession) (le:12211) (re:13197) (di:complement) D90789 D90789 g1742424 Escherichia coli 562 -11534837 300562 dipeptide transport atp-binding protein dppd. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #279(33.5-33.9 min.)) (nt:orf_id:o279#2; similar to (swissprot accession) (le:4314) (re:5300) (di:complement) D90790 D90790 g1742435 Escherichia coli 562 -11534837 7500922227 b1484 putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completegenome.) (nt:f328; this 328 aa orf is 44 pct identical (3 gaps)) (le:5267) (re:6253) (di:complement) AE000245 AE000245 g1787759 Escherichia coli 562 -11534837 223825 dipeptide transport atp-binding protein dppd. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf_id:o279#2; similar to (swissprot accession) (le:12211) (re:13197) (di:complement) D90789 D90789 g1742424 Escherichia coli 562 -11534837 6500730979 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1484 b1484 Escherichia coli 562 -11534837

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849551	10739	32895	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849552	10740	32896	825	274

Description

5000692269 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1485 b1485 Escherichia coli 562 -11534838
7500922228 yddq (de:hypothetical abc transporter permease protein yddq) (db:swissprot) YDDQ_ECOLI P77463 ESCHERICHIA COLI 562 -11534838 7000691326 probable oligopeptide transport protein b1485:probable oligopeptide permease b1485 (cl:oligopeptide permease protein oppb) (db:pir2.dat) H64901 H64901 Escherichia coli 562 -11534838 223816 dipeptide transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf_id:o279#3; similar to (swissprot accession) (le:13194) (re:14090) (di:complement) D90789 D90789 g1742425 Escherichia coli 562 -11534838 300563 dipeptide transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #279(33.5-33.9 min.)) (nt:orf_id:o279#3; similar to (swissprot accession) (le:5297) (re:6193) (di:complement) D90790 D90790 g1742436 Escherichia coli 562 -11534838 7500922230 b1485 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completegenome.) (nt:f298; this 298 aa orf is 46 pct identical (7 gaps)) (le:6250) (re:7146) (di:complement) AE000245 AE000245 g1787760 Escherichia coli 562 -11534838 223826 dipeptide transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf_id:o279#3; similar to (swissprot accession) (le:13194) (re:14090) (di:complement) D90789 D90789 g1742425 Escherichia coli 562 -11534838 6500730980 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1485 b1485 Escherichia coli 562 -11534838

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849555	10741	32897	402	133

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849561	10742	32898	375	124

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849575	10743	32899	987	328

Description

5000692270 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1486 b1486 Escherichia coli 562 -11534839
7500922231 yddr (de:hypothetical abc transporter permease protein yddr) (db:swissprot) YDDR_ECOLI P77308 ESCHERICHIA COLI 562 -11534839 7000691327 peptide transport system permease protein b1486 (cl:transmembrane protein dppb) (db:pir2.dat) A64902 A64902 Escherichia coli 562 -11534839 223817 dipeptide transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)).) (nt:orf_id:o279#4; similar to (swissprot accession) (le:14087) (re:15109) (di:complement) D90789 D90789 g1742426 Escherichia coli 562 -11534839 300564 dipeptide transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #279(33.5-33.9 min.)).) (nt:orf_id:o279#4; similar to (swissprot accession) (le:6190) (re:7212) (di:complement) D90790 D90790 g1742437 Escherichia coli 562 -11534839 7500922233 b1486 putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completegenome.) (nt:f340; this 340 aa orf is 47 pct identical (7 gaps)) (le:7143) (re:8165) (di:complement) AE000245 AE000245 g1787761 Escherichia coli 562 -11534839 223827 dipeptide transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)).) (nt:orf_id:o279#4; similar to (swissprot accession) (le:14087) (re:15109) (di:complement) D90789 D90789 g1742426 Escherichia coli 562 -11534839 6500730981 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1486 b1486 Escherichia coli 562 -11534839

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849579	10744	32900	324	107

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849583	10745	32901	504	167

Description

5000692271 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1487 b1487 Escherichia coli 562 -11534840
7500922234 ydds (de:putative binding protein ydds precursor) (db:swissprot) YDDS_ECOLI P76128 ESCHERICHIA COLI 562 -11534840 7000691328 probable oligopeptide-binding periplasmic protein b1487 precursor (cl:dipeptide transport protein) (db:pir2.dat) B64902 B64902 Escherichia coli 562 -11534840 7500922236 b1487 putative hemin-binding lipoprotein (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completegenome.) (nt:f516; 28 pct identical (32 gaps) to 505 residues) (le:8167) (re:9717) (di:complement) AE000245 AE000245 g1787762 Escherichia coli 562 -11534840 6500730982 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1487 b1487 Escherichia coli 562 -11534840

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849603	10746	32902	183	60

Description

5000692272 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1488 b1488 Escherichia coli 562 -11534841
7000691329 hypothetical protein b1488 (db:pir2.dat) C64902 C64902
Escherichia coli 562 -11534841 223819 d-alanyl-d-alanine dipeptidase ec 3.4.13.- (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #278(33.3-33.7 min.)) (nt:orf_id:o279#6; similar to (swissprot accession) (le:16675) (re:17256) (di:complement) D90789 D90789 g1742428 Escherichia coli 562 -11534841 223829 d-alanyl-d-alanine dipeptidase ec 3.4.13.- (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #279(33.5-33.9 min.)) (nt:orf_id:o279#6; similar to (swissprot accession) (le:8778) (re:9359) (di:complement) D90790 D90790 g1742439 Escherichia coli 562 -11534841 300572 d-alanyl-d-alanine dipeptidase ec 3.4.13.- (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #280(33.7-34.1 min.)) (nt:orf_id:o279#6; similar to (swissprot accession) (le:132) (re:713) (di:complement) D90791 D90791 g1742446 Escherichia coli 562 -11534841 300566 b1488 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 135 of 400 of the completegenome.) (nt:f193; 41 pct identical (22 gaps) to 154 residues) (le:9731) (re:10312) (di:complement) AE000245 AE000245 g1787763 Escherichia coli 562 -11534841 223835 d-alanyl-d-alanine dipeptidase ec 3.4.13.- (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #280(33.7-34.1 min.)) (nt:orf_id:o279#6; similar to (swissprot accession) (le:132) (re:713) (di:complement) D90791 D90791 g1742446 Escherichia coli 562 -11534841 6500730983 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1488 b1488 Escherichia coli 562 -11534841

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849604	10747	32903	249	83

Description

5000692273 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1489 b1489 Escherichia coli 562 -11534842
7000691330 hypothetical protein b1489 (db:pir2.dat) D64902 D64902
Escherichia coli 562 -11534842 7500960010 b1489 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 136 of 400 of the completegenome.) (nt:f807; this 807 aa orf is 31 pct identical (12 gaps)) (le:191) (re:2614) (di:complement) AE000246 AE000246 g1787765 Escherichia coli 562 -11534842 6500730984 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1489 b1489 Escherichia coli 562 -11534842

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849606	10748	32904	294	97

Description

5000692274 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1490 b1490 Escherichia coli 562 -11534843
7000691331 hypothetical protein b1490 (db:pir2.dat) E64902 E64902
Escherichia coli 562 -11534843 223831 yhck (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #279(33.5-33.9 min.)) (nt:orf_id:o279#8; similar to (swissprot accession) (le:12041) (re:13423) (di:complement) D90790 D90790 g1742441 Escherichia coli 562 -11534843
300574 yhck (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #280(33.7-34.1 min.)) (nt:orf_id:o279#8; similar to (swissprot accession) (le:3395) (re:4777) (di:complement) D90791 D90791 g1742448 Escherichia coli 562 -11534843 300568 b1490 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 136 of 400 of the completegenome.) (nt:f460; this 460 aa orf is 26 pct identical (7 gaps)) (le:2615) (re:3997) (di:complement) AE000246 AE000246 g1787766 Escherichia coli 562 -11534843 223837 yhck (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #280(33.7-34.1 min.)) (nt:orf_id:o279#8; similar to (swissprot accession) (le:3395) (re:4777) (di:complement) D90791 D90791 g1742448 Escherichia coli 562 -11534843 6500730985 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1490 b1490 Escherichia coli 562 -11534843

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849612	10749	32905	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849633	10750	32906	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849635	10751	32907	621	206

Description

5000692275 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1491 b1491 Escherichia coli 562 -11534844
7000691332 hypothetical protein b1491 (db:pir2.dat) F64902 F64902
Escherichia coli 562 -11534844 7500960011 b1491 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 136 of 400 of the completegenome.) (nt:f439; this 439 aa orf is 30 pct identical (20 gaps)) (le:4361) (re:5680) (di:complement) AE000246 AE000246 g1787767 Escherichia coli 562 -11534844 6500730986 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1491 b1491 Escherichia coli 562 -11534844

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849636	10752	32908	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849638	10753	32909	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849645	10754	32910	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849651	10755	32911	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849658	10756	32912	342	113

Description

6500730987 ydda:b1496 hypothetical abc transporter in gadb 5region
 (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1496
 b1496 Escherichia coli 562 -11534845 111265 ydda (de:intergenic region
 (cds102)) (db:swissprot) YDDA_ECOLI P31826 ESCHERICHIA COLI 562 -11534845
 7000687521 ydda probable abc-type transport protein ydda (cl:atp-binding
 cassette homology) (db:pir2.dat) C64903 C64903 Escherichia coli 562
 -11534845 7500922210 ydda putative atp-binding component of a transport
 (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia
 coli k-12 mg1655 section 136 of 400 of the completegenome.) (nt:f561; 100
 pct identical to ydda_ecoli sw:) (le:14514) (re:16199) (di:complement)
 AE000246 AE000246 g1787772 Escherichia coli 562 -11534845 5000692279
 (de:(ecoli_1456) (pn:hypothetical abc transporter atp-binding protein in
 gadb 5"region:cds102) (gn:ydda) (gtcfc:13.7:14.1) (ec:) (ydda_ecoli)
 (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1456
 ECOLI_1456 Escherichia coli 562 10123353

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849674	10757	32913	183	60

Description

5000692280 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli) b1497 b1497 Escherichia coli 562 -11534846
 7000691333 hypothetical protein b1497 (cl:probable arylsulfatase regulatory
 protein atsb) (db:pir2.dat) D64903 D64903 Escherichia coli 562 -11534846
 7500960012 b1497 putative enzyme (fn:putative enzyme; not classified)
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 137 of 400 of the
 completegenome.) (nt:f390; uug start; this 390 aa orf is 43 pct) (le:210)
 (re:1382) (di:complement) AE000247 AE000247 g1787774 Escherichia coli 562
 -11534846 6500730988 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
 (rileyfc:5.7.0) (db:gtc-escherichia coli) b1497 b1497 Escherichia coli 562
 -11534846

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849685	10758	32914	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849694	10759	32915	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849709	10760	32916	951	316

Description

5000692281 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1498 b1498 Escherichia coli 562 -11534847
7000691334 arylsulfatase homolog b1498 (db:pir2.dat) E64903 E64903
Escherichia coli 562 -11534847 223848 arylsulfatase precursor ec 3.1.6.1 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #301(34.0-34.3 min.)) (nt:orf_id:o301#1; similar to (swissprot accession) (le:2530) (re:4245) (di:complement) D90792 D90792 g1742460 Escherichia coli 562 -11534847 300585 b1498 putative sulfatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 137 of 400 of the completegenome.) (nt:f571; uug start; this 571 aa orf is 32 pct) (le:1419) (re:3134) (di:complement) AE000247 AE000247 g1787775 Escherichia coli 562 -11534847 6500730989 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1498 b1498 Escherichia coli 562 -11534847

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849722	10761	32917	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849728	10762	32918	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849749	10763	32919	864	287

Description

5000692282 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1499 b1499 Escherichia coli 562 -11534848
7000691335 transcription regulator homolog b1499 precursor (cl:hypothetical protein f242a) (db:pir2.dat) F64903 F64903 Escherichia coli 562 -11534848
7500960013 b1499 putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 137 of 400 of the completegenome.) (nt:f253; this 253 aa orf is 34 pct identical (3 gaps)) (le:3503) (re:4264) (di:complement) AE000247 AE000247 g1787776 Escherichia coli 562 -11534848 6500730990 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1499 b1499 Escherichia coli 562 -11534848

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849758	10764	32920	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849773	10765	32921	876	291

Description

5000692283 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1500 b1500 Escherichia coli 562 -11534849
7000691336 hypothetical protein b1500 (db:pir2.dat) G64903 G64903
Escherichia coli 562 -11534849 7500960014 b1500 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 137 of 400 of the completegenome.) (nt:f65; this 65 aa orf is 38 pct identical (4 gaps)) (le:4339) (re:4536) (di:complement) AE000247 AE000247 g1787777 Escherichia coli 562 -11534849 6500730991 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1500 b1500 Escherichia coli 562 -11534849

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849775	10766	32922	501	166

Description

5000692284 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1501 b1501 Escherichia coli 562 -11534850
7000691337 hypothetical protein b1501 (db:pir2.dat) H64903 H64903
Escherichia coli 562 -11534850 223850 formate dehydrogenase a chain ec 1.2.1.2 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #301(34.0-34.3 min.)) (nt:orf_id:o301#3; similar to (swissprot accession) (le:5898) (re:8177) (di:complement) D90792 D90792 g1742462 Escherichia coli 562 -11534850 300587 b1501 putative oxidoreductase:major subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 137 of 400 of the completegenome.) (nt:f759; this 759 aa orf is 32 pct identical (41 gaps)) (le:4784) (re:7063) (di:complement) AE000247 AE000247 g1787778 Escherichia coli 562 -11534850 6500730992 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1501 b1501 Escherichia coli 562 -11534850

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849793	10767	32923	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849798	10768	32924	504	167

Description

5000692285 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1502 b1502 Escherichia coli 562 -11534851
7000691338 probable fimbrial protein b1502 (cl:fimbrial protein fimh) (db:pir2.dat) A64904 A64904 Escherichia coli 562 -11534851 223851 fimh protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #301(34.0-34.3 min.)) (nt:orf_id:o301#4; similar to (swissprot accession) (le:8511) (re:9425) (di:complement) D90792 D90792 g1742463 Escherichia coli 562 -11534851 300596 fimh protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #302(34.1-34.5 min.)) (nt:orf_id:o301#4; similar to (swissprot accession) (le:2555) (re:3469) (di:complement) D90793 D90793 g1742472 Escherichia coli 562 -11534851 300588 b1502 putative adhesin:similar to fimh protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 137 of 400 of the completegenome.) (nt:f304; this 304 aa orf is 47 pct identical (5 gaps)) (le:7397) (re:8311) (di:complement) AE000247 AE000247 g1787779 Escherichia coli 562 -11534851 223859 fimh protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #302(34.1-34.5 min.)) (nt:orf_id:o301#4; similar to (swissprot accession) (le:2555) (re:3469) (di:complement) D90793 D90793 g1742472 Escherichia coli 562 -11534851 6500730993 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1502 b1502 Escherichia coli 562 -11534851

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849813	10769	32925	414	137

Description

GTC ORF with score 99 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c46a5.) (nt:similar to eosinophil peroxidase and) (le:148:548:817:1236) (re:421:770:965:1732) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849819	10770	32926	600	199

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849820	10771	32927	864	287

Description

5000692286 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1503 b1503 Escherichia coli 562 -11534852
7000691339 fimbrial protein precursor b1503 (cl:conserved hypothetical protein b1503) (db:pir2.dat) B64904 B64904 Escherichia coli 562 -11534852
223852 fimg protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #301(34.0-34.3 min.)) (nt:orf_id:o301#5; similar to (swissprot accession) (le:9484) (re:9987) (di:complement) D90792 D90792 g1742464 Escherichia coli 562 -11534852 300597 fimg protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #302(34.1-34.5 min.)) (nt:orf_id:o301#5; similar to (swissprot accession) (le:3528) (re:4031) (di:complement) D90793 D90793 g1742473 Escherichia coli 562 -11534852 300589 b1503 putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 137 of 400 of the completegenome.) (nt:f167; this 167 aa orf is 57 pct identical (0 gaps)) (le:8370) (re:8873) (di:complement) AE000247 AE000247 g1787780 Escherichia coli 562 -11534852 223860 fimg protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #302(34.1-34.5 min.)) (nt:orf_id:o301#5; similar to (swissprot accession) (le:3528) (re:4031) (di:complement) D90793 D90793 g1742473 Escherichia coli 562 -11534852 6500730994 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1503 b1503 Escherichia coli 562 -11534852

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849836	10772	32928	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849837	10773	32929	348	115

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849841	10774	32930	357	118

Description

5000692287 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1504 b1504 Escherichia coli 562 -11534853
7000691340 probable fimbrial protein b1504 (cl:type 1 fimbrial protein) (db:pir2.dat) C64904 C64904 Escherichia coli 562 -11534853 223853 fimf protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #301(34.0-34.3 min.)) (nt:orf_id:o301#6; similar to (swissprot accession) (le:10000) (re:10530) (di:complement) D90792 D90792 g1742465 Escherichia coli 562 -11534853 300598 fimf protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #302(34.1-34.5 min.)) (nt:orf_id:o301#6; similar to (swissprot accession) (le:4044) (re:4574) (di:complement) D90793 D90793 g1742474 Escherichia coli 562 -11534853 300590 b1504 putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 137 of 400 of the completegenome.) (nt:f176; this 176 aa orf is 45 pct identical (2 gaps)) (le:8886) (re:9416) (di:complement) AE000247 AE000247 g1787781 Escherichia coli 562 -11534853 223861 fimf protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #302(34.1-34.5 min.)) (nt:orf_id:o301#6; similar to (swissprot accession) (le:4044) (re:4574) (di:complement) D90793 D90793 g1742474 Escherichia coli 562 -11534853 6500730995 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1504 b1504 Escherichia coli 562 -11534853

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849843	10775	32931	828	275

Description

5000692288 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1505 b1505 Escherichia coli 562 -11534854
7000691341 outer membrane usher protein homolog b1505 (db:pir2.dat) D64904 D64904 Escherichia coli 562 -11534854 7500960015 b1505 putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 137 of 400 of the completegenome.) (nt:f382; this 382 aa orf is 56 pct identical (0 gaps)) (le:9430) (re:10578) (di:complement) AE000247 AE000247 g1787782 Escherichia coli 562 -11534854 6500730996 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1505 b1505 Escherichia coli 562 -11534854

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849850	10776	32932	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849853	10777	32933	486	161

Description

5000692289 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1506 b1506 Escherichia coli 562 -11534855
7000691342 hypothetical protein b1506 (db:pir2.dat) E64904 E64904
Escherichia coli 562 -11534855 7500960016 b1506 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 138 of 400 of the completegenome.) (nt:f59; this 59 aa orf is 35 pct identical (1 gap)) (le:290) (re:469) (di:complement) AE000248 AE000248 g1787784 Escherichia coli 562 -11534855 6500730997 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1506 b1506 Escherichia coli 562 -11534855

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849854	10778	32934	726	241
<u>Description</u>				

5000692290 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1509 b1509 Escherichia coli 562 -11534856
7000691343 hypothetical protein b1509 (db:pir2.dat) H64904 H64904
Escherichia coli 562 -11534856 223865 adhesin aida-i precursor.
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #302(34.1-34.5 min.)) (nt:orf_id:o302#1; similar to (swissprot accession) (le:8402) (re:9802) (di:complement) D90793 D90793 g1742478 Escherichia coli 562 -11534856 300609 adhesin aida-i precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.)) (nt:orf_id:o302#1; similar to (swissprot accession) (le:1075) (re:2475) (di:complement) D90794 D90794 g1742486 Escherichia coli 562 -11534856 300602 b1509 putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 138 of 400 of the completegenome.) (nt:f466; this 466 aa orf is 39 pct identical (25 gaps)) (le:2598) (re:3998) (di:complement) AE000248 AE000248 g1787787 Escherichia coli 562 -11534856 223872 adhesin aida-i precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.)) (nt:orf_id:o302#1; similar to (swissprot accession) (le:1075) (re:2475) (di:complement) D90794 D90794 g1742486 Escherichia coli 562 -11534856 6500730998 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1509 b1509 Escherichia coli 562 -11534856

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849864	10779	32935	756	251
<u>Description</u>				

6500730999 ydek:orft:b1510 hypothetical protein in hipa 5region:hypothetical 136.5 kd lipoprotein in hipb-uxab intergenic region precursor:orft (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1510 b1510 Escherichia coli 562 -11534857 111302 ydek:orft (de:precursor (orft)) (db:swissprot) YDEK_ECOLI P32051 ESCHERICHIA COLI 562 -11534857 7000687531 ydek ydek protein:protein t (db:pir2.dat) A64905 A64905 Escherichia coli 562 -11534857 7500922251 ydek orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 138 of 400 of the completegenome.) (nt:f1325; 99 pct identical to ydek_ecoli sw:) (le:4042) (re:8019) (di:complement) AE000248 AE000248 g1787788 Escherichia coli 562 -11534857 5000692291 (de:(ecoli_1470) (pn:hypothetical 65) (gn:ydek) (gtcfc:13.7:14.1) (ec:) (ydek_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1470 ECOLI_1470 Escherichia coli 562 10123360

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849871	10780	32936	903	300

Description

6500731000 ydev:b1511 hypothetical protein:hypothetical sugar kinase in hipb-uxab intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1511 b1511 Escherichia coli 562 -11534858
4000707672 ydev (de:hypothetical sugar kinase in hipb-uxab intergenic region) (db:swissprot) YDEV_ECOLI P77432 ESCHERICHIA COLI 562 -11534858
7000687532 ydev sugar kinase homolog ydev (db:pir2.dat) B64905 B64905 Escherichia coli 562 -11534858 223867 xylulose kinase ec 2.7.1.17 xylulokinase . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #302(34.1-34.5 min.)) (nt:orf_id:o302#4; similar to (swissprot accession) (le:14356) (re:15948) (di:complement) D90793 D90793 g1742480 Escherichia coli 562 -11534858 300611 xylulose kinase ec 2.7.1.17 xylulokinase . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.)) (nt:orf_id:o302#4; similar to (swissprot accession) (le:7029) (re:8621) (di:complement) D90794 D90794 g1742488 Escherichia coli 562 -11534858 300604 ydev putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 138 of 400 of the completegenome.) (nt:f530; this 530 aa orf is 25 pct identical (21 gaps)) (le:8550) (re:10142) (di:complement) AE000248 AE000248 g1787789 Escherichia coli 562 -11534858 223874 xylulose kinase ec 2.7.1.17 xylulokinase . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.)) (nt:orf_id:o302#4; similar to (swissprot accession) (le:7029) (re:8621) (di:complement) D90794 D90794 g1742488 Escherichia coli 562 -11534858 5000692292 (de:(ecoli_1471) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1471 ECOLI_1471 Escherichia coli 562 10119670

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849883	10781	32937	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849886	10782	32938	663	220

Description

5000692293 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1512 b1512 Escherichia coli 562 -11534859
 7500922259 ydew (de:hypothetical transcriptional regulator in hipb-uxab intergenic region) (db:swissprot) YDEW_ECOLI P76141 ESCHERICHIA COLI 562 -11534859 7000691344 probable transcription regulator ydew (db:pir2.dat) C64905 C64905 Escherichia coli 562 -11534859 7500922261 ydew putative transcriptional regulator:sorc family (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 139 of 400 of the completegenome.) (nt:f317; this 317 aa orf is 27 pct identical (16 gaps)) (le:70) (re:1023) (di:complement) AE000249 AE000249 g1787791 Escherichia coli 562 -11534859 6500731001 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1512 b1512 Escherichia coli 562 -11534859

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849887	10783	32939	294	97

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849888	10784	32940	378	126

Description

5000692294 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1513 b1513 Escherichia coli 562 -11534860
7500922262 ydex (de:hypothetical abc transporter atp-binding protein ydex) (db:swissprot) YDEX_ECOLI P77257 ESCHERICHIA COLI 562 -11534860 7000691345 probable sugar transport atp-binding protein b1513 (cl:atp-binding cassette homology) (db:pir2.dat) D64905 D64905 Escherichia coli 562 -11534860 223876 ribose transport atp-binding protein rbsa. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.)) (nt:orf_id:o302-303#1; similar to (swissprot accession) (le:9903) (re:11438) (di:direct) D90794 D90794 g1742490 Escherichia coli 562 -11534860 7500922264 b1513 putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 139 of 400 of the completegenome.) (nt:o511; this 511 aa orf is 39 pct identical (24 gaps)) (le:1272) (re:2807) (di:direct) AE000249 AE000249 g1787792 Escherichia coli 562 -11534860 7500922265 ego10a aerobic growth essential protein (fn:essential for aerobic growth) (db:genpept-bct2) (de:escherichia coli aerobic growth essential protein (ego10a) gene,complete cds.) (le:1) (re:1536) (di:direct) AF089855 AF089855 g3661533 Escherichia coli 562 -11534860 300613 ribose transport atp-binding protein rbsa. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.)) (nt:orf_id:o302-303#1; similar to (swissprot accession) (le:9903) (re:11438) (di:direct) D90794 D90794 g1742490 Escherichia coli 562 -11534860
6500731002 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1513 b1513 Escherichia coli 562 -11534860

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849893	10785	32941	762	253

Description

5000692295 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1514 b1514 Escherichia coli 562 -11534861
7500922266 ydey (de:hypothetical abc transporter permease protein ydey) (db:swissprot) YDEY_ECOLI P77672 ESCHERICHIA COLI 562 -11534861 7000691346
probable sugar transport permease protein b1514 (cl:l-arabinose transport system permease arah) (db:pir2.dat) E64905 E64905 Escherichia coli 562 -11534861 223877 arah l-arabinose transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.)) (nt:orf_id:o303#2; similar to (swissprot accession) (le:11432) (re:12460) (di:direct) D90794 D90794 g1742491 Escherichia coli 562 -11534861
7500922268 ydey putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 139 of 400 of the completegenome.) (nt:o342; this 342 aa orf is 30 pct identical (5 gaps)) (le:2801) (re:3829) (di:direct) AE000249 AE000249 g1787793 Escherichia coli 562 -11534861 300614 arah l-arabinose transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.)) (nt:orf_id:o303#2; similar to (swissprot accession) (le:11432) (re:12460) (di:direct) D90794 D90794 g1742491 Escherichia coli 562 -11534861 6500731003 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1514 b1514 Escherichia coli 562 -11534861

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849909	10786	32942	663	220
<u>Description</u>				
5000692296 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1515 b1515 Escherichia coli 562 -11534862				
7500922269 ydez (de:hypothetical abc transporter permease protein ydez) (db:swissprot) YDEZ_ECOLI P77651 ESCHERICHIA COLI 562 -11534862 7000691347 probable sugar transport permease protein b1515 (cl:l-arabinose transport system permease arah) (db:pir2.dat) F64905 F64905 Escherichia coli 562 -11534862 223878 ribose transport system permease protein rbsc. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.)) (nt:orf_id:o303-4#1; similar to (swissprot accession) (le:12460) (re:13452) (di:direct) D90794 D90794 g1742492 Escherichia coli 562 -11534862				
7500922271 ydez putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 139 of 400 of the completegenome.) (nt:o330; this 330 aa orf is 37 pct identical (6 gaps)) (le:3829) (re:4821) (di:direct) AE000249 AE000249 g1787794 Escherichia coli 562 -11534862 300615 ribose transport system permease protein rbsc. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #303(34.3-34.6 min.)) (nt:orf_id:o303-4#1; similar to (swissprot accession) (le:12460) (re:13452) (di:direct) D90794 D90794 g1742492 Escherichia coli 562 -11534862 6500731004 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1515 b1515 Escherichia coli 562 -11534862				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849913	10787	32943	726	241
<u>Description</u>				
5000692297 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1516 b1516 Escherichia coli 562 -11534863				
7000691348 sugar-binding protein homolog b1516 precursor (db:pir2.dat) G64905 G64905 Escherichia coli 562 -11534863 7500960017 b1516 putative lacI-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 139 of 400 of the completegenome.) (nt:o340; this 340 aa orf is 25 pct identical (15 gaps)) (le:4833) (re:5855) (di:direct) AE000249 AE000249 g1787795 Escherichia coli 562 -11534863 6500731005 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1516 b1516 Escherichia coli 562 -11534863				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849931	10788	32944	264	87
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849946	10789	32945	330	109
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849957	10790	32946	417	138
<u>Description</u>				

6500731006 yneb:b1517 hypothetical protein:hypothetical 31.9 kd protein in hipb-uxab intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1517 b1517 Escherichia coli 562 -11534864
 4000708199 yneb (de:hypothetical 31.9 kd protein in hipb-uxab intergenic region) (db:swissprot) YNEB_ECOLI P76143 ESCHERICHIA COLI 562 -11534864
 7000688160 conserved hypothetical protein b1517 (db:pir2.dat) H64905 H64905 Escherichia coli 562 -11534864 7500951780 yneb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 139 of 400 of the completegenome.) (nt:o291; this 291 aa orf is 40 pct identical (6 gaps)) (le:5882) (re:6757) (di:direct) AE000249 AE000249 g1787796 Escherichia coli 562 -11534864 5000692298 (de:(ecoli_1477) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1477 ECOLI_1477 Escherichia coli 562 10123363

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849960	10791	32947	678	225
<u>Description</u>				

5000692299 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1518 b1518 Escherichia coli 562 -11534865
 7500951781 yneb (de:hypothetical 11.3 kd protein in hipb-uxab intergenic region) (db:swissprot) YNEC_ECOLI P76144 ESCHERICHIA COLI 562 -11534865
 7000691349 hypothetical protein b1518 (db:pir2.dat) A64906 A64906 Escherichia coli 562 -11534865 7500951783 b1518 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 139 of 400 of the completegenome.) (nt:o96; this 96 aa orf is 31 pct identical (1 gap)) (le:6781) (re:7071) (di:direct) AE000249 AE000249 g1787797 Escherichia coli 562 -11534865 6500731007 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1518 b1518 Escherichia coli 562 -11534865

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849972	10792	32948	507	168

Description

GTC ORF with score 111 to: (or:Boreogadus saida) (db:genpept-vrt)
 (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene,
 complete cds.) (nt:cleavage of polyprotein at conserved spacers r or)
 (le:209:281) (re:211:1801) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849980	10793	32949	582	193

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849982	10794	32950	711	236

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501849992	10795	32951	390	129

Description

5000692300 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli) b1519 b1519 Escherichia coli 562 -11534866
 7000691350 biotin biosynthesis protein homolog b1519 (cl:bioc homology)
 (db:pir2.dat) B64906 B64906 Escherichia coli 562 -11534866 7500960018 b1519
 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2)
 (de:escherichia coli k-12 mg1655 section 139 of 400 of the completgenome.)
 (nt:o252; this 252 aa orf is 28 pct identical (18 gaps)) (le:7128) (re:7886)
 (di:direct) AE000249 AE000249 g1787798 Escherichia coli 562 -11534866
 6500731008 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli) b1519 b1519 Escherichia coli 562 -11534866

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501849997	10796	32952	1857	618

Description

5000692301 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1520 b1520 Escherichia coli 562 -11534867
 7000691351 probable membrane protein b1520 (db:pir2.dat) C64906 C64906 Escherichia coli 562 -11534867 7500960019 b1520 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 139 of 400 of the completegenome.) (nt:f321; this 321 aa orf is 27 pct identical (11 gaps)) (le:7890) (re:8855) (di:complement) AE000249 AE000249 g1787799 Escherichia coli 562 -11534867 6500731009 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1520 b1520 Escherichia coli 562 -11534867

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850007	10797	32953	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850024	10798	32954	666	221

Description

5000692302 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1522 b1522 Escherichia coli 562 -11534868
 7000691352 probable membrane protein b1522 (db:pir2.dat) E64906 E64906 Escherichia coli 562 -11534868 7500960020 b1522 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:f315; uug start; this 315 aa orf is 28 pct) (le:144) (re:1091) (di:complement) AE000250 AE000250 g1787802 Escherichia coli 562 -11534868 6500731010 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1522 b1522 Escherichia coli 562 -11534868

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850047	10799	32955	402	133

Description

5000692303 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1523 b1523 Escherichia coli 562 -11534869
7500951786 yneg (de:hypothetical 13.5 kd protein in uxab-marc intergenic region) (db:swissprot) YNEG_ECOLI P76148 ESCHERICHIA COLI 562 -11534869
7000691353 hypothetical protein b1523 (db:pir2.dat) F64906 F64906 Escherichia coli 562 -11534869 7500951788 b1523 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:f119; this 119 aa orf is 25 pct identical (6 gaps)) (le:1203) (re:1562) (di:complement) AE000250 AE000250 g1787803 Escherichia coli 562 -11534869 6500731011 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1523 b1523 Escherichia coli 562 -11534869

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850059	10800	32956	525	174

Description

6500731012 yneh:b1524 hypothetical protein:hypothetical 33.5 kd protein in uxab-marr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1524 b1524 Escherichia coli 562 -11534870
5500686627 yneh (de:hypothetical 33.5 kd protein in uxab-marr intergenic region) (db:swissprot) YNEH_ECOLI P77470 ESCHERICHIA COLI 562 -11534870
7000688163 yneh glutaminase homolog yneh (cl:hypothetical protein b1524) (db:pir2.dat) G64906 G64906 Escherichia coli 562 -11534870 223882 glutaminase:kidney isoform precursor ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #304(34.6-34.9 min.)) (nt:orf_id:o304#10; similar to (swissprot accession) (le:8191) (re:9117) (di:complement) D90795 D90795 g1742497 Escherichia coli 562 -11534870 223890 glutaminase:kidney isoform precursor ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #305(34.7-35.1 min.)) (nt:orf_id:o304#10; similar to (swissprot accession) (le:1474) (re:2400) (di:complement) D90796 D90796 g1742506 Escherichia coli 562 -11534870 300619 yneh putative glutaminase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:f308; this 308 aa orf is 38 pct identical (6 gaps)) (le:1562) (re:2488) (di:complement) AE000250 AE000250 g1787804 Escherichia coli 562 -11534870 5000692304 (de:ecoli_1484) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) ECOLI_1484 ECOLI_1484 Escherichia coli 562 10119679

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850061	10801	32957	432	144

Description

5000692305 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1525 b1525 Escherichia coli 562 -11534871
7000691354 aldehyde dehydrogenase homolog b1525 (cl:aldehyde dehydrogenase (nad+):aldehyde dehydrogenase homology) (db:pir2.dat) H64906 H64906
Escherichia coli 562 -11534871 7500960021 b1525 putative aldehyde dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:f470; this 470 aa orf is 32 pct identical (3 gaps)) (le:2552) (re:3964) (di:complement) AE000250 AE000250 g1787805 Escherichia coli 562 -11534871
6500731013 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1525 b1525 Escherichia coli 562 -11534871

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850063	10802	32958	291	96

Description

6500731014 ynej:b1526 hypothetical protein:hypothetical transcriptional regulator in uxab-marr intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1526 b1526 Escherichia coli 562 -11534872 4000708150 ynej (de:hypothetical transcriptional regulator in uxab-marr intergenic region) (db:swissprot) YNEJ_ECOLI P77309 ESCHERICHIA COLI 562 -11534872 7000688164 ynej probable transcription regulator ynej (cl:pseudomonas putida regulatory protein catr) (db:pir2.dat) A64907 A64907 Escherichia coli 562 -11534872 223885 pectinase gene transcriptional regulator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #304(34.6-34.9 min.)) (nt:orf_id:o304#13; similar to (swissprot accession) (le:10668) (re:11549) (di:direct) D90795 D90795 g1742500 Escherichia coli 562 -11534872 223893 pectinase gene transcriptional regulator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #305(34.7-35.1 min.)) (nt:orf_id:o304#13; similar to (swissprot accession) (le:3951) (re:4832) (di:direct) D90796 D90796 g1742509 Escherichia coli 562 -11534872 300622 ynej putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:o293; this 293 aa orf is 27 pct identical (10 gaps)) (le:4041) (re:4922) (di:direct) AE000250 AE000250 g1787806 Escherichia coli 562 -11534872 5000692306 (de:(ecoli_1486) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1486 ECOLI_1486 Escherichia coli 562 10119682

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850065	10803	32959	405	134

Description

5000692307 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1527 b1527 Escherichia coli 562 -11534873
7000691355 hypothetical protein b1527 (db:pir2.dat) B64907 B64907
Escherichia coli 562 -11534873 7500960022 b1527 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:o371; this 371 aa orf is 31 pct identical (7 gaps)) (le:5000) (re:6115) (di:direct) AE000250 AE000250
g1787807 Escherichia coli 562 -11534873 6500731015 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1527 b1527 Escherichia coli 562 -11534873

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850066	10804	32960	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850069	10805	32961	591	196

Description

6500731016 ydea:b1528 hypothetical protein in marr 5region:hypothetical 42.5 kd protein in uxab-marr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1528 b1528 Escherichia coli 562 -11534874 111281 ydea (de:hypothetical 42.5 kd protein in uxab-marr intergenic region) (db:swissprot) YDEA_ECOLI P31122 ESCHERICHIA COLI 562 -11534874 7000687525 ydea chloramphenicol resistance protein homolog ydea (cl:streptomyces lividans chloramphenicol resistance protein) (db:pir2.dat) C64907 C64907 Escherichia coli 562 -11534874 223886 ydea protein araj precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #304(34.6-34.9 min.)) (nt:orf_id:o304#15; similar to (swissprot accession) (le:12892) (re:14082) (di:direct) D90795 D90795 g1742501 Escherichia coli 562 -11534874 223894 ydea protein araj precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #305(34.7-35.1 min.)) (nt:orf_id:o304#15; similar to (swissprot accession) (le:6175) (re:7365) (di:direct) D90796 D90796 g1742510 Escherichia coli 562 -11534874 300623 ydea putative resistance / regulatory protein (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:o396; 100 pct identical to fragment ydea_ecoli) (le:6265) (re:7455) (di:direct) AE000250 AE000250 g1787808 Escherichia coli 562 -11534874 5000692308 (de:(ecoli_1488) (pn:hypothetical protein in marr 5"region:fragment) (gn:ydea) (gtcfc:13.7:14.1) (ec:) (ydea_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1488 ECOLI_1488 Escherichia coli 562 10119683

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850075	10806	32962	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850085	10807	32963	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850087	10808	32964	1008	335

Description

6500731017 ydeb:b1529 hypothetical protein in marr 5region:hypothetical 23.6 kd protein in uxab-marr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1529 b1529 Escherichia coli 562 -11534875 111285 marc (de:multiple antibiotic resistance protein marc) (db:swissprot) MARC_ECOLI P31123 ESCHERICHIA COLI 562 -11534875 7000687526 ydeb membrane protein ydeb (db:pir2.dat) D64907 D64907 Escherichia coli 562 -11534875 7500922242 marc multiple antibiotic resistance protein (db:genpept-bct1) (de:escherichia coli multiple antibiotic resistance protein (marc),multiple antibiotic resistance protein (marr), and multipleantibiotic resistance protein (mara) genes, complete cds.) (le:569) (re:1234) (di:complement) ECOMARAR M96235 g3132835 Escherichia coli 562 -11534875 7500922241 ydeb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:f221; residues 66-221 are 100 pct identical) (le:7480) (re:8145) (di:complement) AE000250 AE000250 g1787809 Escherichia coli 562 -11534875 5000692309 (de:(ecoli_1489) (pn:hypothetical 16) (gn:ydeb) (gtcfc:13.7:14.1) (ec:) (ydeb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1489 ECOLI_1489 Escherichia coli 562 10123372

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850094	10809	32965	240	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850096	10810	32966	264	87

Description

6500731018 yded:b1533 hypothetical 28.7 kd protein in marb-dcp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1533 b1533 Escherichia coli 562 -11534876 111288 yded (de:hypothetical 28.7 kd protein in marb-dcp intergenic region) (db:swissprot) YDED_ECOLI P31125 ESCHERICHIA COLI 562 -11534876 7000687527 yded probable membrane protein yded (db:pir2.dat) H64907 H64907 Escherichia coli 562 -11534876 223899 yded (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #305(34.7-35.1 min.)) (nt:orf_id:o306#4; similar to (swissprot accession) (le:9385) (re:10185) (di:complement) D90796 D90796 g1742515 Escherichia coli 562 -11534876 223912 yded (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #306(34.8-35.1 min.)) (nt:orf_id:o306#4; similar to (swissprot accession) (le:2834) (re:3634) (di:complement) D90797 D90797 g1742529 Escherichia coli 562 -11534876 300631 yded orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 140 of 400 of the completegenome.) (nt:f266; 100 pct identical to yded_ecoli sw:) (le:9475) (re:10275) (di:complement) AE000250 AE000250 g1787813 Escherichia coli 562 -11534876 5000692310 (de:(ecoli_1493) (pn:hypothetical 28) (gn:yded) (gtcfc:13.7:14.1) (ec:) (yded_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1493 ECOLI_1493 Escherichia coli 562 10053018

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850103	10811	32967	249	82

Description

6500731019 ydef:ydee:b1534 hypothetical protein in marb-dcp intergenic region: hypothetical 42.7 kd protein in marb-dcp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1534 b1534 Escherichia coli 562 -11534877 111290 ydee (de:hypothetical 42.7 kd protein in marb-dcp intergenic region) (db:swissprot) YDEE_ECOLI P31126 ESCHERICHIA COLI 562 -11534877 7000687528 ydee membrane protein ydee (db:pir2.dat) A64908 A64908 Escherichia coli 562 -11534877 7500922247 ydef putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 141 of 400 of the completegenome.) (nt:o395; residues 157-395 are 100 pct identical) (le:147) (re:1334) (di:direct) AE000251 AE000251 g1787815 Escherichia coli 562 -11534877 5000692311 (de:(ecoli_1494) (pn:hypothetical 25) (gn:ydef) (gtcfc:13.7:14.1) (ec:) (ydef_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1494 ECOLI_1494 Escherichia coli 562 10123373

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850108	10812	32968	255	84

Description

6500731020 ydei:b1536 hypothetical 14.1 kd protein in marb-dcp intergenic region:hypothetical 14.1 kd protein in marb-dcp intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1536 b1536 Escherichia coli 562 -11534878 111299 ydei (de:hypothetical 14.1 kd protein in marb-dcp intergenic region precursor) (db:swissprot) YDEI_ECOLI P31130 ESCHERICHIA COLI 562 -11534878 7000687529 ydei ydei protein precursor (cl:hypothetical protein b3024) (db:pir2.dat) C64908 C64908 Escherichia coli 562 -11534878 223903 ydei (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #305(34.7-35.1 min..)) (nt:orf_id:o306#8; similar to (swissprot accession) (le:13252) (re:13644) (di:complement) D90796 D90796 g1742519 Escherichia coli 562 -11534878 223916 ydei (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #306(34.8-35.1 min..)) (nt:orf_id:o306#8; similar to (swissprot accession) (le:6701) (re:7093) (di:complement) D90797 D90797 g1742533 Escherichia coli 562 -11534878 300635 ydei orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 141 of 400 of the completegenome.) (nt:f130; 100 pct identical to ydei_ecoli sw: p31130) (le:2920) (re:3312) (di:complement) AE000251 AE000251 g1787817 Escherichia coli 562 -11534878 5000692313 (de:(ecoli_1496) (pn:hypothetical 14) (gn:ydei) (gtcfc:13.7:14.1) (ec:) (ydei_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1496 ECOLI_1496 Escherichia coli 562 10053029

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850109	10813	32969	267	88

Description

6500731021 ydej:b1537 hypothetical 18.3 kd protein in marb-dcp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1537 b1537 Escherichia coli 562 -11534879 111301 ydej (de:hypothetical 18.3 kd protein in marb-dcp intergenic region) (db:swissprot) YDEJ_ECOLI P31131 ESCHERICHIA COLI 562 -11534879 7000687530 ydej ydej protein (cl:conserved hypothetical protein aq_1996) (db:pir2.dat) D64908 D64908 Escherichia coli 562 -11534879 223904 ydej (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #305(34.7-35.1 min.)) (nt:orf_id:o306#9; similar to (swissprot accession) (le:13920) (re:14438) (di:direct) D90796 D90796 g1742520 Escherichia coli 562 -11534879 223917 ydej (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #306(34.8-35.1 min.)) (nt:orf_id:o306#9; similar to (swissprot accession) (le:7369) (re:7887) (di:direct) D90797 D90797 g1742534 Escherichia coli 562 -11534879 300636 ydej orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 141 of 400 of the completegenome.) (nt:o172; 100 pct identical to ydej_ecoli sw: p31131) (le:3588) (re:4106) (di:direct) AE000251 AE000251 g1787818 Escherichia coli 562 -11534879 5000692314 (de:(ecoli_1497) (pn:hypothetical 18) (gn:ydej) (gtcfc:13.7:14.1) (ec:) (ydej_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1497 ECOLI_1497 Escherichia coli 562 10053031

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850110	10814	32970	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850122	10815	32971	744	247

Description

5000692316 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1540 b1540 Escherichia coli 562 -11534880
7000687535 ydfh (de:hypothetical transcriptional regulator in dcp-noha intergenic region) (db:swissprot) YDFH_ECOLI P77577 ESCHERICHIA COLI 562 -11534880 7000687536 ydfh probable transcription regulator ydfh (cl:hypothetical protein b1540) (db:pir2.dat) G64908 G64908 Escherichia coli 562 -11534880 223920 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #306(34.8-35.1 min.)) (nt:orf_id:o306#12; similar to (swissprot accession) (le:10948) (re:11634) (di:direct) D90797 D90797 g1742537 Escherichia coli 562 -11534880 300643 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o306#12; similar to (swissprot accession) (le:347) (re:1033) (di:direct) D90798 D90798 g1742542 Escherichia coli 562 -11534880 300639 ydfh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 141 of 400 of the completegenome.) (nt:o228; this 228 aa orf is 31 pct identical (2 gaps)) (le:7167) (re:7853) (di:direct) AE000251 AE000251 g1787821 Escherichia coli 562 -11534880 223924 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o306#12; similar to (swissprot accession) (le:347) (re:1033) (di:direct) D90798 D90798 g1742542 Escherichia coli 562 -11534880 6500731022 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1540 b1540 Escherichia coli 562 -11534880

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850123	10816	32972	426	141

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850125	10817	32973	447	148

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850139	10818	32974	690	229

Description

5000692317 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1541 b1541 Escherichia coli 562 -11534881
7500922296 ydfz (de:hypothetical 7.3 kd protein in dcp-pinq intergenic region) (db:swissprot) YDFZ_ECOLI P76153 ESCHERICHIA COLI 562 -11534881
7000691356 hypothetical protein b1541 (db:pir2.dat) H64908 H64908 Escherichia coli 562 -11534881 7500922298 b1541 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 141 of 400 of the completegenome.) (nt:o67; this 67 aa orf is 33 pct identical (2 gaps)) (le:8030) (re:8233) (di:direct) AE000251 AE000251 g1787822 Escherichia coli 562 -11534881 6500731023 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1541 b1541 Escherichia coli 562 -11534881

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850148	10819	32975	222	73

Description

6500731024 ydfi:b1542 hypothetical protein:hypothetical 53.7 kd protein in dcp-noha intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1542 b1542 Escherichia coli 562 -11534882
4000707868 ydfi (de:hypothetical 53.7 kd protein in dcp-noha intergenic region) (db:swissprot) YDFI_ECOLI P77260 ESCHERICHIA COLI 562 -11534882
7000687537 hypothetical protein b1542 (cl:conserved hypothetical protein yel070w) (db:pir2.dat) A64909 A64909 Escherichia coli 562 -11534882 223921 d-mannionate oxidoreductase ec 1.1.1.57 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #306(34.8-35.1 min.)) (nt:orf_id:o306#14; similar to (swissprot accession) (le:12049) (re:13509) (di:complement) D90797 D90797 g1742538 Escherichia coli 562 -11534882 300644 d-mannionate oxidoreductase ec 1.1.1.57 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o306#14; similar to (swissprot accession) (le:1448) (re:2908) (di:complement) D90798 D90798 g1742543 Escherichia coli 562 -11534882 300640 ydfi putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 141 of 400 of the completegenome.) (nt:f486; this 486 aa orf is 58 pct identical (4 gaps)) (le:8268) (re:9728) (di:complement) AE000251 AE000251 g1787823 Escherichia coli 562 -11534882 223925 d-mannionate oxidoreductase ec 1.1.1.57 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o306#14; similar to (swissprot accession) (le:1448) (re:2908) (di:complement) D90798 D90798 g1742543 Escherichia coli 562 -11534882 5000692318 (de:(ecoli_1502) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1502 ECOLI_1502 Escherichia coli 562 10119691

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850149	10820	32976	756	251

Description

5000692319 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1543 b1543 Escherichia coli 562 -11534883
7500922274 ydfj (de:region) (db:swissprot) YDFJ_ECOLI P77228 ESCHERICHIA COLI 562 -11534883 7000691357 hypothetical protein b1543 (cl:citrate utilization determinant) (db:pir2.dat) B64909 B64909 Escherichia coli 562 -11534883 223926 proline/betaine transporter proline porter ii (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o308#1; similar to (swissprot accession) (le:2997) (re:4280) (di:complement) D90798 D90798 g1742544 Escherichia coli 562 -11534883 7500922276 b1543 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 141 of 400 of the completgenome.) (nt:f427; this 427 aa orf is 31 pct identical (22 gaps)) (le:9817) (re:11100) (di:complement) AE000251 AE000251 g1787824 Escherichia coli 562 -11534883 300645 proline/betaine transporter proline porter ii (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o308#1; similar to (swissprot accession) (le:2997) (re:4280) (di:complement) D90798 D90798 g1742544 Escherichia coli 562 -11534883 6500731025 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1543 b1543 Escherichia coli 562 -11534883

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850161	10821	32977	561	187

Description

5000692320 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1544 b1544 Escherichia coli 562 -11534884
7500922277 ydfk (de:hypothetical 10.1 kd protein in dcp-noha intergenic region) (db:swissprot) YDFK_ECOLI P76154 ESCHERICHIA COLI 562 -11534884 7000691358 hypothetical protein b1544 (db:pir2.dat) C64909 C64909 Escherichia coli 562 -11534884 7500922279 ydfk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completgenome.) (nt:o88; this 88 aa orf is 32 pct identical (4 gaps)) (le:654) (re:920) (di:direct) AE000252 AE000252 g1787826 Escherichia coli 562 -11534884 6500731026 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1544 b1544 Escherichia coli 562 -11534884

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850164	10822	32978	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850166	10823	32979	483	160

Description

5000692321 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1545 b1545 Escherichia coli 562 -11534885
 7000689431 hypothetical protein b1545 (cl:transposase repressor) (db:pir2.dat) D64909 D64909 Escherichia coli 562 -11534885 223927
 transposon tn2501 resolvase. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o308#2; similar to (swissprot accession) (le:5617) (re:6207) (di:direct) D90798 D90798 g1742545 Escherichia coli 562 -11534885 300646 b1545 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:o196; this 196 aa orf is 75 pct identical (0 gaps)) (le:1237) (re:1827) (di:direct) AE000252 AE000252 g1787827 Escherichia coli 562 -11534885 6500731027 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1545 b1545 Escherichia coli 562 -11534885

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850169	10824	32980	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850175	10825	32981	396	131

Description

GTC ORF with score 132 to: (sr:pyrococcus horikoshii (strain:ot3) dna) (db:genpept-bct2) (de:pyrococcus horikoshii ot3 genomic dna, 544001-777000 nt. position(3/7).) (nt:similar to swiss_prot:p39359 percent identity:) (le:210642) (re:211505) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850187	10826	32982	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850188	10827	32983	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850209	10828	32984	486	161

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850210	10829	32985	363	120

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850218	10830	32986	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850244	10831	32987	1584	527

Description

6500731028 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1546 b1546 Escherichia coli 562 -11534886
7500922280 ydfm (de:hypothetical 21.3 kd protein in dcp-noha intergenic region) (db:swissprot) YDFM_ECOLI P76155 ESCHERICHIA COLI 562 -11534886
7000687538 ydfm ynac protein:phage protein-related:ydfm protein (cl:phage t4 tail fiber assembly protein gp38) (db:pir2.dat) E64909 E64909 Escherichia coli 562 -11534886 223928 tail fiber assembly protein g (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min..)) (nt:orf_id:o308#3; similar to (pir accession number) (le:6304) (re:6879) (di:complement) D90798 D90798 g1742546 Escherichia coli 562 -11534886
7500922282 ydfm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:f191; this 191 aa orf is 94 pct identical (0 gaps)) (le:1925) (re:2500) (di:complement) AE000252 AE000252 g2367120 Escherichia coli 562 -11534886 300647 tail fiber assembly protein g (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min..)) (nt:orf_id:o308#3; similar to (pir accession number) (le:6304) (re:6879) (di:complement) D90798 D90798 g1742546 Escherichia coli 562 -11534886

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850249	10832	32988	732	243

Description

5000692323 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1547 b1547 Escherichia coli 562 -11534887
7000691359 hypothetical protein b1547 (cl:phage t4 tail fiber protein gp37) (db:pir2.dat) F64909 F64909 Escherichia coli 562 -11534887 223929 37 tail fiber protein gp37. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min..)) (nt:orf_id:o308#4; similar to (swissprot accession) (le:6879) (re:7841) (di:complement) D90798 D90798 g1742547 Escherichia coli 562 -11534887 300648 b1547 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:f320; this 320 aa orf is 75 pct identical (23 gaps)) (le:2500) (re:3462) (di:complement) AE000252 AE000252 g1787829 Escherichia coli 562 -11534887 6500731029 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1547 b1547 Escherichia coli 562 -11534887

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850254	10833	32989	696	231

Description

6500731030 ydfo:b1549 hypothetical protein:hypothetical 17.0 kd protein in noha-cspj intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1549 b1549 Escherichia coli 562 -11534888
7000687539 ydfo ydfo protein (cl:ydfo protein) (db:pir2.dat) H64909 H64909 Escherichia coli 562 -11534888 7500960024 ydfo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:ol41) (le:4647) (re:5072) (di:direct) AE000252 AE000252 g1787831 Escherichia coli 562 -11534888 4000708201 ydfo_ecoli (de:(gn:ydfo) (de:hypothetical 17.0 kd protein in noha-cspj intergenic region) (sp:p76156)) P76156 P76156 Escherichia coli 562 -11534888 5000692325 (de:(ecoli_1509) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1509 ECOLI_1509 Escherichia coli 562 10123378

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850258	10834	32990	594	198

Description

5000692326 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1550 b1550 Escherichia coli 562 -11534889
7502852245 ydfy (de:hypothetical 6.7 kd protein in noha-cspi intergenic region) (db:swissprot) YDFY_ECOLI P77695 ESCHERICHIA COLI 562 -11534889 7000691360 hypothetical protein b1550 (db:pir2.dat) A64910 A64910 Escherichia coli 562 -11534889 223931 yccl (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.).) (nt:orf_id:o308#7; similar to (swissprot accession) (le:9603) (re:9779) (di:complement) D90798 D90798 g1742549 Escherichia coli 562 -11534889 300650 b1550 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:f58; this 58 aa orf is 32 pct identical (0 gaps)) (le:5224) (re:5400) (di:complement) AE000252 AE000252 g1787832 Escherichia coli 562 -11534889 6500731031 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1550 b1550 Escherichia coli 562 -11534889

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850262	10835	32991	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850278	10836	32992	1590	529

Description

5000692327 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1551 b1551 Escherichia coli 562 -11534890
7000691361 hypothetical protein b1551 (db:pir2.dat) B64910 B64910
Escherichia coli 562 -11534890 7500960025 b1551 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:f63; this 63 aa orf is 30 pct identical (1 gap)) (le:5569) (re:5760) (di:complement) AE000252 AE000252 g1787833 Escherichia coli 562 -11534890 6500731032 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1551 b1551 Escherichia coli 562 -11534890

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850286	10837	32993	441	146

Description

6500731033 cspj:b1552 hypothetical protein:cold shock-like protein cspj (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1552 b1552 Escherichia coli 562 -11534891 4000707754 cspi:cspj (de:cold shock-like protein cspi) (db:swissprot) CSPI_ECOLI P77605 ESCHERICHIA COLI 562 -11534891 7000684928 cspi:cspj cold shock protein homolog cspi (cl:major cold shock protein:cold shock domain homology) (db:pir2.dat) C64910 C64910 Escherichia coli 562 -11534891 223932 cold shock-like protein cspb. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o308#8; similar to (swissprot accession) (le:10449) (re:10661) (di:complement) D90798 D90798 g1742550 Escherichia coli 562 -11534891 300661 cold shock-like protein cspb. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o308#8; similar to (swissprot accession) (le:422) (re:634) (di:complement) D90799 D90799 g1742561 Escherichia coli 562 -11534891 300651 cspi cold shock-like protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:f70; this 70 aa orf is 72 pct identical (0 gaps)) (le:6070) (re:6282) (di:complement) AE000252 AE000252 g1787834 Escherichia coli 562 -11534891 223942 cold shock-like protein cspb. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o308#8; similar to (swissprot accession) (le:422) (re:634) (di:complement) D90799 D90799 g1742561 Escherichia coli 562 -11534891 5000692328 (de:(ecoli_1512) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1512 ECOLI_1512 Escherichia coli 562 10119700

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850291	10838	32994	534	177

Description

5000692329 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1553 b1553 Escherichia coli 562 -11534892
7000691362 hypothetical protein b1553 (db:pir2.dat) D64910 D64910
Escherichia coli 562 -11534892 7500960026 b1553 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:f165; this 165 aa orf is 27 pct identical (8 gaps)) (le:6645) (re:7142) (di:complement) AE000252 AE000252 g1787835 Escherichia coli 562 -11534892 6500731034 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1553 b1553 Escherichia coli 562 -11534892

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850295	10839	32995	516	171

Description

5000692330 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1554 b1554 Escherichia coli 562 -11534893
7000691363 hypothetical protein b1554 (cl:phage t4 lysozyme homology) (db:pir2.dat) E64910 E64910 Escherichia coli 562 -11534893 7500960027 b1554 putative lysozyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:f177; this 177 aa orf is 32 pct identical (15 gaps)) (le:7139) (re:7672) (di:complement) AE000252 AE000252 g1787836 Escherichia coli 562 -11534893 6500731035 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1554 b1554 Escherichia coli 562 -11534893

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850321	10840	32996	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850345	10841	32997	1293	430

Description

5000692331 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1555 b1555 Escherichia coli 562 -11534894
7500922284 ydfr (de:hypothetical 12.1 kd protein in cspi-cspb intergenic region) (db:swissprot) YDFR_ECOLI P76160 ESCHERICHIA COLI 562 -11534894
7000691364 hypothetical protein b1555 (db:pir2.dat) F64910 F64910 Escherichia coli 562 -11534894 7500922286 b1555 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:f103; this 103 aa orf is 36 pct identical (0 gaps)) (le:7669) (re:7980) (di:complement) AE000252 AE000252 g1787837 Escherichia coli 562 -11534894 6500731036 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1555 b1555 Escherichia coli 562 -11534894

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850357	10842	32998	528	176

Description

5000692332 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1556 b1556 Escherichia coli 562 -11534895
7000691365 lysis protein s.b1556 (db:pir2.dat) G64910 G64910 Escherichia coli 562 -11534895 223933 lysis protein s. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o308#12; similar to (swissprot accession) (le:12364) (re:12654) (di:complement) D90798 D90798 g1742551 Escherichia coli 562 -11534895 300662 lysis protein s. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o308#12; similar to (swissprot accession) (le:2337) (re:2627) (di:complement) D90799 D90799 g1742562 Escherichia coli 562 -11534895 300652 b1556 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 142 of 400 of the completegenome.) (nt:f96; 83 pct identical to 71 amino acids) (le:7985) (re:8275) (di:complement) AE000252 AE000252 g1787838 Escherichia coli 562 -11534895 223943 lysis protein s. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o308#12; similar to (swissprot accession) (le:2337) (re:2627) (di:complement) D90799 D90799 g1742562 Escherichia coli 562 -11534895 6500731037 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1556 b1556 Escherichia coli 562 -11534895

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850364	10843	32999	510	169

Description

5000692334 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1559 b1559 Escherichia coli 562 -11534896
 7000691366 hypothetical protein b1559 (db:pir2.dat) B64911 B64911
 Escherichia coli 562 -11534896 7500960028 b1559 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:f260; this 260 aa orf is 41 pct identical (14 gaps)) (le:241) (re:1023) (di:complement) AE000253 AE000253 g1787842 Escherichia coli 562 -11534896 6500731038 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1559 b1559 Escherichia coli 562 -11534896

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850368	10844	33000	435	144

Description

5000692335 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1560 b1560 Escherichia coli 562 -11534897
 7000691367 hypothetical protein b1560 (db:pir2.dat) C64911 C64911
 Escherichia coli 562 -11534897 7500960029 b1560 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:f362; this 362 aa orf is 27 pct identical (14 gaps)) (le:1007) (re:2095) (di:complement) AE000253 AE000253 g1787843 Escherichia coli 562 -11534897 6500731039 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1560 b1560 Escherichia coli 562 -11534897

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501850371	10845	33001	1848	615

Description

6500731040 rem:b1561 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1561 b1561 Escherichia coli 562 -11534898 300657 rem (de:hypothetical rem protein) (db:swissprot) REM_ECOLI P07010 ESCHERICHIA COLI 562 -11534898 135175 rem hypothetical 9k protein relb operon:hypothetical rem protein (db:pir1.dat) (mp:34 min) QQECR9 D22830 Escherichia coli 562 -11534898 223938 rem (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o308#17; similar to (pir accession number) (le:16645) (re:16896) (di:complement) D90798 D90798 g1742556 Escherichia coli 562 -11534898 300667 rem (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o308#17; similar to (pir accession number) (le:6618) (re:6869) (di:complement) D90799 D90799 g1742567 Escherichia coli 562 -11534898 300689 rem (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o308#17; similar to (pir accession number) (le:3394) (re:3645) (di:complement) D90800 D90800 g1742590 Escherichia coli 562 -11534898 5000692336 (db:genpept-bct1) (de:e. coli relb gene region.) (nt:rem protein (aa 1-83)) (le:1464) (re:1715) (di:direct) ECRELB X02405 g42703 Escherichia coli 562 -11534898 238044 rem orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:f83; 100 pct identical to rem_ecoli sw: p07010) (le:2403) (re:2654) (di:complement) AE000253 AE000253 g1787844 Escherichia coli 562 -11534898 93911 rem (de:hypothetical rem protein) (db:swissprot) REM_ECOLI P07010 ESCHERICHIA COLI 562 -11534898 223948 rem (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o308#17; similar to (pir accession number) (le:6618) (re:6869) (di:complement) D90799 D90799 g1742567 Escherichia coli 562 -11534898 223970 rem (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o308#17; similar to (pir accession number) (le:3394) (re:3645) (di:complement) D90800 D90800 g1742590 Escherichia coli 562 -11534898

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501850388	10846	33002	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850411	10847	33003	369	122

Description

6500731041 rele:b1563 hypothetical rele protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1563 b1563 Escherichia coli 562 -11534899 300659 rele (de:hypothetical rele protein) (db:swissprot) RELE_ECOLI P07008 ESCHERICHIA COLI 562 -11534899 135174 rele hypothetical 11k protein relb operon:hypothetical rele protein (db:pir1.dat) (mp:34 min) QQECR1 B22830 Escherichia coli 562 -11534899 223940 rele (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o308#19; similar to (pir accession number) (le:17340) (re:17627) (di:complement) D90798 D90798 g1742558 Escherichia coli 562 -11534899 300669 rele (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o308#19; similar to (pir accession number) (le:7313) (re:7600) (di:complement) D90799 D90799 g1742569 Escherichia coli 562 -11534899 300691 rele (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o308#19; similar to (pir accession number) (le:4089) (re:4376) (di:complement) D90800 D90800 g1742592 Escherichia coli 562 -11534899 5000692337 (db:genpept-bct1) (de:e. coli relb gene region.) (nt:rele protein (aa 1-95)) (le:733) (re:1020) (di:direct) ECRELB X02405 g42701 Escherichia coli 562 -11534899 238042 rele orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:f95; 100 pct identical to rele_ecoli sw: p07008; cg) (le:3098) (re:3385) (di:complement) AE000253 AE000253 g1787846 Escherichia coli 562 -11534899 93889 rele (de:hypothetical rele protein) (db:swissprot) RELE_ECOLI P07008 ESCHERICHIA COLI 562 -11534899 223950 rele (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o308#19; similar to (pir accession number) (le:7313) (re:7600) (di:complement) D90799 D90799 g1742569 Escherichia coli 562 -11534899 223972 rele (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o308#19; similar to (pir accession number) (le:4089) (re:4376) (di:complement) D90800 D90800 g1742592 Escherichia coli 562 -11534899

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850412	10848	33004	450	149

Description

GTC ORF with score 108 to: (sr:drosophila melanogaster (library: lambda gt10 cDNA) third insta) (db:genpept-inv) (de:drosophila melanogaster photoreceptor ets dna binding domainprotein (yan) mrna, complete cds.) (nt:ets-domain at amino acids 398-479; ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850416	10849	33005	423	140
<u>Description</u>				
5000692338 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1565 b1565 Escherichia coli 562 -11534900				
7500922287 ydfv (de:hypothetical 11.3 kd protein in relb-flxa intergenic region) (db:swissprot) YDFV_ECOLI P76163 ESCHERICHIA COLI 562 -11534900				
7000691368 hypothetical protein b1565 (db:pir2.dat) H64911 H64911 Escherichia coli 562 -11534900 7500922289 b1565 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:o101; this 101 aa orf is 27 pct identical (1 gap)) (le:3649) (re:3954) (di:direct) AE000253 AE000253 g1787848 Escherichia coli 562 -11534900 6500731042 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1565 b1565 Escherichia coli 562 -11534900				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850421	10850	33006	498	165
<u>Description</u>				
6500731043 flxa:b1566 hypothetical protein:flxa protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1566 b1566 Escherichia coli 562 -11534901 1500686934 flxa (de:flxa protein) (db:swissprot) FLXA_ECOLI P77609 ESCHERICHIA COLI 562 -11534901 7000685309 hypothetical protein b1566 (db:pir2.dat) A64912 A64912 Escherichia coli 562 -11534901 223096 flxa flxa (sr:escherichia coli (strain:ej500) dna) (db:genpept-bct1) (de:escherichia coli flxa gene, complete cds.) (le:130) (re:462) (di:direct) D89975 D89975 g1753220 Escherichia coli 562 -11534901 7500881642 flxa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:o110; this 110 aa orf is 25 pct identical (2 gaps)) (le:4157) (re:4489) (di:direct) AE000253 AE000253 g1787849 Escherichia coli 562 -11534901 5000692339 (de:(ecoli_1526) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1526 ECOLI_1526 Escherichia coli 562 10063092				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850426	10851	33007	1128	375

Description

5000692340 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1567 b1567 Escherichia coli 562 -11534902
7500922290 ydfw (de:hypothetical 5.9 kd protein in flxa-dicc intergenic region) (db:swissprot) YDFW_ECOLI P76164 ESCHERICHIA COLI 562 -11534902
7000691369 hypothetical protein b1567 (db:pir2.dat) B64912 B64912
Escherichia coli 562 -11534902 7500922292 b1567 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:f49; this 49 aa orf is 35 pct identical (3 gaps)) (le:4926) (re:5075) (di:complement) AE000253 AE000253
g1787850 Escherichia coli 562 -11534902 6500731044 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1567 b1567 Escherichia coli 562 -11534902

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850442	10852	33008	189	62

Description

5000692341 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1568 b1568 Escherichia coli 562 -11534903
7500922293 ydfx (de:hypothetical 11.0 kd protein in flxa-dicc intergenic region) (db:swissprot) YDFX_ECOLI P76165 ESCHERICHIA COLI 562 -11534903
7000691370 hypothetical protein b1568 (db:pir2.dat) C64912 C64912
Escherichia coli 562 -11534903 7500922295 b1568 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:f96; this 96 aa orf is 26 pct identical (1 gap)) (le:5098) (re:5388) (di:complement) AE000253 AE000253
g1787851 Escherichia coli 562 -11534903 6500731045 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1568 b1568 Escherichia coli 562 -11534903

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850443	10853	33009	297	98

Description

6500731046 ydfa:b1571 hypothetical 5.8 kd protein in dica-dicb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1571 b1571 Escherichia coli 562 -11534904 111312 ydfa (de:hypothetical 5.8 kd protein in dica-dicb intergenic region) (db:swissprot) YDFA_ECOLI P29008 ESCHERICHIA COLI 562 -11534904 163288 ydfa hypothetical 6k protein dica-dicb intergenic region (db:pir2.dat) (mp:35 min) B30383 B30383 Escherichia coli 562 -11534904 223954 ydfa (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o309#3; similar to (pir accession number) (le:10475) (re:10630) (di:direct) D90799 D90799 g1742573 Escherichia coli 562 -11534904 300695 ydfa (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o309#3; similar to (pir accession number) (le:7251) (re:7406) (di:direct) D90800 D90800 g1742596 Escherichia coli 562 -11534904 300673 ydfa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:o51; 100 pct identical to ydfa_ecoli sw:) (le:6260) (re:6415) (di:direct) AE000253 AE000253 g1787854 Escherichia coli 562 -11534904 223976 ydfa (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o309#3; similar to (pir accession number) (le:7251) (re:7406) (di:direct) D90800 D90800 g1742596 Escherichia coli 562 -11534904 5000692342 (de:(ecoli_1531) (pn:hypothetical 5) (gn:ydfa) (gtcfc:13.7:14.1) (ec:) (ydfa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1531 ECOLI_1531 Escherichia coli 562 10053042

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850445	10854	33010	477	158

Description

6500731047 ydfb:b1572 hypothetical protein in dica-dicb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1572 b1572 Escherichia coli 562 -11534905 7000690963 ydfb hypothetical 5k protein dica-dicb intergenic region (db:pir2.dat) (mp:35 min) G64912 G64912 Escherichia coli 562 -11534905 7500959822 ydfb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:o56; 100 pct identical to ydfb_ecoli sw: p29009) (le:6375) (re:6545) (di:direct) AE000253 AE000253 g1787855 Escherichia coli 562 -11534905 5000692343 (de:(ecoli_1532) (pn:hypothetical 4) (gn:ydfb) (gtcfc:13.7:14.1) (ec:) (ydfb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1532 ECOLI_1532 Escherichia coli 562 10123388

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850446	10855	33011	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850447	10856	33012	213	70

Description

6500731048 ydfc:b1573 hypothetical 8.3 kd protein in dica-dicb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1573 b1573 Escherichia coli 562 -11534906 111316 ydfc (de:hypothetical 8.3 kd protein in dica-dicb intergenic region) (db:swissprot) YDFC_ECOLI P21418 ESCHERICHIA COLI 562 -11534906 135179 ydfc hypothetical 8k protein dica-dicb intergenic region (db:pir1.dat) (mp:35 min) Q4ECD8 D30383 Escherichia coli 562 -11534906 223956 ydfc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o309#5; similar to (pir accession number) (le:10790) (re:11008) (di:direct) D90799 D90799 g1742575 Escherichia coli 562 -11534906 300697 ydfc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o309#5; similar to (pir accession number) (le:7566) (re:7784) (di:direct) D90800 D90800 g1742598 Escherichia coli 562 -11534906 300675 ydfc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:o72; 100 pct identical to ydfc_ecoli sw: p21418;) (le:6575) (re:6793) (di:direct) AE000253 AE000253 g1787856 Escherichia coli 562 -11534906 223978 ydfc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o309#5; similar to (pir accession number) (le:7566) (re:7784) (di:direct) D90800 D90800 g1742598 Escherichia coli 562 -11534906 5000692344 (de:(ecoli_1533) (pn:hypothetical 8) (gn:ydfc) (gtcfc:13.7:14.1) (ec:) (ydfc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1533 ECOLI_1533 Escherichia coli 562 10053046

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850464	10857	33013	840	280

Description

6500731049 ydfd:b1576 hypothetical 6.8 kd protein in dicb
3region:hypothetical 6.8 kd protein in dicb-intq intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1576
b1576 Escherichia coli 562 -11534907 300677 ydfd (de:hypothetical 6.8 kd
protein in dicb-intq intergenic region) (db:swissprot) YDFD_ECOLI P29010
ESCHERICHIA COLI 562 -11534907 7000687533 ydfd hypothetical 7k protein dicb
3region (db:pir1.dat) (mp:35 min) Q3ECD7 B64913 Escherichia coli 562
-11534907 223958 ydfd (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o309#7; similar to (swissprot
accession) (le:11761) (re:11952) (di:direct) D90799 D90799 g1742577
Escherichia coli 562 -11534907 300699 ydfd (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.))
(nt:orf_id:o309#7; similar to (swissprot accession) (le:8537) (re:8728)
(di:direct) D90800 D90800 g1742600 Escherichia coli 562 -11534907
5000692345 (db:genpept-bct1) (de:e. coli genes dica, dicb, dicc and dicf.)
(nt:put. orf5 (7kd)) (le:2213) (re:2404) (di:direct) ECDICABC X07465 g41281
Escherichia coli 562 -11534907 232682 ydfd orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
143 of 400 of the completegenome.) (nt:o63; 100 pct identical to ydfd_ecoli
sw: p29010;) (le:7546) (re:7737) (di:direct) AE000253 AE000253 g1787858
Escherichia coli 562 -11534907 111318 ydfd (de:hypothetical 6.8 kd protein
in dicb-intq intergenic region) (db:swissprot) YDFD_ECOLI P29010 ESCHERICHIA
COLI 562 -11534907 223980 ydfd (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o309#7; similar to (swissprot
accession) (le:8537) (re:8728) (di:direct) D90800 D90800 g1742600
Escherichia coli 562 -11534907

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850474	10858	33014	486	161

Description

5000692347 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1578 b1578 Escherichia coli 562 -11534908
7500974859 b1578 orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the
completegenome.) (nt:o218; orf in is2 element; 100 pct identical to)
(le:8633) (re:9289) (di:direct) AE000253 AE000253 g1787860 Escherichia coli
562 -11534908 6500731050 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b1578 b1578 Escherichia coli 562
-11534908

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850475	10859	33015	276	91

Description

5000692348 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1579 b1579 Escherichia coli 562 -11534909
7000691371 hypothetical protein b1579 (cl:hypothetical protein b1579) (db:pir2.dat) E64913 E64913 Escherichia coli 562 -11534909 7500960030 b1579 putative transposase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:o398; this 398 aa orf is 23 pct identical (28 gaps)) (le:9264) (re:10460) (di:direct) AE000253 AE000253 g1787861 Escherichia coli 562 -11534909 6500731051 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1579 b1579 Escherichia coli 562 -11534909

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850480	10860	33016	471	156

Description

5000692350 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1582 b1582 Escherichia coli 562 -11534910
7500951802 ynfa (de:hypothetical 11.9 kd protein in rspa-speg intergenic region) (db:swissprot) YNFA_ECOLI P76169 ESCHERICHIA COLI 562 -11534910
7000689515 hypothetical protein b1582 (cl:hypothetical protein b1582) (db:pir2.dat) H64913 H64913 Escherichia coli 562 -11534910 7500951804 b1582 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 144 of 400 of the completegenome.) (nt:f108; this 108 aa orf is 39 pct identical (2 gaps)) (le:2575) (re:2901) (di:complement) AE000254 AE000254 g1787865 Escherichia coli 562 -11534910 6500731052 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1582 b1582 Escherichia coli 562 -11534910

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850486	10861	33017	366	121

Description

5000692351 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1583 b1583 Escherichia coli 562 -11534911
7500951805 ynfB (de:hypothetical 12.9 kd protein in rspa-speg intergenic region precursor) (db:swissprot) YNFB_ECOLI P76170 ESCHERICHIA COLI 562 -11534911 7000691372 hypothetical protein b1583 (db:pir2.dat) A64914 A64914 Escherichia coli 562 -11534911 7500951807 b1583 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 144 of 400 of the completegenome.) (nt:ol13; this 113 aa orf is 27 pct identical (2 gaps)) (le:3036) (re:3377) (di:direct) AE000254 AE000254 g1787866 Escherichia coli 562 -11534911 6500731053 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1583 b1583 Escherichia coli 562 -11534911

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850487	10862	33018	603	200

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850510	10863	33019	1884	627

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850521	10864	33020	276	91

Description

6500731054 ynfC:b1585 hypothetical protein:hypothetical 27.9 kd protein in speg-mlc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1585 b1585 Escherichia coli 562 -11534912
1500686257 ynfC (de:hypothetical 27.9 kd protein in speg-mlc intergenic region) (db:swissprot) YNFC_ECOLI P76171 ESCHERICHIA COLI 562 -11534912
7000688166 hypothetical protein b1585 (db:pir2.dat) C64914 C64914 Escherichia coli 562 -11534912 7500951808 ynfC orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 144 of 400 of the completegenome.) (nt:f248; this 248 aa orf is 33 pct identical (3 gaps)) (le:3975) (re:4721) (di:complement) AE000254 AE000254 g1787868 Escherichia coli 562 -11534912 5000692352 (de:(ecoli_1544) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1544 ECOLI_1544 Escherichia coli 562 10061007

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501850537	10865	33021	1218	406

Description

5000692353 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1586 b1586 Escherichia coli 562 -11534913

7500951809 ynfD (de:hypothetical 12.1 kd protein in speg-dgsa intergenic region precursor) (db:swissprot) YNFD_ECOLI P76172 ESCHERICHIA COLI 562 -11534913 7000691373 hypothetical protein b1586 (db:pir2.dat) D64914 D64914 Escherichia coli 562 -11534913 7500951811 b1586 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 144 of 400 of the completegenome.) (nt:o115; this 115 aa orf is 30 pct identical (2 gaps)) (le:4751) (re:5098) (di:direct) AE000254 AE000254 g1787869 Escherichia coli 562 -11534913 6500731055 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1586 b1586 Escherichia coli 562 -11534913

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501850540	10866	33022	558	185

Description

5000692354 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1587 b1587 Escherichia coli 562 -11534914

7000691374 dimethylsulfoxide reductase:chain a1 precursor:anaerobic (ec:1.8.--) (db:pir2.dat) E64914 E64914 Escherichia coli 562 -11534914

223989 anaerobic dimethyl sulfoxide reductase chain a (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #310(35.7-36.0 min.).) (nt:orf_id:o311#1; similar to (swissprot accession) (le:2696) (re:5122) (di:direct) D90801 D90801 g1742610 Escherichia coli 562 -11534914 223999 anaerobic dimethyl sulfoxide reductase chain a (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #311(35.7-36.1 min.).) (nt:orf_id:o311#1; similar to (swissprot accession) (le:723) (re:3149) (di:direct) D90802 D90802 g1742621 Escherichia coli 562 -11534914 300707 b1587 putative oxidoreductase:major subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 144 of 400 of the completegenome.) (nt:o808; this 808 aa orf is 67 pct identical (10 gaps)) (le:5297) (re:7723) (di:direct) AE000254 AE000254 g1787870 Escherichia coli 562 -11534914 6500731056 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1587 b1587 Escherichia coli 562 -11534914

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850541	10867	33023	402	133

Description

5000692355 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1588 b1588 Escherichia coli 562 -11534915
7000691375 dimethylsulfoxide reductase:chain a2 precursor:anaerobic
(ec:1.8.-.-) (db:pir2.dat) F64914 F64914 Escherichia coli 562 -11534915
223990 anaerobic dimethyl sulfoxide reductase chain a (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #310(35.7-36.0 min..))
(nt:orf_id:o311#2; similar to (swissprot accession) (le:5180) (re:7606)
(di:direct) D90801 D90801 g1742611 Escherichia coli 562 -11534915 224000
anaerobic dimethyl sulfoxide reductase chain a (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #311(35.7-36.1 min..))
(nt:orf_id:o311#2; similar to (swissprot accession) (le:3207) (re:5633)
(di:direct) D90802 D90802 g1742622 Escherichia coli 562 -11534915 300708
b1588 putative oxidoreductase:major subunit (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 144
of 400 of the completegenome.) (nt:o808; this 808 aa orf is 66 pct identical
(15 gaps)) (le:7781) (re:10207) (di:direct) AE000254 AE000254 g1787871
Escherichia coli 562 -11534915 6500731057 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1588 b1588
Escherichia coli 562 -11534915

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850572	10868	33024	2064	687

Description

5000692356 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1589 b1589 Escherichia coli 562 -11534916

7000691376 dimethylsulfoxide reductase:chain b1:anaerobic (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (ec:1.8.-.-) (db:pir2.dat) G64914 G64914 Escherichia coli 562 -11534916 223991 dimethylsulfoxide reductase ec 1.8.-.- chain (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #310(35.7-36.0 min.)) (nt:orf_id:o311#3; similar to (pir accession number) (le:7617) (re:8234) (di:direct) D90801 D90801 g1742612 Escherichia coli 562 -11534916 224001 dimethylsulfoxide reductase ec 1.8.-.- chain (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #311(35.7-36.1 min.)) (nt:orf_id:o311#3; similar to (pir accession number) (le:5644) (re:6261) (di:direct) D90802 D90802 g1742623 Escherichia coli 562 -11534916 300709 b1589 putative oxidoreductase:fe-s subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 144 of 400 of the completegenome.) (nt:o205; this 205 aa orf is 94 pct identical (2 gaps)) (le:10218) (re:10835) (di:direct) AE000254 AE000254 g1787872 Escherichia coli 562 -11534916 6500731058 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1589 b1589 Escherichia coli 562 -11534916

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850585	10869	33025	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850586	10870	33026	246	81

Description

5000692357 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1590 b1590 Escherichia coli 562 -11534917

7000691377 probable dimethylsulfoxide reductase:chain c1:anaerobic (cl:probable dimethylsulfoxide reductase chain c) (ec:1.8.-.-) (db:pir2.dat) H64914 H64914 Escherichia coli 562 -11534917 7500960031 b1590 putative dmsc reductase anchor subunit (fn:putative enzyme; degradation of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 144 of 400 of the completegenome.) (nt:o284; 56 pct identical (3 gaps) to dmssc_ecoli) (le:10837) (re:11691) (di:direct) AE000254 AE000254 g1787873 Escherichia coli 562 -11534917 6500731059 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1590 b1590 Escherichia coli 562 -11534917

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850590	10871	33027	618	205

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850613	10872	33028	363	120

Description

5000692358 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1591 b1591 Escherichia coli 562 -11534918

7500951812 ynfj (de:hypothetical 23.6 kd protein in speg-dgsa intergenic region precursor) (db:swissprot) YNFI_ECOLI P76174 ESCHERICHIA COLI 562 -11534918 7000689512 ycdy protein homolog b1591 (cl:escherichia coli ycdy protein) (db:pir2.dat) A64915 A64915 Escherichia coli 562 -11534918

7500951814 b1591 putative oxidoreductase component (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 144 of 400 of the completegenome.) (nt:o207; this 207 aa orf is 38 pct identical (3 gaps)) (le:11725) (re:12348) (di:direct) AE000254 AE000254 g1787874 Escherichia coli 562 -11534918 6500731060 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1591 b1591 Escherichia coli 562 -11534918

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850620	10873	33029	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850649	10874	33030	1446	481

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850682	10875	33031	198	65

Description

5000692359 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1592 b1592 Escherichia coli 562 -11534919
 7000691378 hypothetical protein b1592 (db:pir2.dat) B64915 B64915 Escherichia coli 562 -11534919 7500960032 b1592 putative chloride channel (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 145 of 400 of the completegenome.) (nt:o438; this 438 aa orf is 31 pct identical (30 gaps)) (le:98) (re:1414) (di:direct) AE000255 AE000255 g1787876 Escherichia coli 562 -11534919 6500731061 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1592 b1592 Escherichia coli 562 -11534919

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850707	10876	33032	606	201

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850713	10877	33033	426	141

Description

5000692360 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1593 b1593 Escherichia coli 562 -11534920
 7000691379 dethiobiotin synthase homolog b1593 (cl:dethiobiotin synthase) (db:pir2.dat) C64915 C64915 Escherichia coli 562 -11534920 223995 dethiobiotin synthase ec 6.3.3.3 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #310(35.7-36.0 min.)) (nt:orf_id:o311#7; similar to (pir accession number) (le:11151) (re:11858) (di:complement) D90801 D90801 g1742616 Escherichia coli 562 -11534920 224005 dethiobiotin synthase ec 6.3.3.3 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #311(35.7-36.1 min.)) (nt:orf_id:o311#7; similar to (pir accession number) (le:9178) (re:9885) (di:complement) D90802 D90802 g1742627 Escherichia coli 562 -11534920 300713 b1593 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 145 of 400 of the completegenome.) (nt:f235; this 235 aa orf is 52 pct identical (5 gaps)) (le:1367) (re:2074) (di:complement) AE000255 AE000255 g1787877 Escherichia coli 562 -11534920 6500731062 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1593 b1593 Escherichia coli 562 -11534920

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850718	10878	33034	741	246

Description

6500731063 ynf1:b1595 hypothetical protein:hypothetical transcriptional regulator in mlc-asr intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1595 b1595 Escherichia coli 562 -11534921 4000708151 ynf1 (de:hypothetical transcriptional regulator in mlc-asr intergenic region) (db:swissprot) YNFL_ECOLI P77559 ESCHERICHIA COLI 562 -11534921 7000688167 hypothetical protein b1595 (cl:pseudomonas putida regulatory protein catr) (db:pir2.dat) E64915 E64915 Escherichia coli 562 -11534921 223997 als operon regulatory protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #310(35.7-36.0 min.).) (nt:orf_id:o311#9; similar to (swissprot accession) (le:13326) (re:14219) (di:complement) D90801 D90801 g1742618 Escherichia coli 562 -11534921 224007 als operon regulatory protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #311(35.7-36.1 min.).) (nt:orf_id:o311#9; similar to (swissprot accession) (le:11353) (re:12246) (di:complement) D90802 D90802 g1742629 Escherichia coli 562 -11534921 300715 ynf1 putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 145 of 400 of the completegenome.) (nt:f297; this 297 aa orf is 35 pct identical (3 gaps)) (le:3542) (re:4435) (di:complement) AE000255 AE000255 g1787879 Escherichia coli 562 -11534921 5000692362 (de:(ecoli_1554) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1554 ECOLI_1554 Escherichia coli 562 10119718

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850720	10879	33035	474	157

Description

6500731064 ynmf:b1596 hypothetical protein:hypothetical 45.3 kd protein in mlc-asr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1596 b1596 Escherichia coli 562 -11534922 117034 ynmf (de:hypothetical 45.3 kd protein in mlc-asr intergenic region) (db:swissprot) YNFM_ECOLI P43531 ESCHERICHIA COLI 562 -11534922 7000688168 hypothetical protein b1596 (cl:probable antibiotic resistance protein yybf) (db:pir2.dat) F64915 F64915 Escherichia coli 562 -11534922 224008 bicyclomycin resistance protein sulfonamide (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #311(35.7-36.1 min.)) (nt:orf_id:o311#10; similar to (swissprot accession) (le:12353) (re:13606) (di:direct) D90802 D90802 g1742630 Escherichia coli 562 -11534922 300716 ynmf putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 145 of 400 of the completegenome.) (nt:o417; this 417 aa orf is 43 pct identical (0 gaps)) (le:4542) (re:5795) (di:direct) AE000255 AE000255 g1787880 Escherichia coli 562 -11534922 5000692363 (de:(ecoli_1555) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1555 ECOLI_1555 Escherichia coli 562 10119720

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850725	10880	33036	822	274

Description

5000692365 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1598 b1598 Escherichia coli 562 -11534923 7000691380 hypothetical protein b1598 (db:pir2.dat) H64915 H64915 Escherichia coli 562 -11534923 7500960033 b1598 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 145 of 400 of the completegenome.) (nt:o273; this 273 aa orf is 24 pct identical (26 gaps)) (le:6803) (re:7624) (di:direct) AE000255 AE000255 g1787882 Escherichia coli 562 -11534923 6500731065 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1598 b1598 Escherichia coli 562 -11534923

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850729	10881	33037	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850734	10882	33038	585	194

Description

5000692366 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1599 b1599 Escherichia coli 562 -11534924
7000691381 hypothetical protein b1599 (cl:suge protein) (db:pir2.dat)
A64916 A64916 Escherichia coli 562 -11534924 224011 putative ethidium bromide resistance protein e1 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #311(35.7-36.1 min.)) (nt:orf_id:o311#14; similar to (swissprot accession) (le:15474) (re:15803) (di:complement) D90802 D90802 g1742633 Escherichia coli 562 -11534924 224016 putative ethidium bromide resistance protein e1 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf_id:o311#14; similar to (swissprot accession) (le:526) (re:855) (di:complement) D90803 D90803 g1742639 Escherichia coli 562 -11534924 300719 b1599 possible chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 145 of 400 of the completegenome.) (nt:f109; this 109 aa orf is 33 pct identical (0 gaps)) (le:7663) (re:7992) (di:complement) AE000255 AE000255 g1787883 Escherichia coli 562 -11534924 6500731066 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1599 b1599 Escherichia coli 562 -11534924

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850738	10883	33039	195	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850757	10884	33040	765	254

Description

5000692367 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1600 b1600 Escherichia coli 562 -11534925
7000691382 hypothetical protein b1600 (cl:suge protein) (db:pir2.dat)
B64916 B64916 Escherichia coli 562 -11534925 224012 putative ethidium bromide resistance protein e1 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #311(35.7-36.1 min.)) (nt:orf_id:o311#15; similar to (swissprot accession) (le:15790) (re:16155) (di:complement) D90802 D90802 g1742634 Escherichia coli 562 -11534925 224017 putative ethidium bromide resistance protein e1 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf_id:o311#15; similar to (swissprot accession) (le:842) (re:1207) (di:complement) D90803 D90803 g1742640 Escherichia coli 562 -11534925 300720 b1600 possible chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 145 of 400 of the completgenome.) (nt:f121; this 121 aa orf is 29 pct identical (1 gap)) (le:7979) (re:8344) (di:complement) AE000255 AE000255 g1787884 Escherichia coli 562 -11534925 6500731067 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1600 b1600 Escherichia coli 562 -11534925

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850759	10885	33041	1326	441

Description

5000692368 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1601 b1601 Escherichia coli 562 -11534926
7000691383 hypothetical protein b1601 (cl:conserved hypothetical protein hi0338) (db:pir2.dat) C64916 C64916 Escherichia coli 562 -11534926 224013 yhht (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #311(35.7-36.1 min.)) (nt:orf_id:o311#16; similar to (swissprot accession) (le:16567) (re:17601) (di:direct) D90802 D90802 g1742635 Escherichia coli 562 -11534926 224018 yhht (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf_id:o311#16; similar to (swissprot accession) (le:1619) (re:2653) (di:direct) D90803 D90803 g1742641 Escherichia coli 562 -11534926 300721 b1601 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 145 of 400 of the completgenome.) (nt:o344; this 344 aa orf is 46 pct identical (0 gaps)) (le:8756) (re:9790) (di:direct) AE000255 AE000255 g1787885 Escherichia coli 562 -11534926 6500731068 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1601 b1601 Escherichia coli 562 -11534926

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850760	10886	33042	615	204

Description

5000692369 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1604 b1604 Escherichia coli 562 -11534927
 7500922304 ydgh (de:hypothetical 33.9 kd protein in pnta-rsta intergenic region precursor) (db:swissprot) YDGH_ECOLI P76177 ESCHERICHIA COLI 562 -11534927 7000691384 conserved hypothetical protein b1604 precursor (db:pir2.dat) F64916 F64916 Escherichia coli 562 -11534927 7500922306 b1604 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 146 of 400 of the completegenome.) (nt:o314; this 314 aa orf is 26 pct identical (3 gaps)) (le:369) (re:1313) (di:direct) AE000256 AE000256 g1787889 Escherichia coli 562 -11534927 6500731069 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1604 b1604 Escherichia coli 562 -11534927

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850792	10887	33043	249	82

Description

5000692370 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1605 b1605 Escherichia coli 562 -11534928
 7502852246 ydgi (de:putative arginine/ornithine antiporter) (db:swissprot) ARCD_ECOLI P77429 ESCHERICHIA COLI 562 -11534928 7000691385 probable membrane protein b1605 precursor (cl:l-lysine transport protein) (db:pir2.dat) G64916 G64916 Escherichia coli 562 -11534928 224021 arginine/ornithine antiporter. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf_id:o312#4; similar to (swissprot accession) (le:7263) (re:8645) (di:direct) D90803 D90803 g1742644 Escherichia coli 562 -11534928 224031 arginine/ornithine antiporter. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf_id:o312#4; similar to (swissprot accession) (le:3377) (re:4759) (di:direct) D90804 D90804 g1742655 Escherichia coli 562 -11534928 300726 b1605 putative arginine/ornithine antiporter (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 146 of 400 of the completegenome.) (nt:o460; this 460 aa orf is 46 pct identical (26 gaps)) (le:1499) (re:2881) (di:direct) AE000256 AE000256 g1787890 Escherichia coli 562 -11534928 6500731070 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1605 b1605 Escherichia coli 562 -11534928

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850794	10888	33044	645	214

Description

6500731071 ydgb:b1606 hypothetical protein:hypothetical oxidoreductase in pnta-rsta intergenic region (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1606 b1606 Escherichia coli 562 -11534929 111334 ydgb (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YDGB_ECOLI P52109 ESCHERICHIA COLI 562 -11534929 7000687542 ydgb probable oxidoreductase:ydgb (cl:short-chain alcohol dehydrogenase homology) (ec:1.-.-.-) (db:pir2.dat) H64916 H64916 Escherichia coli 562 -11534929 224022 ydgb (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf_id:o312#5; similar to (swissprot accession) (le:8682) (re:9404) (di:direct) D90803 D90803 g1742645 Escherichia coli 562 -11534929 224032 ydgb (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf_id:o312#5; similar to (swissprot accession) (le:4796) (re:5518) (di:direct) D90804 D90804 g1742656 Escherichia coli 562 -11534929 300727 ydgb putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 146 of 400 of the completegenome.) (nt:o240; this 240 aa orf is 31 pct identical (19 gaps)) (le:2918) (re:3640) (di:direct) AE000256 AE000256 g1787891 Escherichia coli 562 -11534929 5000692371 (de:(ecoli_1565) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1565 ECOLI_1565 Escherichia coli 562 10119728

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850799	10889	33045	297	98

Description

6500731072 ydgc:b1607 hypothetical protein:hypothetical 12.5 kd protein in pnta-rsta intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1607 b1607 Escherichia coli 562 -11534930 111336 ydgc (de:hypothetical 12.5 kd protein in pnta-rsta intergenic region) (db:swissprot) YDGC_ECOLI P52110 ESCHERICHIA COLI 562 -11534930 7000687543 probable membrane protein ydgc precursor (db:pir2.dat) A64917 A64917 Escherichia coli 562 -11534930 224023 ydgc membrane protein glpm. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #312(36.0-36.3 min.)) (nt:orf_id:o312#7; similar to (swissprot accession) (le:9401) (re:9736) (di:complement) D90803 D90803 g1742646 Escherichia coli 562 -11534930 224033 ydgc membrane protein glpm. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf_id:o312#7; similar to (swissprot accession) (le:5515) (re:5850) (di:complement) D90804 D90804 g1742657 Escherichia coli 562 -11534930 300728 ydgc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 146 of 400 of the completegenome.) (nt:f111; this 111 aa orf is 25 pct identical (6 gaps)) (le:3637) (re:3972) (di:complement) AE000256 AE000256 g1787892 Escherichia coli 562 -11534930 5000692372 (de:(ecoli_1566) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1566 ECOLI_1566 Escherichia coli 562 10119729

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850801	10890	33046	399	132
<u>Description</u>				
5000692375 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1614 b1614 Escherichia coli 562 -11534931				
7000687540 ydga (de:hypothetical 54.7 kd protein im mana-gusc intergenic region) (db:swissprot) YDGA_ECOLI P77804 ESCHERICHIA COLI 562 -11534931				
7000687541 ydga probable membrane protein ydga (cl:hypothetical protein b1614) (db:pir2.dat) H64917 H64917 Escherichia coli 562 -11534931 224040 yihf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #313(36.1-36.4 min.)) (nt:orf_id:o312#14; similar to (swissprot accession) (le:13672) (re:15180) (di:direct) D90804 D90804 g1742664 Escherichia coli 562 -11534931				
300739 yihf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf_id:o312#14; similar to (swissprot accession) (le:4536) (re:6044) (di:direct) D90805 D90805 g1742669 Escherichia coli 562 -11534931				
300735 ydga orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 147 of 400 of the completegenome.) (nt:o502; this 502 aa orf is 35 pct identical (20 gaps)) (le:1429) (re:2937) (di:direct) AE000257 AE000257 g1787900 Escherichia coli 562 -11534931				
224044 yihf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf_id:o312#14; similar to (swissprot accession) (le:4536) (re:6044) (di:direct) D90805 D90805 g1742669 Escherichia coli 562 -11534931				
6500731073 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1614 b1614 Escherichia coli 562 -11534931				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501850803	10891	33047	231	76

Description

5000692379 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1624 b1624 Escherichia coli 562 -11534932

7000691386 conserved hypothetical protein b1624 (cl:conserved hypothetical protein b1624) (db:pir2.dat) B64919 B64919 Escherichia coli 562 -11534932

224053 virulence factor mvim. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf_id:o314#10; similar to (swissprot accession) (le:17952) (re:19031) (di:complement) D90805 D90805 g1742678 Escherichia coli 562 -11534932 224060 virulence factor mvim. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #315(36.6-36.9 min.)) (nt:orf_id:o314#10; similar to (swissprot accession) (le:6264) (re:7343) (di:complement) D90806 D90806 g1742686 Escherichia coli 562 -11534932 300750 virulence factor mvim. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o314#10; similar to (swissprot accession) (le:874) (re:1953) (di:complement) D90807 D90807 g1742694 Escherichia coli 562 -11534932 300773 virulence factor mvim. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o314#10; similar to (swissprot accession) (le:6365) (re:7444) (di:complement) D90808 D90808 g1742718 Escherichia coli 562 -11534932 300748 b1624 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:f359; residues 74-259 are 45 pct identical to) (le:3989) (re:5068) (di:complement) AE000258 AE000258 g1787911 Escherichia coli 562 -11534932 224067 virulence factor mvim. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o314#10; similar to (swissprot accession) (le:874) (re:1953) (di:complement) D90807 D90807 g1742694 Escherichia coli 562 -11534932 224090 virulence factor mvim. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o314#10; similar to (swissprot accession) (le:6365) (re:7444) (di:complement) D90808 D90808 g1742718 Escherichia coli 562 -11534932 6500731074 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1624 b1624 Escherichia coli 562 -11534932

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850806	10892	33048	363	120

Description

5000692380 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1625 b1625 Escherichia coli 562 -11534933
7500922314 ydgt (de:hypothetical 8.4 kd protein in add-nth intergenic region) (db:swissprot) YDGT_ECOLI P76179 ESCHERICHIA COLI 562 -11534933
7000691387 modulating protein ymoa homolog b1625 (cl:modulating protein ymoa) (db:pir2.dat) C64919 C64919 Escherichia coli 562 -11534933 7500922316 b1625 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:o71; this 71 aa orf is 42 pct identical (4 gaps)) (le:5670) (re:5885) (di:direct) AE000258 AE000258 g1787912 Escherichia coli 562 -11534933
6500731075 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1625 b1625 Escherichia coli 562 -11534933

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850811	10893	33049	291	97

Description

5000692381 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1626 b1626 Escherichia coli 562 -11534934
7000691388 probable membrane protein b1626 (db:pir2.dat) D64919 D64919 Escherichia coli 562 -11534934 7500922310 b1626 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:o154; this 154 aa orf is 27 pct identical (5 gaps)) (le:5947) (re:6411) (di:direct) AE000258 AE000258 g1787913 Escherichia coli 562 -11534934 7500922308 ydgk (de:hypothetical 17.3 kd protein in add-nth intergenic region) (db:swissprot) YDGK_ECOLI P76180 ESCHERICHIA COLI 562 -11534934 6500731076 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1626 b1626 Escherichia coli 562 -11534934

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850815	10894	33050	579	192

Description

5000692382 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1627 b1627 Escherichia coli 562 -11534935
7000691389 probable membrane protein b1627 (cl:conserved hypothetical protein h1688) (db:pir2.dat) E64919 E64919 Escherichia coli 562 -11534935
7500960034 b1627 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:o193; this 193 aa orf is 33 pct identical (2 gaps)) (le:6488) (re:7069) (di:direct) AE000258 AE000258 g1787914 Escherichia coli 562 -11534935 6500731077 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1627 b1627 Escherichia coli 562 -11534935

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850841	10895	33051	327	108

Description

5000692383 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1628 b1628 Escherichia coli 562 -11534936

7000691390 probable iron-sulfur protein b1628 precursor:rnfb protein homolog (cl:conserved hypothetical protein h1684:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) F64919 F64919 Escherichia coli 562 -11534936 224061 ferredoxin ii. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #315(36.6-36.9 min.)) (nt:orf_id:o316#4; similar to (swissprot accession) (le:9344) (re:9922) (di:direct) D90806 D90806 g1742687 Escherichia coli 562 -11534936 224068 ferredoxin ii. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o316#4; similar to (swissprot accession) (le:3954) (re:4532) (di:direct) D90807 D90807 g1742695 Escherichia coli 562 -11534936 300774 ferredoxin ii. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o316#4; similar to (swissprot accession) (le:9445) (re:10023) (di:direct) D90808 D90808 g1742719 Escherichia coli 562 -11534936 300751 b1628 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:o192; this 192 aa orf is 40 pct identical (2 gaps)) (le:7069) (re:7647) (di:direct) AE000258 AE000258 g1787915 Escherichia coli 562 -11534936 224091 ferredoxin ii. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o316#4; similar to (swissprot accession) (le:9445) (re:10023) (di:direct) D90808 D90808 g1742719 Escherichia coli 562 -11534936 6500731078 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1628 b1628 Escherichia coli 562 -11534936

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850847	10896	33052	279	92

Description

5000692384 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1629 b1629 Escherichia coli 562 -11534937
7000691391 probable iron-sulfur protein b1629:rnfc protein homolog b1629 (db:pir2.dat) G64919 G64919 Escherichia coli 562 -11534937 224062 glucose repression mediator protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #315(36.6-36.9 min.)) (nt:orf_id:o316#5; similar to (swissprot accession) (le:9915) (re:12137) (di:direct) D90806 D90806 g1742688 Escherichia coli 562 -11534937 224069 glucose repression mediator protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o316#5; similar to (swissprot accession) (le:4525) (re:6747) (di:direct) D90807 D90807 g1742696 Escherichia coli 562 -11534937 300775 glucose repression mediator protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o316#5; similar to (swissprot accession) (le:10016) (re:12238) (di:direct) D90808 D90808 g1742720 Escherichia coli 562 -11534937 300752 b1629 putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:o740; this 740 aa orf is 30 pct identical (9 gaps)) (le:7640) (re:9862) (di:direct) AE000258 AE000258 g1787916 Escherichia coli 562 -11534937 224092 glucose repression mediator protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o316#5; similar to (swissprot accession) (le:10016) (re:12238) (di:direct) D90808 D90808 g1742720 Escherichia coli 562 -11534937
6500731079 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1629 b1629 Escherichia coli 562 -11534937

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850848	10897	33053	396	131

Description

6500731080 ydgo:b1630 hypothetical protein:hypothetical 38.1 kd protein in add-nth intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1630 b1630 Escherichia coli 562 -11534938
5500686524 ydgo (de:hypothetical 38.1 kd protein in add-nth intergenic region) (db:swissprot) YDGO_ECOLI P76182 ESCHERICHIA COLI 562 -11534938
7000687545 ydgo probable membrane protein ydgo precursor (db:pir2.dat) H64919 H64919 Escherichia coli 562 -11534938 7500922311 ydgo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:o352; residues 7-306 are 46 pct identical to) (le:9863) (re:10921) (di:direct) AE0000258 AE0000258 g1787917 Escherichia coli 562 -11534938 5000692385 (de:(ecoli_1589) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1589 ECOLI_1589 Escherichia coli 562 10123403

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850858	10898	33054	231	76

Description

5000692386 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1631 b1631 Escherichia coli 562 -11534939
7000691392 conserved hypothetical protein b1631 (cl:hypothetical protein hi1687) (db:pir2.dat) A64920 A64920 Escherichia coli 562 -11534939 224063 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #315(36.6-36.9 min.)) (nt:orf_id:o316#10; similar to (swissprot accession) (le:13200) (re:13820) (di:direct) D90806 D90806 g1742689 Escherichia coli 562 -11534939 224070 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o316#10; similar to (swissprot accession) (le:7810) (re:8430) (di:direct) D90807 D90807 g1742697 Escherichia coli 562 -11534939 300776 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o316#10; similar to (swissprot accession) (le:13301) (re:13921) (di:direct) D90808 D90808 g1742721 Escherichia coli 562 -11534939 300753 b1631 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:o206; this 206 aa orf is 48 pct identical (1 gap)) (le:10925) (re:11545) (di:direct) AE000258 AE000258 g1787918 Escherichia coli 562 -11534939 224093 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o316#10; similar to (swissprot accession) (le:13301) (re:13921) (di:direct) D90808 D90808 g1742721 Escherichia coli 562 -11534939 6500731081 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1631 b1631 Escherichia coli 562 -11534939

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850859	10899	33055	885	294

Description

6500731082 ydgq:b1632 hypothetical protein:hypothetical 24.5 kd protein in add-nth intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1632 b1632 Escherichia coli 562 -11534940
4000708202 ydgq (de:hypothetical 24.5 kd protein in add-nth intergenic region) (db:swissprot) YDQO_ECOLI P77179 ESCHERICHIA COLI 562 -11534940
7000687546 ydgq probable membrane protein ydgq (cl:conserved hypothetical protein h1688) (db:pir2.dat) B64920 B64920 Escherichia coli 562 -11534940
224064 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #315(36.6-36.9 min.)) (nt:orf_id:o316#11; similar to (swissprot accession) (le:13824) (re:14519) (di:direct) D90806 D90806 g1742690 Escherichia coli 562 -11534940 224071 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o316#11; similar to (swissprot accession) (le:8434) (re:9129) (di:direct) D90807 D90807 g1742698 Escherichia coli 562 -11534940 300777 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o316#11; similar to (swissprot accession) (le:13925) (re:14620) (di:direct) D90808 D90808 g1742722 Escherichia coli 562 -11534940 300754 ydgq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 148 of 400 of the completegenome.) (nt:o231; this 231 aa orf is 37 pct identical (8 gaps)) (le:11549) (re:12244) (di:direct) AE000258 AE000258 g1787919 Escherichia coli 562 -11534940 224094 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #317(36.6-36.9 min.)) (nt:orf_id:o316#11; similar to (swissprot accession) (le:13925) (re:14620) (di:direct) D90808 D90808 g1742722 Escherichia coli 562 -11534940 5000692387 (de:(ecoli_1591) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1591 ECOLI_1591 Escherichia coli 562 10119743

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850868	10900	33056	333	110

Description

5000692388 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1634 b1634 Escherichia coli 562 -11534941
7000687547 ydgr (de:hypothetical 54.0 kd protein in nth-gst intergenic region) (db:swissprot) YDGR_ECOLI P77304 ESCHERICHIA COLI 562 -11534941
7000687548 probable membrane protein b1634 (cl:peptide transporter protein) (db:pir2.dat) D64920 D64920 Escherichia coli 562 -11534941 224073
di-tripeptide transporter. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o316#13; similar to (swissprot accession) (le:10375) (re:11877) (di:direct) D90807 D90807 g1742700 Escherichia coli 562 -11534941 300756 ydgr putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:o500; this 500 aa orf is 52 pct identical (4 gaps)) (le:376) (re:1878) (di:direct) AE000259 AE000259 g1787922 Escherichia coli 562 -11534941
6500731083 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1634 b1634 Escherichia coli 562 -11534941

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850875	10901	33057	675	224

Description

5000692389 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1636 b1636 Escherichia coli 562 -11534942
5500685712 pdxy (ec:2.7.1.35) (de:pyridoxamine kinase, (pm kinase)) (db:swissprot) PDXY_ECOLI P77150 ESCHERICHIA COLI 562 -11534942 7000686108
ydgs probable pyridoxal kinase:ydgs (ec:2.7.1.35) (db:pir2.dat) F64920 F64920 Escherichia coli 562 -11534942 224075 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o316#15; similar to (swissprot accession) (le:12632) (re:13495) (di:complement) D90807 D90807 g1742702 Escherichia coli 562 -11534942
300758 pdxy pyridoxal kinase 2 / pyridoxine kinase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:f287; this 287 aa orf is 51 pct identical (3 gaps)) (le:2633) (re:3496) (di:complement) AE000259 AE000259 g1787924 Escherichia coli 562 -11534942 6500731084 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1636 b1636 Escherichia coli 562 -11534942

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850880	10902	33058	366	121

Description

6500731085 ydha:b1639 hypothetical protein in pdxh 5region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1639 b1639 Escherichia coli 562 -11534943 164192 ydha ydha protein (db:pir2.dat) A43261 A43261 Escherichia coli 562 -11534943 224078 ydha orf1 5 of pdxh (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o316#18; similar to (pir accession number) (le:15672) (re:15920) (di:complement) D90807 D90807 g1742705 Escherichia coli 562 -11534943 300761 (fn:unknown) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli pyridoxamine 5'-phosphate oxidase (pdxh) gene,complete cds, tyrosyl-trna synthetase (tyrs) gene, 3' end, orf, 5'end.) (nt:orf; putative) (le:<1) (re:251) (di:di... ECOTYSPDH M92351 g148096 Escherichia coli 562 -11534943 236236 ydha orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:f109; 100 pct identical to fragment ydha_ecoli) (le:5673) (re:5921) (di:complement) AE000259 AE000259 g1787927 Escherichia coli 562 -11534943 5000692390 (de:(ecoli_1598) (pn:hypothetical protein in pdxh 5"region:fragment) (gn:ydha) (gtcfc:13.7:14.1) (ec:)(ydha_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1598 ECOLI_1598 Escherichia coli 562 10053078

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850881	10903	33059	273	90

Description

5000692391 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1640 b1640 Escherichia coli 562 -11534944 7000691393 conserved hypothetical protein b1640 (cl:hypothetical protein hi0753) (db:pir2.dat) B64921 B64921 Escherichia coli 562 -11534944 224079 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.)) (nt:orf_id:o316#19; similar to (swissprot accession) (le:16099) (re:17208) (di:complement) D90807 D90807 g1742706 Escherichia coli 562 -11534944 300762 b1640 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:f369; this 369 aa orf is 50 pct identical (15 gaps)) (le:6100) (re:7209) (di:complement) AE000259 AE000259 g1787928 Escherichia coli 562 -11534944 6500731086 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1640 b1640 Escherichia coli 562 -11534944

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850886	10904	33060	198	65

Description

6500731087 slyb:b1641 hypothetical protein:outer membrane lipoprotein slyb precursor (gtcfc:11.2) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1641 b1641 Escherichia coli 562 -11534945 7000691394 slyb outer membrane lipoprotein slyb precursor (cl:pal cross-reacting lipoprotein) (db:pir2.dat) C64921 C64921 Escherichia coli 562 -11534945 7500960035 slyb putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:ol55; 75 pct identical amino acid sequence and) (le:7483) (re:7950) (di:direct) AE000259 AE000259 g1787929 Escherichia coli 562 -11534945 5000692392 (de:(ecoli_1600) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1600 ECOLI_1600 Escherichia coli 562 10123404

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850887	10905	33061	486	161

Description

6500731088 slya:b1642 hypothetical protein:transcriptional regulator slya (gtcfc:10.2:10.2) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1642 b1642 Escherichia coli 562 -11534946 118645 slya (de:transcriptional regulator slya) (db:swissprot) SLYA_ECOLI P55740 ESCHERICHIA COLI 562 -11534946 300764 salmolyisin cytolysin slya . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #316(36.7-37.1 min.).) (nt:orf_id:o316#22; similar to (swissprot accession) (le:17995) (re:18435) (di:complement) D90807 D90807 g1742708 Escherichia coli 562 -11534946 224081 slya transcriptional regulator for cryptic hemolysin (fn:regulator; adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:f146; this 146 aa orf is 90 pct identical (0 gaps)) (le:7997) (re:8437) (di:complement) AE000259 AE000259 g1787930 Escherichia coli 562 -11534946 7000686609 slya slya protein (fn:regulatory protein) (db:genpept) (de:escherichia coli slya gene.) (le:176) (re:616) (di:direct) ECAJ10965 AJ010965 g4127820 Escherichia coli 562 -11534946 5000692393 (de:(ecoli_1601) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1601 ECOLI_1601 Escherichia coli 562 -11534946

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850894	10906	33062	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850901	10907	33063	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850907	10908	33064	240	79

Description

5000692394 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1643 b1643 Escherichia coli 562 -11534947
 7500922325 ydhi (de:hypothetical 8.9 kd protein in slyA-sodC intergenic region) (db:swissprot) YDHI_ECOLI P76184 ESCHERICHIA COLI 562 -11534947
 7000691395 probable membrane protein b1643 (db:pir2.dat) E64921 E64921 Escherichia coli 562 -11534947 7500922327 b1643 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:o78; this 78 aa orf is 37 pct identical (8 gaps)) (le:8632) (re:8868) (di:direct) AE000259 AE000259 g1787931 Escherichia coli 562 -11534947 6500731089 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1643 b1643 Escherichia coli 562 -11534947

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850913	10909	33065	843	280

Description

5000692395 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1644 b1644 Escherichia coli 562 -11534948
 7500922328 ydhj (de:hypothetical 33.0 kd protein in slyA-sodC intergenic region) (db:swissprot) YDHJ_ECOLI P76185 ESCHERICHIA COLI 562 -11534948
 7000691396 probable membrane protein b1644 (cl:escherichia coli hypothetical protein b1644) (db:pir2.dat) F64921 F64921 Escherichia coli 562 -11534948 7500922330 b1644 putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:o299; this 299 aa orf is 41 pct identical (1 gap)) (le:8829) (re:9728) (di:direct) AE000259 AE000259 g1787932 Escherichia coli 562 -11534948 6500731090 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1644 b1644 Escherichia coli 562 -11534948

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850922	10910	33066	441	147

Description

5000692396 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1645 b1645 Escherichia coli 562 -11534949
7000691397 probable membrane protein b1645 (db:pir2.dat) G64921 G64921 Escherichia coli 562 -11534949 7500960036 b1645 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:o670; this 670 aa orf is 25 pct identical (35 gaps)) (le:9728) (re:11740) (di:direct) AE000259 AE000259 g1787933 Escherichia coli 562 -11534949 6500731091 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1645 b1645 Escherichia coli 562 -11534949

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850927	10911	33067	387	128

Description

GTC ORF with score 426 to: (fn:catalyst for urea hydrolysis; plays a pivotal) (db:genpept-pln2) (ec:3.5.1.5) (de:coccidioides immitis urease (ure) gene, complete cds.) (nt:believed to be expressed during sporulation in) (le:864:1092:1253:1395:1878) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501850928	10912	33068	270	89

Description

GTC ORF with score 332 to: (fn:catalyst for urea hydrolysis; plays a pivotal) (db:genpept-pln2) (ec:3.5.1.5) (de:coccidioides immitis urease (ure) gene, complete cds.) (nt:believed to be expressed during sporulation in) (le:864:1092:1253:1395:1878) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850953	10913	33069	549	182

Description

5000692398 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1647 b1647 Escherichia coli 562 -11534950
 7500922322 ydhf (de:hypothetical oxidoreductase in sodc-nema intergenic region) (db:swissprot) YDHF_ECOLI P76187 ESCHERICHIA COLI 562 -11534950
 7000691398 probable oxidoreductase:b1647 (ec:1.-.-.-) (db:pir2.dat) A64922 A64922 Escherichia coli 562 -11534950 7500922324 b1647 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 150 of 400 of the completegenome.) (nt:f298; this 298 aa orf is 51 pct identical (5 gaps)) (le:71) (re:967) (di:complement) AE000260 AE000260 g1787936 Escherichia coli 562 -11534950 6500731092 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1647 b1647 Escherichia coli 562 -11534950

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850960	10914	33070	1155	384

Description

5000692399 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1648 b1648 Escherichia coli 562 -11534951
 7500922331 ydhl (de:hypothetical 14.4 kd protein in sodc-nema intergenic region precursor) (db:swissprot) YDHL_ECOLI P76188 ESCHERICHIA COLI 562 -11534951 7000691399 probable membrane protein b1648 (db:pir2.dat) B64922 B64922 Escherichia coli 562 -11534951 7500922333 b1648 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 150 of 400 of the completegenome.) (nt:f125) (le:1016) (re:1393) (di:complement) AE000260 AE000260 g1787937 Escherichia coli 562 -11534951 6500731093 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1648 b1648 Escherichia coli 562 -11534951

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850975	10915	33071	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850976	10916	33072	294	97

Description

5000692400 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1649 b1649 Escherichia coli 562 -11534952
7000691400 conserved hypothetical protein b1649 (db:pir2.dat) C64922 C64922 Escherichia coli 562 -11534952 7500960037 b1649 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 150 of 400 of the completegenome.) (nt:o199; residues 18-121 are 26 pct identical to 104) (le:1358) (re:1957) (di:direct) AE000260 AE000260 g1787938 Escherichia coli 562 -11534952 6500731094 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1649 b1649 Escherichia coli 562 -11534952

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850977	10917	33073	315	104

Description

6500731095 nema:b1650 hypothetical protein:n-ethylmaleimide reductase:n-ethylmaleimide reducing enzyme (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1650 b1650 Escherichia coli 562 -11534953 1500687142 nema (ec:1.-.-.-) (de:enzyme)) (db:swissprot) NEMA_ECOLI P77258 ESCHERICHIA COLI 562 -11534953 7000685957 nema probable n-ethylmaleimide reductase:nema:hypothetical protein b1650 (cl:nadph dehydrogenase chain oye2) (ec:1.-.-.-) (db:pir2.dat) (mp:37 min) JC5605 JC5605 Escherichia coli 562 -11534953 222987 nema n-ethylmaleimide reducing enzyme (sr:escherichia coli (strain:w3110) dna, clone_lib:kohara linkage clon) (db:genpept-bct1) (de:escherichia coli dna for n-ethylmaleimide reducing enzyme, completecds, lactoylglutathion lyase n-terminal, partial cds.) (le:124) (re:1221) (di:direct) D86931 D86931 g1711244 Escherichia coli 562 -11534953 303356 nema n-ethylmaleimide reductase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 150 of 400 of the completegenome.) (nt:o365; this 365 aa orf is 41 pct identical (23 gaps)) (le:1994) (re:3091) (di:direct) AE000260 AE000260 g1787939 Escherichia coli 562 -11534953 5000692401 (de:(ecoli_1609) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1609 ECOLI_1609 Escherichia coli 562 10063836

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850982	10918	33074	990	329

Description

6500731096 ydhd:b1654 hypothetical protein in lhr 5region:hypothetical 12.9 kd protein in lhr-sodb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1654 b1654 Escherichia coli 562 -11534954 111351 ydhd (de:12.9 kd protein in lhr-sodb intergenic region) (db:swissprot) YDHD_ECOLI P37010 ESCHERICHIA COLI 562 -11534954 7000687551 ydhd probable glutaredoxin-like protein ydhd (cl:conserved hypothetical protein h1165) (db:pir2.dat) H64922 H64922 Escherichia coli 562 -11534954 224098 ydhd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #318(37.2-37.6 min.)) (nt:orf_id:o317#10; similar to (swissprot accession) (le:5346) (re:5693) (di:complement) D90809 D90809 g1742727 Escherichia coli 562 -11534954 7500922319 ydhd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 150 of 400 of the completegenome.) (nt:f115; 100 pct identical to fragment ydhd_ecoli) (le:9089) (re:9436) (di:complement) AE000260 AE000260 g1787943 Escherichia coli 562 -11534954 5000692403 (de:(ecoli_1613) (pn:hypothetical protein in lhr 5"region:fragment) (gn:ydhd) (gtcfc:13.7:14.1) (ec:) (ydhd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1613 ECOLI_1613 Escherichia coli 562 10119752

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850983	10919	33075	639	212

Description

6500731097 ydho:b1655 hypothetical protein:hypothetical 29.9 kd protein in lhr-sodb intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1655 b1655 Escherichia coli 562 -11534955 4000708204 ydho (de:hypothetical 29.9 kd protein in lhr-sodb intergenic region precursor) (db:swissprot) YDHO_ECOLI P76190 ESCHERICHIA COLI 562 -11534955 7000687552 hypothetical protein b1655 precursor (db:pir2.dat) A64923 A64923 Escherichia coli 562 -11534955 7500922334 ydho putative lipoprotein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 150 of 400 of the completegenome.) (nt:o271; this 271 aa orf is 27 pct identical (10 gaps)) (le:9770) (re:10585) (di:direct) AE000260 AE000260 g1787944 Escherichia coli 562 -11534955 5000692404 (de:(ecoli_1614) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1614 ECOLI_1614 Escherichia coli 562 10123411

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850985	10920	33076	969	322

Description

5000692405 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1657 b1657 Escherichia coli 562 -11534956
7000689507 chloramphenicol resistance protein homolog b1657 (cl:streptomyces lividans chloramphenicol resistance protein) (db:pir2.dat) C64923 C64923 Escherichia coli 562 -11534956 224101 protein araj precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #318(37.2-37.6 min.)) (nt:orf_id:o317#13; similar to (swissprot accession) (le:7713) (re:8882) (di:complement) D90809 D90809 g1742730 Escherichia coli 562 -11534956 224110 protein araj precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o317#13; similar to (swissprot accession) (le:107) (re:1276) (di:complement) D90810 D90810 g1742740 Escherichia coli 562 -11534956 300779 b1657 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 151 of 400 of the completegenome.) (nt:f389; residues 10-254 are 34 pct identical to) (le:837) (re:2006) (di:complement) AE000261 AE000261 g1787947 Escherichia coli 562 -11534956 6500731098 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1657 b1657 Escherichia coli 562 -11534956

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501850989	10921	33077	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851005	10922	33078	339	112

Description

GTC ORF with score 122 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f4i1 genomic sequence,complete sequence.) (nt:unknown protein) (le:107535:107864:108265) (re:107707:107980:108299) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851006	10923	33079	732	244

Description

6500731099 ydhb:b1659 hypothetical transcriptional regulator in cfa-purr
intergenic region:hypothetical transcriptional regulator in purr-cfa
intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1659 b1659 Escherichia coli 562 -11534957 111349
ydhb (de:hypothetical transcriptional regulator in purr-cfa intergenic
region) (db:swissprot) YDHB_ECOLI P37598 ESCHERICHIA COLI 562 -11534957
7000687549 ydhb probable transcription regulator ydbh (cl:probable
transcription regulator ybbs) (db:pir2.dat) E64923 E64923 Escherichia coli
562 -11534957 7500922317 ydhb putative transcriptional regulator lysr-type
(fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 151 of 400 of the completegenome.) (nt:f310; 100
pct identical to ydhb_ecoli sw: p37598) (le:3582) (re:4514) (di:complement)
AE000261 AE000261 g1787949 Escherichia coli 562 -11534957 5000692406
(de:(ecoli_1618) (pn:hypothetical transcriptional regulator in cfa-purr
intergenic region) (gn:ydhb) (gtcfc:13.7:14.1) (ec:) (ydhb_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1618
ECOLI_1618 Escherichia coli 562 10053079

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851015	10924	33080	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851021	10925	33081	402	133

Description

6500731100 ydhe:b1663 hypothetical protein in ribc 5region:hypothetical 49.4 kd protein in ribc-pykf intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1663 b1663 Escherichia coli 562 -11534958 7000691840 ydhe hypothetical protein in ribc 5region (cl:conserved hypothetical protein hi1612) (db:pir2.dat) A64924 A64924 Escherichia coli 562 -11534958 295372 ydhe (db:genpept-bct1) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:hypothetical protein ydhe) (le:861) (re:2234) (di:direct) ECU68703 U68703 g1549276 Escherichia coli 562 -11534958 239764 ydhe putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 151 of 400 of the completgenome.) (nt:o457; 99 pct identical to fragment ydhe_ecoli) (le:8173) (re:9546) (di:direct) AE000261 AE000261 g1787953 Escherichia coli 562 -11534958 5000692408 (de:(ecoli_1622) (pn:hypothetical protein in ribc 5"region:fragment) (gn:ydhe) (gtcfc:13.7:14.1) (ec:) (ydhe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1622 ECOLI_1622 Escherichia coli 562 10123413

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851028	10926	33082	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851034	10927	33083	1611	536

Description

5000692409 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1664 b1664 Escherichia coli 562 -11534959
7000691401 hypothetical protein b1664 (db:pir2.dat) B64924 B64924
Escherichia coli 562 -11534959 224109 adhesin aida-i precursor.
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #318(37.2-37.6 min.)) (nt:orf_id:o319#8; similar to (swissprot accession) (le:16464) (re:17720) (di:complement) D90809 D90809 g1742738 Escherichia coli 562 -11534959 300787 adhesin aida-i precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o319#8; similar to (swissprot accession) (le:8858) (re:10114) (di:complement) D90810 D90810 g1742748 Escherichia coli 562 -11534959 295373 (db:genpept-bct1) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:hypothetical protein) (le:2275) (re:3531) (di:complement) ECU68703 U68703 g1549277 Escherichia coli 562 -11534959 239765 b1664 possible enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 151 of 400 of the completegenome.) (nt:f418; this 418 aa orf is 31 pct identical (50 gaps)) (le:9587) (re:10843) (di:complement) AE000261 AE000261 g1787954 Escherichia coli 562 -11534959 224118 adhesin aida-i precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o319#8; similar to (swissprot accession) (le:8858) (re:10114) (di:complement) D90810 D90810 g1742748 Escherichia coli 562 -11534959 6500731101 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1664 b1664 Escherichia coli 562 -11534959

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851036	10928	33084	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851053	10929	33085	1176	391

Description

GTC ORF with score 656 to: (sr:homo sapiens adult male brain cdna to mrna, clone_lib:pbluescripti) (db:genpept-pri3) (de:homo sapiens mrna for kiaa0801 protein, complete cds.) (nt:hg03949 cdna clone for kiaa0801 has 923-bp and) (le:145) (re:3243) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851056	10930	33086	1023	340

Description

5000692410 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1667 b1667 Escherichia coli 562 -11534960
 7502852247 ydhr (de:hypothetical 11.3 kd protein in ribe-pykf intergenic region precursor) (db:swissprot) YDHR_ECOLI P77225 ESCHERICHIA COLI 562 -11534960 7000691402 hypothetical protein b1667 (db:pir2.dat) C64924 C64924 Escherichia coli 562 -11534960 295374 (db:genpept-bct1) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:hypothetical protein) (le:4104) (re:4409) (di:direct) ECU68703 U68703 g1549278 Escherichia coli 562 -11534960 239766 b1667 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 152 of 400 of the completegenome.) (nt:o101; this 101 aa orf is 23 pct identical (2 gaps)) (le:441) (re:746) (di:direct) AE000262 AE000262 g1787956 Escherichia coli 562 -11534960 6500731102 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1667 b1667 Escherichia coli 562 -11534960

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851058	10931	33087	399	132

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851081	10932	33088	756	252

Description

5000692411 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1668 b1668 Escherichia coli 562 -11534961
 7000691403 hypothetical protein b1668 (db:pir2.dat) D64924 D64924 Escherichia coli 562 -11534961 295375 (db:genpept-bct1) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:hypothetical protein) (le:4535) (re:6139) (di:direct) ECU68703 U68703 g1549279 Escherichia coli 562 -11534961 239767 b1668 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 152 of 400 of the completegenome.) (nt:o534; this 534 aa orf is 38 pct identical (6 gaps)) (le:872) (re:2476) (di:direct) AE000262 AE000262 g1787957 Escherichia coli 562 -11534961 6500731103 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1668 b1668 Escherichia coli 562 -11534961

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851084	10933	33089	480	159

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851089	10934	33090	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851092	10935	33091	348	115

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851095	10936	33092	489	162

Description

5000692412 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1669 b1669 Escherichia coli 562 -11534962
7000691404 hypothetical protein b1669 (db:pir2.dat) E64924 E64924
Escherichia coli 562 -11534962 300788 circumsporozoite protein precursor (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o319#12; similar to (pir accession number) (le:12734) (re:13546) (di:complement) D90810 D90810 g1742749 Escherichia coli 562 -11534962 295376 (db:genpept-bct1) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:hypothetical protein) (le:6151) (re:6963) (di:complement) ECU68703 U68703 g1549280 Escherichia coli 562 -11534962 239768 b1669 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 152 of 400 of the completegenome.) (nt:f270; this 270 aa orf is 24 pct identical (3 gaps)) (le:2488) (re:3300) (di:complement) AE000262 AE000262 g1787958 Escherichia coli 562 -11534962 224119 circumsporozoite protein precursor (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o319#12; similar to (pir accession number) (le:12734) (re:13546) (di:complement) D90810 D90810 g1742749 Escherichia coli 562 -11534962 6500731104 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1669 b1669 Escherichia coli 562 -11534962

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501851096	10937	33093	333	110

Description

6500731105 ydhu:b1670 hypothetical protein:phsc protein homolog (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1670 b1670 Escherichia coli 562 -11534963 1500687009 ydhu (de:phsc protein homolog) (db:swissprot) PHSC_ECOLI P77409 ESCHERICHIA COLI 562 -11534963 7000686141 hypothetical protein b1670 (db:pir2.dat) F64924 F64924 Escherichia coli 562 -11534963 300789 membrane anchoring protein phsc. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o319#14; similar to (swissprot accession) (le:13550) (re:14335) (di:complement) D90810 D90810 g1742750 Escherichia coli 562 -11534963 295377 (db:genpept-bct1) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:hypothetical protein) (le:6967) (re:7752) (di:complement) ECU68703 U68703 g1549281 Escherichia coli 562 -11534963 239769 ydhu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 152 of 400 of the completegenome.) (nt:f261; this 261 aa orf is 57 pct identical (3 gaps)) (le:3304) (re:4089) (di:complement) AE000262 AE000262 g1787959 Escherichia coli 562 -11534963 224120 membrane anchoring protein phsc. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o319#14; similar to (swissprot accession) (le:13550) (re:14335) (di:complement) D90810 D90810 g1742750 Escherichia coli 562 -11534963 5000692413 (de:(ecoli_1627) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1627 ECOLI_1627 Escherichia coli 562 10063342

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851097	10938	33094	192	64

Description

5000692414 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1671 b1671 Escherichia coli 562 -11534964
7000691405 hypothetical protein b1671 (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) G64924 G64924 Escherichia coli 562 -11534964 300790 thiosulfate reductase electron transport protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o319#15; similar to (swissprot accession) (le:14332) (re:15051) (di:complement) D90810 D90810 g1742751 Escherichia coli 562 -11534964 295378 (db:genpept-bct1) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:hypothetical protein) (le:7749) (re:8468) (di:complement) ECU68703 U68703 g1549282 Escherichia coli 562 -11534964 239770 b1671 putative oxidoreductase:fe-s subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 152 of 400 of the completegenome.) (nt:f239; this 239 aa orf is 50 pct identical (3 gaps)) (le:4086) (re:4805) (di:complement) AE000262 AE000262 g1787960 Escherichia coli 562 -11534964 224121 thiosulfate reductase electron transport protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o319#15; similar to (swissprot accession) (le:14332) (re:15051) (di:complement) D90810 D90810 g1742751 Escherichia coli 562 -11534964 6500731106 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1671 b1671 Escherichia coli 562 -11534964

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851102	10939	33095	369	122

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851118	10940	33096	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851121	10941	33097	420	139

Description

5000692415 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1672 b1672 Escherichia coli 562 -11534965
7000691406 hypothetical protein b1672 (db:pir2.dat) H64924 H64924
Escherichia coli 562 -11534965 295379 (db:genpept-bct1) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:hypothetical protein) (le:8481) (re:9128) (di:complement) ECU68703 U68703 g1549283 Escherichia coli 562 -11534965 239771 b1672 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 152 of 400 of the completegenome.) (nt:f215; this 215 aa orf is 23 pct identical (9 gaps)) (le:4818) (re:5465) (di:complement) AE000262 AE000262 g1787961 Escherichia coli 562 -11534965 6500731107 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1672 b1672 Escherichia coli 562 -11534965

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851126	10942	33098	303	100

Description

5000692416 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1673 b1673 Escherichia coli 562 -11534966
7500922336 ydhv (de:hypothetical 77.9 kd protein in ribe-pykf intergenic region) (db:swissprot) YDHV_ECOLI P76192 ESCHERICHIA COLI 562 -11534966
7000691407 hypothetical protein b1673 (db:pir2.dat) A64925 A64925
Escherichia coli 562 -11534966 7500922338 b1673 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 152 of 400 of the completegenome.) (nt:f700; 34 pct identical (2 gaps) to 66 residues) (le:5469) (re:7571) (di:complement) AE000262 AE000262 g1787962 Escherichia coli 562 -11534966 6500731108 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1673 b1673 Escherichia coli 562 -11534966

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851134	10943	33099	891	296

Description

GTC ORF with score 1016 to: (sr:plasmid ptrab3) (db:genpept-bct1) (de:agrobacterium vitis plasmid ptrab3 tartrate utilization generegion, including lysr-like regulator (ttua), membrane protein(ttub), tartrate dehydrogenase (ttuc and ttuc'), enzyme ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851137	10944	33100	750	249

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851154	10945	33101	453	150

Description

5000692417 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1674 b1674 Escherichia coli 562 -11534967
7000691408 hypothetical protein b1674 (db:pir2.dat) B64925 B64925
Escherichia coli 562 -11534967 300791 respiratory nitrate reductase 1 b chain ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o319#18; similar to (swissprot accession) (le:17838) (re:18464) (di:complement) D90810 D90810 g1742752 Escherichia coli 562 -11534967 295381 (db:genpept-bct1) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:hypothetical protein) (le:11255) (re:11881) (di:complement) ECU68703 U68703 g1549285 Escherichia coli 562 -11534967 239773 b1674 putative oxidoreductase:fe-s subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 152 of 400 of the completegenome.) (nt:f208; 30 pct identical (21 gaps) to 154 residues) (le:7592) (re:8218) (di:complement) AE000262 AE000262 g1787963 Escherichia coli 562 -11534967 224122 respiratory nitrate reductase 1 b chain ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #319(37.4-37.8 min.)) (nt:orf_id:o319#18; similar to (swissprot accession) (le:17838) (re:18464) (di:complement) D90810 D90810 g1742752 Escherichia coli 562 -11534967 6500731109 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1674 b1674 Escherichia coli 562 -11534967

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851161	10946	33102	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851164	10947	33103	417	138
<u>Description</u>				
5000692418 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1675 b1675 Escherichia coli 562 -11534968				
7000691409 hypothetical protein b1675 (db:pir2.dat) C64925 C64925 Escherichia coli 562 -11534968 295382 (db:genpept-bct1) (de:escherichia coli k-12 mg1655 genome, ribc-pykf region.) (nt:hypothetical protein) (le:12336) (re:12545) (di:complement) ECU68703 U68703 g1549286 Escherichia coli 562 -11534968 239774 b1675 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 152 of 400 of the completegenome.) (nt:f69; this 69 aa orf is 28 pct identical (2 gaps)) (le:8673) (re:8882) (di:complement) AE000262 AE000262 g1787964 Escherichia coli 562 -11534968 6500731110 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1675 b1675 Escherichia coli 562 -11534968				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851165	10948	33104	408	135
<u>Description</u>				
5000692419 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1678 b1678 Escherichia coli 562 -11534969				
7500951834 ynhg (de:hypothetical 36.1 kd protein in lpp-arod intergenic region precursor) (db:swissprot) YNHG_ECOLI P76193 ESCHERICHIA COLI 562 -11534969 7000691410 hypothetical protein b1678 (cl:conserved hypothetical protein b0819) (db:pir2.dat) F64925 F64925 Escherichia coli 562 -11534969				
7500951836 ynhg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 153 of 400 of the completegenome.) (nt:f334; residues 76-305 are 48 pct identical (6 gaps)) (le:593) (re:1597) (di:complement) AE000263 AE000263 g1787968 Escherichia coli 562 -11534969 6500731111 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1678 b1678 Escherichia coli 562 -11534969				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851170	10949	33105	357	119

Description

5000692420 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1679 b1679 Escherichia coli 562 -11534970
7500951825 ynha (de:hypothetical 15.8 kd protein in lpp-arod intergenic
region) (db:swissprot) YNHA_ECOLI P76194 ESCHERICHIA COLI 562 -11534970
7000691411 hypothetical protein b1679 (cl:hypothetical protein b2811)
(db:pir2.dat) G64925 G64925 Escherichia coli 562 -11534970 7500951827 ynha
orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 153 of 400 of the completgenome.) (nt:f138; this
138 aa orf is 22 pct identical (0 gaps)) (le:1746) (re:2162) (di:complement)
AE000263 AE000263 g1787969 Escherichia coli 562 -11534970 6500731112
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1679 b1679 Escherichia coli 562 -11534970

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851171	10950	33106	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851174	10951	33107	336	111

Description

5000692421 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1680 b1680 Escherichia coli 562 -11534971
7000691412 hypothetical protein b1680 (cl:nifs protein) (db:pir2.dat)
H64925 H64925 Escherichia coli 562 -11534971 224135 nifs protein.
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3
min.)) (nt:orf_id:o320#17; similar to (swissprot accession) (le:17025)
(re:18245) (di:direct) D90811 D90811 g1742766 Escherichia coli 562 -11534971
300810 nifs protein. (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #321(38.1-38.4 min.)) (nt:orf_id:o320#17; similar to
(swissprot accession) (le:4413) (re:5633) (di:direct) D90812 D90812 g1742773
Escherichia coli 562 -11534971 300804 b1680 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
153 of 400 of the completegenome.) (nt:f406; this 406 aa orf is 28 pct
identical (12 gaps)) (le:2175) (re:3395) (di:complement) AE000263 AE000263
g1787970 Escherichia coli 562 -11534971 224141 nifs protein.
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #321(38.1-38.4
min.)) (nt:orf_id:o320#17; similar to (swissprot accession) (le:4413)
(re:5633) (di:direct) D90812 D90812 g1742773 Escherichia coli 562 -11534971
6500731113 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1680 b1680 Escherichia coli 562 -11534971

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851207	10952	33108	819	272

Description

5000692422 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1681 b1681 Escherichia coli 562 -11534972
7500951828 ynhc (de:hypothetical 46.8 kd protein in lpp-arod intergenic region) (db:swissprot) YNHC_ECOLI P77689 ESCHERICHIA COLI 562 -11534972
7000691413 hypothetical protein b1681 (db:pir2.dat) A64926 A64926 Escherichia coli 562 -11534972 224134 ycf24 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.)) (nt:orf_id:o320#15; similar to (swissprot accession) (le:15757) (re:17028) (di:direct) D90811 D90811 g1742765 Escherichia coli 562 -11534972 300803 ycf24 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #321(38.1-38.4 min.)) (nt:orf_id:o320#15; similar to (swissprot accession) (le:3145) (re:4416) (di:direct) D90812 D90812 g1742772 Escherichia coli 562 -11534972 300809 ynhc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 153 of 400 of the completegenome.) (nt:f423; this 423 aa orf is 29 pct identical (1 gap)) (le:3392) (re:4663) (di:complement) AE000263 AE000263 g1787971 Escherichia coli 562 -11534972 224140 ycf24 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.)) (nt:orf_id:o320#15; similar to (swissprot accession) (le:15757) (re:17028) (di:direct) D90811 D90811 g1742765 Escherichia coli 562 -11534972 6500731114 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1681 b1681 Escherichia coli 562 -11534972

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501851211	10953	33109	744	247

Description

5000692423 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1682 b1682 Escherichia coli 562 -11534973

7500951830 ynhd (de:probable atp-dependent transporter ynhd) (db:swissprot) YNHD_ECOLI P77499 ESCHERICHIA COLI 562 -11534973 7000691414 hypothetical protein b1682 (cl:atp-binding cassette homology) (db:pir2.dat) B64926 B64926 Escherichia coli 562 -11534973 224133 ycf24 multidrug resistance protein 1 p-glycoprotein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.)) (nt:orf_id:o320#14; similar to (swissprot accession) (le:15036) (re:15782) (di:direct) D90811 D90811 g1742764 Escherichia coli 562 -11534973 300802 ycf24 multidrug resistance protein 1 p-glycoprotein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #321(38.1-38.4 min.)) (nt:orf_id:o320#14; similar to (swissprot accession) (le:2424) (re:3170) (di:direct) D90812 D90812 g1742771 Escherichia coli 562 -11534973 300808 ynhd putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 153 of 400 of the completegenome.) (nt:f248; this 248 aa orf is 56 pct identical (0 gaps)) (le:4638) (re:5384) (di:complement) AE000263 AE000263 g1787972 Escherichia coli 562 -11534973 224139 ycf24 multidrug resistance protein 1 p-glycoprotein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.)) (nt:orf_id:o320#14; similar to (swissprot accession) (le:15036) (re:15782) (di:direct) D90811 D90811 g1742764 Escherichia coli 562 -11534973 6500731115 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1682 b1682 Escherichia coli 562 -11534973

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851215	10954	33110	675	224

Description

5000692424 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1683 b1683 Escherichia coli 562 -11534974
7500951832 ynhe (de:hypothetical 56.3 kd protein in lpp-arod intergenic region) (db:swissprot) YNHE_ECOLI P77522 ESCHERICHIA COLI 562 -11534974
7000691415 hypothetical protein b1683 (cl:conserved hypothetical protein b1683) (db:pir2.dat) C64926 C64926 Escherichia coli 562 -11534974 224132 ycf24 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.)) (nt:orf_id:o320#13; similar to (swissprot accession) (le:13500) (re:15026) (di:direct) D90811 D90811 g1742763 Escherichia coli 562 -11534974 300801 ycf24 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #321(38.1-38.4 min.)) (nt:orf_id:o320#13; similar to (swissprot accession) (le:888) (re:2414) (di:direct) D90812 D90812 g1742770 Escherichia coli 562 -11534974 300807 ynhe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 153 of 400 of the completegenome.) (nt:f508; this 508 aa orf is 62 pct identical (18 gaps)) (le:5394) (re:6920) (di:complement) AE000263 AE000263 g1787973 Escherichia coli 562 -11534974 224138 ycf24 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.)) (nt:orf_id:o320#13; similar to (swissprot accession) (le:13500) (re:15026) (di:direct) D90811 D90811 g1742763 Escherichia coli 562 -11534974 6500731116 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1683 b1683 Escherichia coli 562 -11534974

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851231	10955	33111	582	193

Description

6500731117 ydic:b1684 hypothetical protein:hypothetical 13.3 kd protein in lpp-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1684 b1684 Escherichia coli 562 -11534975
1500686178 ydic (de:hypothetical 13.3 kd protein in lpp-arod intergenic region) (db:swissprot) YDIC_ECOLI P77667 ESCHERICHIA COLI 562 -11534975
7000687558 hypothetical protein b1684 (cl:conserved hypothetical protein hi0376) (db:pir2.dat) D64926 D64926 Escherichia coli 562 -11534975 224131 hesb protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.)) (nt:orf_id:o320#12; similar to (swissprot accession) (le:13162) (re:13530) (di:direct) D90811 D90811 g1742762 Escherichia coli 562 -11534975 300806 hesb protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #321(38.1-38.4 min.)) (nt:orf_id:o320#12; similar to (swissprot accession) (le:550) (re:918) (di:direct) D90812 D90812 g1742769 Escherichia coli 562 -11534975 300800 ydic orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 153 of 400 of the completengenome.) (nt:f122; this 122 aa orf is 42 pct identical (0 gaps)) (le:6890) (re:7258) (di:complement) AE000263 AE000263 g1787974 Escherichia coli 562 -11534975 224137 hesb protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #321(38.1-38.4 min.)) (nt:orf_id:o320#12; similar to (swissprot accession) (le:550) (re:918) (di:direct) D90812 D90812 g1742769 Escherichia coli 562 -11534975 5000692425 (de:(ecoli_1641) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1641 ECOLI_1641 Escherichia coli 562 10060786

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851233	10956	33112	1050	349

Description

5000692426 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1685 b1685 Escherichia coli 562 -11534976
7500922350 ydih (de:hypothetical 10.5 kd protein in lpp-arod intergenic region) (db:swissprot) YDIH_ECOLI P76195 ESCHERICHIA COLI 562 -11534976
7000691416 hypothetical protein b1685 (db:pir2.dat) E64926 E64926 Escherichia coli 562 -11534976 7500922352 b1685 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 153 of 400 of the completengenome.) (nt:f89; f89; this 89 aa orf is 36 pct identical) (le:7806) (re:8075) (di:complement) AE000263 AE000263 g1787975 Escherichia coli 562 -11534976 6500731118 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1685 b1685 Escherichia coli 562 -11534976

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851234	10957	33113	231	76

Description

5000692427 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1686 b1686 Escherichia coli 562 -11534977
 7000691417 conserved hypothetical protein b1686 (db:pir2.dat) F64926 F64926 Escherichia coli 562 -11534977 224130 coma operon protein 2.
 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.)) (nt:orf_id:o320#10; similar to (swissprot accession) (le:11916) (re:12326) (di:direct) D90811 D90811 g1742761 Escherichia coli 562 -11534977 300799 b1686 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 153 of 400 of the completegenome.) (nt:f136; 59 pct identical amino acid sequence and) (le:8094) (re:8504) (di:complement) AE000263 AE000263 g1787976 Escherichia coli 562 -11534977 6500731119 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1686 b1686 Escherichia coli 562 -11534977

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851241	10958	33114	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851245	10959	33115	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851270	10960	33116	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851278	10961	33117	420	139

Description

GTC ORF with score 161 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid c54g10, complete sequence.) (nt:similar to mitochondrial carrier protein; cdna est) (le:14550:14684:15041) (re:14585:14813:15343) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851281	10962	33118	345	114

Description

6500731120 ydij:b1687 hypothetical protein:hypothetical 113.2 kd protein in lpp-arod intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1687 b1687 Escherichia coli 562 -11534978 5500686544 ydij (de:hypothetical 113.2 kd protein in lpp-arod intergenic region) (db:swissprot) YDIJ_ECOLI P77748 ESCHERICHIA COLI 562 -11534978 7000687562 hypothetical protein b1687 (db:pir2.dat) G64926 G64926 Escherichia coli 562 -11534978 224129 glycolate oxidase subunit glcd. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.).) (nt:orf_id:o320#9; similar to (swissprot accession) (le:8863) (re:11919) (di:direct) D90811 D90811 g1742760 Escherichia coli 562 -11534978 300798 ydij putative oxidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 153 of 400 of the completegenome.) (nt:f1018; this 1018 aa orf is 20 pct identical) (le:8501) (re:11557) (di:complement) AE000263 AE000263 g1787977 Escherichia coli 562 -11534978 5000692428 (de:(ecoli_1644) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1644 ECOLI_1644 Escherichia coli 562 10119768

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851319	10963	33119	252	83

Description

5000692429 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1688 b1688 Escherichia coli 562 -11534979 7000691418 hypothetical protein b1688 (db:pir2.dat) H64926 H64926 Escherichia coli 562 -11534979 224128 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.).) (nt:orf_id:o320#8; similar to (swissprot accession) (le:7362) (re:8474) (di:complement) D90811 D90811 g1742759 Escherichia coli 562 -11534979 300797 b1688 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 154 of 400 of the completegenome.) (nt:o370; this 370 aa orf is 20 pct identical (13 gaps)) (le:320) (re:1432) (di:direct) AE000264 AE000264 g1787979 Escherichia coli 562 -11534979 6500731121 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1688 b1688 Escherichia coli 562 -11534979

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851321	10964	33120	513	170

Description

5000692430 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1689 b1689 Escherichia coli 562 -11534980
 7500922355 ydil (de:hypothetical 15.0 kd protein in lpp-arod intergenic region) (db:swissprot) YDIL_ECOLI P76196 ESCHERICHIA COLI 562 -11534980
 7000691419 hypothetical protein b1689 (db:pir2.dat) A64927 A64927 Escherichia coli 562 -11534980 7500922357 b1689 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 154 of 400 of the completegenome.) (nt:o127; uug start; this 127 aa orf is 36 pct) (le:1834) (re:2217) (di:direct) AE000264 AE000264 g1787980
 Escherichia coli 562 -11534980 6500731122 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1689 b1689
 Escherichia coli 562 -11534980

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851324	10965	33121	510	169

Description

5000692431 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1690 b1690 Escherichia coli 562 -11534981
 7000689499 hypothetical protein b1690 (cl:hypothetical protein b1691) (db:pir2.dat) B64927 B64927 Escherichia coli 562 -11534981 7500955799 b1690 putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 154 of 400 of the completegenome.) (nt:o404; this 404 aa orf is 23 pct identical (25 gaps)) (le:2317) (re:3531) (di:direct) AE000264 AE000264 g1787981
 Escherichia coli 562 -11534981 6500731123 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1690 b1690
 Escherichia coli 562 -11534981

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851329	10966	33122	1731	576

Description

5000692432 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1691 b1691 Escherichia coli 562 -11534982
 7000689498 hypothetical protein b1691 (cl:hypothetical protein b1691) (db:pir2.dat) C64927 C64927 Escherichia coli 562 -11534982 7500955798 b1691 putative amino acid/amine transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 154 of 400 of the completegenome.) (nt:o423; this 423 aa orf is 20 pct identical (22 gaps)) (le:3752) (re:5023) (di:direct) AE000264 AE000264 g1787982
 Escherichia coli 562 -11534982 6500731124 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1691 b1691
 Escherichia coli 562 -11534982

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851339	10967	33123	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851346	10968	33124	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851363	10969	33125	240	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851370	10970	33126	600	200

Description

5000692435 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1695 b1695 Escherichia coli 562 -11534983
7000691420 hypothetical protein b1695 (cl:acyl-coa dehydrogenase) (db:pir2.dat) G64927 G64927 Escherichia coli 562 -11534983 7500960038 b1695 putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 154 of 400 of the completegenome.) (nt:o401; this 401 aa orf is 48 pct identical (3 gaps)) (le:8388) (re:9593) (di:direct) AE000264 AE000264 g1787986 Escherichia coli 562 -11534983 6500731125 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1695 b1695 Escherichia coli 562 -11534983

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851375	10971	33127	324	107

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851377	10972	33128	219	72

Description

5000692436 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1696 b1696 Escherichia coli 562 -11534984
 7502852248 ydip (de:hypothetical transcriptional regulator in arod-pps intergenic region) (db:swissprot) YDIP_ECOLI P77402 ESCHERICHIA COLI 562 -11534984 7000691421 hypothetical protein b1696 (db:pir2.dat) H64927 H64927 Escherichia coli 562 -11534984 224143 msm operon regulatory protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #321(38.1-38.4 min.)) (nt:orf_id:o321#2; similar to (swissprot accession) (le:7756) (re:8667) (di:complement) D90812 D90812 g1742775 Escherichia coli 562 -11534984 300812 b1696 putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 154 of 400 of the completegenome.) (nt:f303; this 303 aa orf is 23 pct identical (13 gaps)) (le:9636) (re:10547) (di:complement) AE000264 AE000264 g1787987 Escherichia coli 562 -11534984 6500731126 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1696 b1696 Escherichia coli 562 -11534984

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851378	10973	33129	1038	345

Description

6500731127 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1697 b1697 Escherichia coli 562 -11534985
 5500686546 ydiq (de:putative electron transfer flavoprotein subunit ydiq) (db:swissprot) YDIQ_ECOLI P76201 ESCHERICHIA COLI 562 -11534985 7000687563 electron transfer flavoprotein beta chain homolog b1697 (cl:electron transfer flavoprotein beta chain) (db:pir2.dat) A64928 A64928 Escherichia coli 562 -11534985 7500922358 ydiq putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 155 of 400 of the completegenome.) (nt:o254; 55 pct identical (5 gaps) to the 256 aa) (le:236) (re:1000) (di:direct) AE000265 AE000265 g2367123 Escherichia coli 562 -11534985

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851384	10974	33130	630	209

Description

GTC ORF with score 141 to: (fn:involved in rhamnolipids synthesis) (db:genpept-bct2) (de:pseudomonas aeruginosa ctra, beta-ketoacyl reductase (rhlg), andregulator protein (rcsf) genes, complete cds.) (nt:rhlg) (le:1723) (re:2757) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851387	10975	33131	495	164

Description

GTC ORF with score 116 to: (db:genpept-bct2) (de:cenarchaeum symbiosum strain a hypothetical protein 01 gene,complete cds; 23s ribosomal rna and 16s ribosomal rna genes,complete sequence; glutamate-1-semialdehyde aminotransferase (gsat)and hypothetical...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851399	10976	33132	642	213

Description

5000692438 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1698 b1698 Escherichia coli 562 -11534986
5500686547 ydir (de:putative electron transfer flavoprotein subunit ydir) (db:swissprot) YDIR_ECOLI P77378 ESCHERICHIA COLI 562 -11534986 7000687564 electron transfer flavoprotein alpha chain homolog b1698 (cl:electron transfer flavoprotein alpha chain fixb) (db:pir2.dat) B64928 B64928 Escherichia coli 562 -11534986 224145 fixb protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #321(38.1-38.4 min.).)
(nt:orf_id:o321#4; similar to (swissprot accession) (le:9767) (re:10705) (di:direct) D90812 D90812 g1742777 Escherichia coli 562 -11534986 300814 ydir putative flavoprotein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 155 of 400 of the completengenome.) (nt:o312; this 312 aa orf is 45 pct identical (4 gaps)) (le:1020) (re:1958) (di:direct) AE000265 AE000265 g1787990 Escherichia coli 562 -11534986 6500731128 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1698 b1698 Escherichia coli 562 -11534986

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851405	10977	33133	330	109

Description

5000692439 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1699 b1699 Escherichia coli 562 -11534987
7000687565 ydis (ec:1.5.5.-) (de:(ec 1.5.5.-)) (db:swissprot) YDIS_ECOLI P77337 ESCHERICHIA COLI 562 -11534987 7000687566 fixc protein homolog b1699 (cl:fixc protein) (db:pir2.dat) C64928 C64928 Escherichia coli 562 -11534987 224146 fixc protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #321(38.1-38.4 min.).) (nt:orf_id:o321#6; similar to (swissprot accession) (le:10761) (re:12050) (di:direct) D90812 D90812 g1742778 Escherichia coli 562 -11534987 300815 ydis flavoprotein:probably electron transport (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 155 of 400 of the completegenome.) (nt:o429; this 429 aa orf is 60 pct identical (1 gap)) (le:2014) (re:3303) (di:direct) AE000265 AE000265 g1787991 Escherichia coli 562 -11534987
6500731129 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1699 b1699 Escherichia coli 562 -11534987

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851408	10978	33134	480	159

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851418	10979	33135	753	250

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851419	10980	33136	534	177

Description

5000692440 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1700 b1700 Escherichia coli 562 -11534988
7000687567 ydit (de:ferredoxin like protein ydit) (db:swissprot) YDIT_ECOLI P77714 ESCHERICHIA COLI 562 -11534988 7000687568 fixx protein homolog b1700 (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) D64928 D64928 Escherichia coli 562 -11534988 224147 ferredoxin like protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #321(38.1-38.4 min.)) (nt:orf_id:o321#7; similar to (swissprot accession) (le:12047) (re:12340) (di:direct) D90812 D90812 g1742779 Escherichia coli 562 -11534988 300816 ydit orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 155 of 400 of the completegenome.) (nt:o97; this 97 aa orf is 63 pct identical (0 gaps)) (le:3300) (re:3593) (di:direct) AE000265 AE000265 g1787992 Escherichia coli 562 -11534988
6500731130 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1700 b1700 Escherichia coli 562 -11534988

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851425	10981	33137	366	121

Description

6500731131 ydia:b1703 hypothetical 19.8 kd protein in ppsa-aroh intergenic region:hypothetical 31.2 kd protein in ppsa-aroh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1703 b1703 Escherichia coli 562 -11534989 111358 ydia (de:hypothetical 31.2 kd protein in ppsa-aroh intergenic region) (db:swissprot) YDIA_ECOLI P03822 ESCHERICHIA COLI 562 -11534989 7000687556 ydia hypothetical ydia protein ppsa-aroh intergenic region (cl:ydia protein) (db:pir1.dat) (mp:37 min) QQECAD G64928 Escherichia coli 562 -11534989 7500922339 ydia orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 155 of 400 of the completegenome.) (nt:o277; 100 pct identical to fragment ydia_ecoli) (le:8064) (re:8897) (di:direct) AE000265 AE000265 g1787995 Escherichia coli 562 -11534989 5000692442 (de:(ecoli_1660) (pn:hypothetical 19) (gn:ydia) (gtcfc:13.7:14.1) (ec:) (ydia_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1660 ECOLI_1660 Escherichia coli 562 10123430

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851426	10982	33138	261	86

Description

6500731132 ydie:b1705 hypothetical 7.1 kd protein in aroh-nlpc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1705 b1705 Escherichia coli 562 -11534990 111362 ydie (de:hypothetical 7.1 kd protein in aroh-nlpc intergenic region) (db:swissprot) YDIE_ECOLI P40721 ESCHERICHIA COLI 562 -11534990 7000687560 ydie hypothetical 7.1 kd protein in aroh-nlpc intergenic region (cl:hemp protein) (db:pir2.dat) A64929 A64929 Escherichia coli 562 -11534990 224153 ydie (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf_id:o322#6; similar to (swissprot accession) (le:6358) (re:6549) (di:direct) D90813 D90813 g1742786 Escherichia coli 562 -11534990 300822 ydie orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:o63; 100 pct identical to ydie_ecoli sw: p40721) (le:96) (re:287) (di:direct) AE000266 AE000266 g1787998 Escherichia coli 562 -11534990 5000692443 (de:(ecoli_1662) (pn:hypothetical 7) (gn:ydie) (gtcfc:13.7:14.1) (ec:) (ydie_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1662 ECOLI_1662 Escherichia coli 562 10053092

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851447	10983	33139	1689	562

Description

GTC ORF with score 143 to: (or:Sus scrofa) (fn:gel formation, gastric epithelial protection) (sr:pig) (db:genpept-mam) (de:sus scrofa yorkshire/chester white/hampshire clone pgm-ssz-9bgastatic mucin mrna, partial cds.) (le:<1) (re:1584) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851450	10984	33140	2556	851

Description

5000692444 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1706 b1706 Escherichia coli 562 -11534991
7500922359 ydiu (de:hypothetical 54.4 kd protein in aroh-nlpc intergenic region) (db:swissprot) YDIU_ECOLI P77649 ESCHERICHIA COLI 562 -11534991
7000691422 hypothetical protein b1706 (cl:hypothetical protein b1706) (db:pir2.dat) B64929 B64929 Escherichia coli 562 -11534991 224154 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf_id:o322#7; similar to (swissprot accession) (le:6553) (re:7989) (di:complement) D90813 D90813 g1742787 Escherichia coli 562 -11534991 7500922361 b1706 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f478; this 478 aa orf is 39 pct identical (17 gaps)) (le:291) (re:1727) (di:complement) AE000266 AE000266 g1787999 Escherichia coli 562 -11534991 300823 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #322(38.4-38.8 min.)) (nt:orf_id:o322#7; similar to (swissprot accession) (le:6553) (re:7989) (di:complement) D90813 D90813 g1742787 Escherichia coli 562 -11534991 6500731133 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1706 b1706 Escherichia coli 562 -11534991

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851466	10985	33141	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851477	10986	33142	618	205

Description

5000692445 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1707 b1707 Escherichia coli 562 -11534992
7000691423 hypothetical protein b1707 (db:pir2.dat) C64929 C64929 Escherichia coli 562 -11534992 7500960039 b1707 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 156 of 400 of the completegenome.) (nt:f237; this 237 aa orf is 21 pct identical (6 gaps)) (le:1790) (re:2503) (di:complement) AE000266 AE000266 g1788000 Escherichia coli 562 -11534992 6500731134 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1707 b1707 Escherichia coli 562 -11534992

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851485	10987	33143	1401	466

Description

5000692446 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1720 b1720 Escherichia coli 562 -11534993
7000691424 hypothetical protein b1720 (db:pir2.dat) H64930 H64930
Escherichia coli 562 -11534993 7500960040 b1720 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 157 of 400 of the completegenome.) (nt:o157; residues 63-120 are 32 pct identical to) (le:3077) (re:3550) (di:direct) AE000267 AE000267 g1788014
Escherichia coli 562 -11534993 6500731135 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1720 b1720
Escherichia coli 562 -11534993

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851487	10988	33144	504	167

Description

5000692447 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1721 b1721 Escherichia coli 562 -11534994
7000691425 hypothetical protein b1721 (db:pir2.dat) A64931 A64931
Escherichia coli 562 -11534994 224178 ankyrin-like regulatory protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.)) (nt:orf_id:o324#2; similar to (swissprot accession) (le:13163) (re:14578) (di:direct) D90814 D90814 g1742812 Escherichia coli 562 -11534994
224184 ankyrin-like regulatory protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #324(38.8-39.1 min.)) (nt:orf_id:o324#2; similar to (swissprot accession) (le:3108) (re:4523) (di:direct) D90815 D90815 g1742819
Escherichia coli 562 -11534994 300837 b1721 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 157 of 400 of the completegenome.) (nt:o471; this 471 aa orf is 31 pct identical (5 gaps)) (le:3561) (re:4976) (di:direct) AE000267 AE000267 g1788015
Escherichia coli 562 -11534994 6500731136 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1721 b1721 Escherichia coli 562 -11534994

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851492	10989	33145	792	263

Description

5000692448 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1722 b1722 Escherichia coli 562 -11534995
 7502852249 ydiy (de:hypothetical 27.6 kd protein in arpb-pfkb intergenic region precursor) (db:swissprot) YDIY_ECOLI P76206 ESCHERICHIA COLI 562 -11534995 7000691426 hypothetical protein b1722 (db:pir2.dat) B64931 B64931 Escherichia coli 562 -11534995 7500960041 b1722 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 157 of 400 of the completegenome.) (nt:f252; this 252 aa orf is 25 pct identical (6 gaps)) (le:5308) (re:6066) (di:complement) AE000267 AE000267 g1788016 Escherichia coli 562 -11534995 6500731137 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1722 b1722 Escherichia coli 562 -11534995

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851531	10990	33146	1443	480

Description

GTC ORF with score 294 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851534	10991	33147	603	201

Description

5000692449 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1724 b1724 Escherichia coli 562 -11534996
 7500922362 ydiz (de:hypothetical 10.9 kd protein in pfkb-ceda intergenic region) (db:swissprot) YDIZ_ECOLI P76207 ESCHERICHIA COLI 562 -11534996
 7000691427 hypothetical protein b1724 (db:pir2.dat) D64931 D64931 Escherichia coli 562 -11534996 7500922364 b1724 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 157 of 400 of the completegenome.) (nt:o96; this 96 aa orf is 29 pct identical (2 gaps)) (le:7383) (re:7673) (di:direct) AE000267 AE000267 g1788018 Escherichia coli 562 -11534996 6500731138 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1724 b1724 Escherichia coli 562 -11534996

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851536	10992	33148	2271	756
<u>Description</u>				
5000692450 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1725 b1725 Escherichia coli 562 -11534997				
7000691428 hypothetical protein b1725 (cl:hypothetical protein b1725) (db:pir2.dat) E64931 E64931 Escherichia coli 562 -11534997 224180 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #323(38.6-39.0 min.)) (nt:orf_id:o324#5; similar to (swissprot accession) (le:17381) (re:18241) (di:direct) D90814 D90814 g1742814 Escherichia coli 562 -11534997 224186 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #324(38.8-39.1 min.)) (nt:orf_id:o324#5; similar to (swissprot accession) (le:7326) (re:8186) (di:direct) D90815 D90815 g1742821 Escherichia coli 562 -11534997 224190 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #325(38.9-39.2 min.)) (nt:orf_id:o324#5; similar to (swissprot accession) (le:385) (re:1245) (di:direct) D90816 D90816 g1742826 Escherichia coli 562 -11534997 300839 b1725 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 157 of 400 of the completengenome.) (nt:o286; this 286 aa orf is 87 pct identical (0 gaps)) (le:7779) (re:8639) (di:direct) AE000267 AE000267 g1788019 Escherichia coli 562 -11534997 6500731139 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1725 b1725 Escherichia coli 562 -11534997				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851540	10993	33149	753	250
<u>Description</u>				
5000692451 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1726 b1726 Escherichia coli 562 -11534998				
7500951846 ynib (de:hypothetical 20.4 kd protein in pfkb-ceda intergenic region) (db:swissprot) YNIB_ECOLI P76208 ESCHERICHIA COLI 562 -11534998				
7000691429 hypothetical protein b1726 (db:pir2.dat) F64931 F64931 Escherichia coli 562 -11534998 7500951848 b1726 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 157 of 400 of the completengenome.) (nt:f178; this 178 aa orf is 30 pct identical (13 gaps)) (le:8680) (re:9216) (di:complement) AE000267 AE000267 g1788020 Escherichia coli 562 -11534998 6500731140 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1726 b1726 Escherichia coli 562 -11534998				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851541	10994	33150	768	255

Description

5000692452 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1727 b1727 Escherichia coli 562 -11534999
7500951849 ynic (de:hypothetical 24.3 kd protein in pfkb-ceda intergenic region) (db:swissprot) YNIC_ECOLI P77247 ESCHERICHIA COLI 562 -11534999
7000691430 hypothetical protein b1727 (cl:hypothetical protein b2690) (db:pir2.dat) G64931 G64931 Escherichia coli 562 -11534999 224187
phosphoglycolate phosphatase ec 3.1.3.18 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #324(38.8-39.1 min.)) (nt:orf_id:o324#7; similar to (swissprot accession) (le:8910) (re:9578) (di:direct) D90815 D90815 g1742822 Escherichia coli 562 -11534999 300840 phosphoglycolate phosphatase ec 3.1.3.18 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #325(38.9-39.2 min.)) (nt:orf_id:o324#7; similar to (swissprot accession) (le:1969) (re:2637) (di:direct) D90816 D90816 g1742827 Escherichia coli 562 -11534999 7500951851 ynic putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 157 of 400 of the completegenome.) (nt:o222; this 222 aa orf is 31 pct identical (15 gaps)) (le:9363) (re:10031) (di:direct) AE000267 AE000267 g1788021 Escherichia coli 562 -11534999 224191 phosphoglycolate phosphatase ec 3.1.3.18 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #324(38.8-39.1 min.)) (nt:orf_id:o324#7; similar to (swissprot accession) (le:8910) (re:9578) (di:direct) D90815 D90815 g1742822 Escherichia coli 562 -11534999 6500731141 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1727 b1727 Escherichia coli 562 -11534999

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851550	10995	33151	735	244

Description

GTC ORF with score 146 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851554	10996	33152	651	216

Description

5000692453 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1728 b1728 Escherichia coli 562 -11535000
7000691431 hypothetical protein b1728 (db:pir2.dat) H64931 H64931
Escherichia coli 562 -11535000 7500960042 b1728 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 158 of 400 of the completegenome.) (nt:o200; this 200 aa orf is 32 pct identical (15 gaps)) (le:106) (re:708) (di:direct) AE000268 AE000268 g1788023 Escherichia coli 562 -11535000 6500731142 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1728 b1728 Escherichia coli 562 -11535000

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851556	10997	33153	450	149

Description

5000692454 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1729 b1729 Escherichia coli 562 -11535001
7000691432 hypothetical protein b1729 (cl:bacillus subtilis sodium-glutamate symporter homolog yhc1) (db:pir2.dat) A64932 A64932
Escherichia coli 562 -11535001 224188 proton/sodium-glutamate symport protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #324(38.8-39.1 min.)) (nt:orf_id:o324#9; similar to (swissprot accession) (le:10464) (re:11855) (di:direct) D90815 D90815 g1742823 Escherichia coli 562 -11535001 224192 proton/sodium-glutamate symport protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #325(38.9-39.2 min.)) (nt:orf_id:o324#9; similar to (swissprot accession) (le:3523) (re:4914) (di:direct) D90816 D90816 g1742828 Escherichia coli 562 -11535001 300841 b1729 part of a kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 158 of 400 of the completegenome.) (nt:o463; this 463 aa orf is 55 pct identical (3 gaps)) (le:841) (re:2232) (di:direct) AE000268 AE000268 g1788024 Escherichia coli 562 -11535001 6500731143 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1729 b1729 Escherichia coli 562 -11535001

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851562	10998	33154	522	173

Description

5000692455 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1730 b1730 Escherichia coli 562 -11535002
 7502852250 ydjo (de:hypothetical 30.7 kd protein in pkfb-ceda intergenic region) (db:swissprot) YDJO_ECOLI P76210 ESCHERICHIA COLI 562 -11535002
 7000691433 hypothetical protein b1730 (db:pir2.dat) B64932 B64932 Escherichia coli 562 -11535002 7500960043 b1730 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 158 of 400 of the completegenome.) (nt:f271; this 271 aa orf is 22 pct identical (12 gaps)) (le:2236) (re:3051) (di:complement) AE000268 AE000268 g1788025 Escherichia coli 562 -11535002 6500731144 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1730 b1730 Escherichia coli 562 -11535002

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851577	10999	33155	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851585	11000	33156	438	145

Description

GTC ORF with score 260 to: (or:Glomerella cingulata) (db:genpept-pln1) (de:colletotrichum gloeosporioides nitrogen starvation-inducedglutamine rich protein mrna, complete cds.) (nt:glutamine rich protein similar to glutenins;) (le:74) (re:721) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851603	11001	33157	330	109

Description

5000692456 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1731 b1731 Escherichia coli 562 -11535003
 7500878514 ceda (de:cell division activator ceda) (db:swissprot) CEDA_ECOLI P76211 ESCHERICHIA COLI 562 -11535003 7000691434 hypothetical protein b1731 (db:pir2.dat) C64932 C64932 Escherichia coli 562 -11535003 7500878516 b1731 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 158 of 400 of the completegenome.) (nt:f87; this 87 aa orf is 24 pct identical (3 gaps)) (le:3328) (re:3591) (di:complement) AE000268 AE000268 g1788026 Escherichia coli 562 -11535003 6500731145 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1731 b1731 Escherichia coli 562 -11535003

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851608	11002	33158	1647	548
<u>Description</u>				
5000692459 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1741 b1741 Escherichia coli 562 -11535004				
7000691435 hypothetical protein b1741 (db:pir2.dat) E64933 E64933 Escherichia coli 562 -11535004 7500960044 b1741 putative excinuclease subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.) (nt:o295) (le:2289) (re:3176) (di:direct) AE000269 AE000269 g1788037 Escherichia coli 562 -11535004 6500731146 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1741 b1741 Escherichia coli 562 -11535004				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851620	11003	33159	441	146
<u>Description</u>				
5000692460 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1742 b1742 Escherichia coli 562 -11535005				
7000691436 hypothetical protein b1742 (db:pir2.dat) F64933 F64933 Escherichia coli 562 -11535005 7500960045 b1742 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.) (nt:f212; this 212 aa orf is 30 pct identical (7 gaps)) (le:3136) (re:3774) (di:complement) AE000269 AE000269 g1788038 Escherichia coli 562 -11535005 6500731147 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1742 b1742 Escherichia coli 562 -11535005				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501851623	11004	33160	792	263

Description

6500731148 spy:b1743 hypothetical protein:spheroplast protein y precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1743 b1743 Escherichia coli 562 -11535006 5500685996 spy (de:spheroplast protein y precursor) (db:swissprot) SPY_ECOLI P77754 ESCHERICHIA COLI 562 -11535006 7000686671 hypothetical protein b1743 (db:pir2.dat) G64933 G64933 Escherichia coli 562 -11535006 224211 yiio (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #326(39.1-39.4 min.)) (nt:orf_id:o326#12; similar to (swissprot accession) (le:10500) (re:10985) (di:complement) D90817 D90817 g1742848 Escherichia coli 562 -11535006 300859 yiio (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #327(39.2-39.5 min.)) (nt:orf_id:o326#12; similar to (swissprot accession) (le:4868) (re:5353) (di:complement) D90818 D90818 g1742855 Escherichia coli 562 -11535006 308427 spy spheroplast protein y (db:genpept-bct1) (de:e.coli spy gene.) (le:1032) (re:1517) (di:direct) ECSPYGENE Y07714 g1655583 Escherichia coli 562 -11535006 238296 spy periplasmic protein related to spheroblast (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.) (nt:f161; this 161 aa orf is 29 pct identical (6 gaps)) (le:3914) (re:4399) (di:complement) AE000269 AE000269 g1788039 Escherichia coli 562 -11535006 224217 yiio (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #327(39.2-39.5 min.)) (nt:orf_id:o326#12; similar to (swissprot accession) (le:4868) (re:5353) (di:complement) D90818 D90818 g1742855 Escherichia coli 562 -11535006 300853 spy spheroplast protein y (db:genpept-bct1) (de:e.coli spy gene.) (le:1032) (re:1517) (di:direct) ECSPYGENE Y07714 g1655583 Escherichia coli 562 -11535006 5000692461 (de:(ecoli_1700) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1700 ECOLI_1700 Escherichia coli 562 10119807

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501851627	11005	33161	768	255

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851638	11006	33162	414	137

Description

6500731149 ydjs:b1744 hypothetical protein:hypothetical 35.8 kd protein in spy-cstc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1744 b1744 Escherichia coli 562 -11535007 5500686548 aste (ec:3.1.-.-) (de:succinylglutamate desuccinylase,) (db:swissprot) ASTE_ECOLI P76215 ESCHERICHIA COLI 562 -11535007 7000687571 hypothetical protein b1744 (db:pir2.dat) H64933 H64933 Escherichia coli 562 -11535007 7500922387 ydjs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.) (nt:f322) (le:4729) (re:5697) (di:complement) AE000269 AE000269 g1788040 Escherichia coli 562 -11535007 5000692462 (de:(ecoli_1701) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1701 ECOLI_1701 Escherichia coli 562 10123445

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851640	11007	33163	1644	548

Description

5000692463 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1745 b1745 Escherichia coli 562 -11535008 7502852251 astb (ec:3.-.-.-) (de:succinylarginine dihydrolase,) (db:swissprot) ASTB_ECOLI P76216 ESCHERICHIA COLI 562 -11535008 7000691437 hypothetical protein b1745 (db:pir2.dat) A64934 A64934 Escherichia coli 562 -11535008 7500960046 b1745 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.) (nt:f447) (le:5690) (re:7033) (di:complement) AE000269 AE000269 g1788041 Escherichia coli 562 -11535008 6500731150 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1745 b1745 Escherichia coli 562 -11535008

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851657	11008	33164	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851664	11009	33165	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851665	11010	33166	279	92

Description

5000692464 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1746 b1746 Escherichia coli 562 -11535009
 7502852252 astd (ec:1.2.1.-) (de:succinylglutamic semialdehyde dehydrogenase,) (db:swissprot) ASTD_ECOLI P76217 ESCHERICHIA COLI 562 -11535009 7000691438 hypothetical protein b1746 (db:pir2.dat) B64934 B64934 Escherichia coli 562 -11535009 7500960047 b1746 putative aldehyde dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.) (nt:f492; 30 pct identical (13 gaps) to 465 residues) (le:7030) (re:8508) (di:complement) AE000269 AE000269 g1788042 Escherichia coli 562 -11535009 6500731151 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1746 b1746 Escherichia coli 562 -11535009

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851666	11011	33167	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851669	11012	33168	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851677	11013	33169	666	221

Description

5000692465 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1747 b1747 Escherichia coli 562 -11535010
 7502852253 asta (ec:2.-.-.-) (de:arginine succinyltransferase,) (db:swissprot) ASTA_ECOLI P76218 ESCHERICHIA COLI 562 -11535010 7000691439 hypothetical protein b1747 (db:pir2.dat) C64934 C64934 Escherichia coli 562 -11535010 7500960048 b1747 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.) (nt:f344; 26 pct identical (5 gaps) to 90 residues) (le:8505) (re:9539) (di:complement) AE000269 AE000269 g1788043 Escherichia coli 562 -11535010 6500731152 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1747 b1747 Escherichia coli 562 -11535010

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851678	11014	33170	597	198

Description

7000687572 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1750 b1750 Escherichia coli 562 -11535011
7000687573 hypothetical protein b1750 (cl:hypothetical protein b1750) (db:pir2.dat) F64934 F64934 Escherichia coli 562 -11535011 7500960050 ydix orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completegenome.) (nt:o252; this 252 aa orf is 33 pct identical (7 gaps)) (le:1178) (re:1936) (di:direct) AE000270 AE000270 g1788047 Escherichia coli 562 -11535011 6500731153 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1750 b1750 Escherichia coli 562 -11535011 5000692467 (de:(ecoli_1707) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1707 ECOLI_1707 Escherichia coli 562 -11535011

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851679	11015	33171	222	73

Description

5000692468 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1751 b1751 Escherichia coli 562 -11535012
7000687574 ydij (de:hypothetical 30.4 kd protein in xtha-gdha intergenic region) (db:swissprot) YDIJ_ECOLI P76220 ESCHERICHIA COLI 562 -11535012
7000687575 hypothetical protein b1751 (db:pir2.dat) G64934 G64934 Escherichia coli 562 -11535012 7500922389 ydij orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completegenome.) (nt:o279) (le:1779) (re:2618) (di:direct) AE000270 AE000270 g1788048 Escherichia coli 562 -11535012 6500731154 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1751 b1751 Escherichia coli 562 -11535012

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851681	11016	33172	237	78

Description

5000692469 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1752 b1752 Escherichia coli 562 -11535013
7000687576 ydjz (de:hypothetical 26.2 kd protein in xtha-gdha intergenic region) (db:swissprot) YDJZ_ECOLI P76221 ESCHERICHIA COLI 562 -11535013
7000687577 hypothetical protein b1752 (db:pir2.dat) H64934 H64934
Escherichia coli 562 -11535013 7500922390 ydjz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completegenome.) (nt:o235; this 235 aa orf is 29 pct identical (10 gaps)) (le:2633) (re:3340) (di:direct) AE000270 AE000270
g1788049 Escherichia coli 562 -11535013 6500731155 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1752 b1752 Escherichia coli 562 -11535013

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851685	11017	33173	276	92

Description

5000692470 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1753 b1753 Escherichia coli 562 -11535014
5500686632 ynja (de:hypothetical 20.5 kd protein in xtha-gdha intergenic region) (db:swissprot) YNJA_ECOLI P76222 ESCHERICHIA COLI 562 -11535014
7000688169 hypothetical protein b1753 (db:pir2.dat) A64935 A64935
Escherichia coli 562 -11535014 7500951864 ynja orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completegenome.) (nt:o182; this 182 aa orf is 20 pct identical (4 gaps)) (le:3340) (re:3888) (di:direct) AE000270 AE000270
g1788050 Escherichia coli 562 -11535014 6500731156 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1753 b1753 Escherichia coli 562 -11535014

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851698	11018	33174	423	140

Description

5000692471 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1754 b1754 Escherichia coli 562 -11535015
7000691440 hypothetical protein b1754 (db:pir2.dat) B64935 B64935
Escherichia coli 562 -11535015 7500960051 b1754 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completegenome.) (nt:o389; this 389 aa orf is 26 pct identical (14 gaps)) (le:3895) (re:5064) (di:direct) AE000270 AE000270
g1788051 Escherichia coli 562 -11535015 6500731157 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1754 b1754 Escherichia coli 562 -11535015

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851700	11019	33175	951	316

Description

GTC ORF with score 133 to: (sr:thale cress) (db:genpept-pln1) (de:sequence of bac tlg11 from arabidopsis thaliana chromosome 1,complete sequence.) (nt:contains similarity to human dimethylaniline) (le:51751:52311:52845) (re:51978:52682:53558) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851703	11020	33176	666	221

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851704	11021	33177	372	123

Description

5000692472 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1755 b1755 Escherichia coli 562 -11535016
7000691441 hypothetical protein b1755 (db:pir2.dat) C64935 C64935
Escherichia coli 562 -11535016 7500960052 b1755 putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completegenome.) (nt:o496; 23 pct identical (9 gaps) to 244 residues) (le:5082) (re:6572) (di:direct) AE000270 AE000270 g1788052 Escherichia coli 562 -11535016
6500731158 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1755 b1755 Escherichia coli 562 -11535016

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851739	11022	33178	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851744	11023	33179	549	182

Description

5000692473 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1756 b1756 Escherichia coli 562 -11535017
7000691442 hypothetical protein b1756 (cl:atp-binding cassette homology) (db:pir2.dat) D64935 D64935 Escherichia coli 562 -11535017 7500960053 b1756 putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completegenome.) (nt:o217; 38 pct identical (4 gaps) to 190 residues) (le:6572) (re:7225) (di:direct) AE000270 AE000270 g1788053 Escherichia coli 562 -11535017 6500731159 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1756 b1756 Escherichia coli 562 -11535017

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851752	11024	33180	1656	551

Description

5000692474 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1757 b1757 Escherichia coli 562 -11535018
7000691443 hypothetical protein b1757 (db:pir2.dat) E64935 E64935 Escherichia coli 562 -11535018 7500951867 b1757 putative thiosulfate sulfur transferase (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completegenome.) (nt:o440; this 440 aa orf is 27 pct identical (23 gaps)) (le:7277) (re:8599) (di:direct) AE000270 AE000270 g1788054 Escherichia coli 562 -11535018 7500951865 ynje (ec:2.8.1.1) (de:putative thiosulfate sulfurtransferase ynje,) (db:swissprot) YNJE_ECOLI P78067 ESCHERICHIA COLI 562 -11535018 6500731160 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1757 b1757 Escherichia coli 562 -11535018

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851761	11025	33181	597	198

Description

5000692475 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1758 b1758 Escherichia coli 562 -11535019
7000691444 hypothetical protein b1758 (db:pir2.dat) F64935 F64935 Escherichia coli 562 -11535019 7500960054 b1758 putative cytochrome oxidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completegenome.) (nt:f208; this 208 aa orf is 25 pct identical (11 gaps)) (le:8608) (re:9234) (di:complement) AE000270 AE000270 g1788055 Escherichia coli 562 -11535019 6500731161 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1758 b1758 Escherichia coli 562 -11535019

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851763	11026	33182	903	300

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851771	11027	33183	234	77

Description

5000692476 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1759 b1759 Escherichia coli 562 -11535020
7000691445 hypothetical protein b1759 (cl:mutt domain homology) (db:pir2.dat) G64935 G64935 Escherichia coli 562 -11535020 224229 mutator mutt protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #328(39.4-39.8 min.)) (nt:orf_id:o328#12; similar to (swissprot accession) (le:13004) (re:13411) (di:direct) D90819 D90819 g1742868 Escherichia coli 562 -11535020 300871 b1759 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completengenome.) (nt:o135; this 135 aa orf is 37 pct identical (5 gaps)) (le:9315) (re:9722) (di:direct) AE000270 AE000270 g1788056 Escherichia coli 562 -11535020 6500731162 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1759 b1759 Escherichia coli 562 -11535020

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851772	11028	33184	657	218

Description

5000692477 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1760 b1760 Escherichia coli 562 -11535021
7000691446 hypothetical protein b1760 (db:pir2.dat) H64935 H64935 Escherichia coli 562 -11535021 7500960055 b1760 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 160 of 400 of the completengenome.) (nt:f90; this 90 aa orf is 26 pct identical (2 gaps)) (le:9688) (re:9960) (di:complement) AE000270 AE000270 g1788057 Escherichia coli 562 -11535021 6500731163 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1760 b1760 Escherichia coli 562 -11535021

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851781	11029	33185	981	326

Description

5000692478 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1762 b1762 Escherichia coli 562 -11535022
7000691447 hypothetical protein b1762 (db:pir2.dat) B64936 B64936
Escherichia coli 562 -11535022 7500960056 b1762 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 161 of 400 of the completegenome.) (nt:f387; alternate name orf 2 of j05076; this 387) (le:1608) (re:2771) (di:complement) AE000271 AE000271 g1788060
Escherichia coli 562 -11535022 6500731164 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1762 b1762
Escherichia coli 562 -11535022

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851784	11030	33186	522	173

Description

6500731165 ydja:b1765 hypothetical 20.1 kd protein in seld-sppa intergenic region:orf183 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1765 b1765 Escherichia coli 562 -11535023 111365 ydja (de:hypothetical 20.1 kd protein in seld-sppa intergenic region (orf183)) (db:swissprot) YDJA_ECOLI P24250 ESCHERICHIA COLI 562 -11535023 163900 ydja hypothetical protein:20k seld-sppa intergenic region (db:pir2.dat) A40360 A40360 Escherichia coli 562 -11535023 224236 ydja (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.).) (nt:orf_id:o329#2; similar to (pir accession number) (le:4982) (re:5533) (di:complement) D90820 D90820 g1742876 Escherichia coli 562 -11535023 300878 (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli orf183 gene, complete cds and seld gene, 5' end.) (nt:orf183) (le:106) (re:657) (di:direct) ECOORF183 M68961 g147021 Escherichia coli 562 -11535023 235298 ydja orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 161 of 400 of the completegenome.) (nt:f183; 100 pct identical to ydja_ecoli sw: p24250;) (le:5902) (re:6453) (di:complement) AE000271 AE000271 g1788063 Escherichia coli 562 -11535023 5000692479 (de:(ecoli_1722) (pn:hypothetical 20) (gn:ydja) (gtcfc:13.7:14.1) (ec:) (ydja_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1722 ECOLI_1722 Escherichia coli 562 10053095

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851788	11031	33187	1119	372

Description

6500731166 ydjb:b1768 hypothetical 23.4 kd protein in ansa 3region
 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1768
 b1768 Escherichia coli 562 -11535024 7000688992 ydjb hypothetical 23.4k
 protein ansa 3 region (db:pir1.dat) (mp:39 min) QQECA5 H64936 Escherichia
 coli 562 -11535024 7500953694 ydjb orf:hypothetical protein (fn:orf;
 unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 161 of
 400 of the completegenome.) (nt:o219; 100 pct identical to ydjb_ecoli sw:
 p21369) (le:9646) (re:10305) (di:direct) AE000271 AE000271 g1788066
 Escherichia coli 562 -11535024 5000692480 (de:(ecoli_1725) (pn:hypothetical
 23) (gn:ydjb) (gtcfc:13.7:14.1) (ec:) (ydjb_ecoli) (keggfc:11.2)
 (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1725 ECOLI_1725 Escherichia
 coli 562 10123460

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851806	11032	33188	852	283

Description

6500731167 ydje:b1769 hypothetical metabolite transport protein in ansa 3region:hypothetical metabolite transport protein in ansa-gapa intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1769 b1769 Escherichia coli 562 -11535025 111370 ydje (de:region) (db:swissprot) YDJE_ECOLI P38055 ESCHERICHIA COLI 562 -11535025 7000687569 ydje hypothetical metabolite transport protein in ansa 3region (cl:hypothetical protein b1775) (db:pir2.dat) A64937 A64937 Escherichia coli 562 -11535025 224240 ydje synaptic vesicle protein 2 sv2 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.)) (nt:orf_id:o329#6; similar to (swissprot accession) (le:9478) (re:10836) (di:complement) D90820 D90820 g1742880 Escherichia coli 562 -11535025 300889 ydje synaptic vesicle protein 2 sv2 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o329#6; similar to (swissprot accession) (le:298) (re:1656) (di:complement) D90821 D90821 g1742888 Escherichia coli 562 -11535025 300882 ydje putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 162 of 400 of the completegenome.) (nt:f452; 100 pct identical to fragment ydje_ecoli) (le:77) (re:1435) (di:complement) AE000272 AE000272 g1788068 Escherichia coli 562 -11535025 224247 ydje synaptic vesicle protein 2 sv2 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o329#6; similar to (swissprot accession) (le:298) (re:1656) (di:complement) D90821 D90821 g1742888 Escherichia coli 562 -11535025 5000692481 (de:(ecoli_1726) (pn:hypothetical metabolite transport protein in ansa:3"region:fragment) (gn:ydje) (gtcfc:13.7:14.1) (ec:) (ydje_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1726 ECOLI_1726 Escherichia coli 562 10119820

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851811	11033	33189	300	99

Description

5000692482 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1770 b1770 Escherichia coli 562 -11535026
7500922383 ydjf (de:hypothetical transcriptional regulator in ansa-gapa intergenic region) (db:swissprot) YDJF_ECOLI P77721 ESCHERICHIA COLI 562 -11535026 7000691448 hypothetical protein b1770 (db:pir2.dat) B64937 B64937 Escherichia coli 562 -11535026 224241 l-fucose operon activator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.)) (nt:orf_id:o329#7; similar to (swissprot accession) (le:10953) (re:11711) (di:complement) D90820 D90820 g1742881 Escherichia coli 562 -11535026 300883 l-fucose operon activator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o329#7; similar to (swissprot accession) (le:1773) (re:2531) (di:complement) D90821 D90821 g1742889 Escherichia coli 562 -11535026 300890 b1770 putative deor-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 162 of 400 of the completegenome.) (nt:f252; this 252 aa orf is 37 pct identical (9 gaps)) (le:1552) (re:2310) (di:complement) AE000272 AE000272 g1788069 Escherichia coli 562 -11535026 224248 l-fucose operon activator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.)) (nt:orf_id:o329#7; similar to (swissprot accession) (le:10953) (re:11711) (di:complement) D90820 D90820 g1742881 Escherichia coli 562 -11535026 6500731168 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1770 b1770 Escherichia coli 562 -11535026

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851837	11034	33190	906	302

Description

5000692483 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1771 b1771 Escherichia coli 562 -11535027

7500922385 ydjg (de:hypothetical oxidoreductase in ansa-rnd intergenic region) (db:swissprot) YDJG_ECOLI P77256 ESCHERICHIA COLI 562 -11535027

7000691449 hypothetical protein b1771 (cl:conserved hypothetical protein ypl088w) (db:pir2.dat) C64937 C64937 Escherichia coli 562 -11535027 224242 iols protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.)) (nt:orf_id:o329#8; similar to (swissprot accession) (le:11848) (re:12828) (di:complement) D90820 D90820 g1742882 Escherichia coli 562 -11535027 300884 iols protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o329#8; similar to (swissprot accession) (le:2668) (re:3648) (di:complement) D90821 D90821 g1742890 Escherichia coli 562 -11535027 300891 b1771 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 162 of 400 of the completegenome.) (nt:f326; this 326 aa orf is 38 pct identical (27 gaps)) (le:2447) (re:3427) (di:complement) AE000272 AE000272 g1788070 Escherichia coli 562 -11535027 224249 iols protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.)) (nt:orf_id:o329#8; similar to (swissprot accession) (le:11848) (re:12828) (di:complement) D90820 D90820 g1742882 Escherichia coli 562 -11535027 6500731169 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1771 b1771 Escherichia coli 562 -11535027

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851843	11035	33191	570	189

Description

5000692484 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1772 b1772 Escherichia coli 562 -11535028
7000691450 hypothetical protein b1772 (cl:ribokinase) (db:pir2.dat) D64937 D64937 Escherichia coli 562 -11535028 224243 2-dehydro-3-deoxygluconokinase ec 2.7.1.45 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.)) (nt:orf_id:o329#9; similar to (swissprot accession) (le:12838) (re:13806) (di:complement) D90820 D90820 g1742883 Escherichia coli 562 -11535028 300892 2-dehydro-3-deoxygluconokinase ec 2.7.1.45 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o329#9; similar to (swissprot accession) (le:3658) (re:4626) (di:complement) D90821 D90821 g1742891 Escherichia coli 562 -11535028 300885 b1772 putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 162 of 400 of the completegenome.) (nt:f322; this 322 aa orf is 34 pct identical (29 gaps)) (le:3437) (re:4405) (di:complement) AE000272 AE000272 g1788071 Escherichia coli 562 -11535028 224250 2-dehydro-3-deoxygluconokinase ec 2.7.1.45 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o329#9; similar to (swissprot accession) (le:3658) (re:4626) (di:complement) D90821 D90821 g1742891 Escherichia coli 562 -11535028 6500731170 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1772 b1772 Escherichia coli 562 -11535028

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851850	11036	33192	531	176

Description

5000692485 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1773 b1773 Escherichia coli 562 -11535029
7000691451 hypothetical protein b1773 (cl:fructose-bisphosphate aldolase ii) (db:pir2.dat) E64937 E64937 Escherichia coli 562 -11535029 224244 tagatose-bisphosphate aldolase agay ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #329(39.7-40.0 min.)) (nt:orf_id:o329#10; similar to (swissprot accession) (le:13790) (re:14626) (di:complement) D90820 D90820 g1742884 Escherichia coli 562 -11535029 300893 tagatose-bisphosphate aldolase agay ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o329#10; similar to (swissprot accession) (le:4610) (re:5446) (di:complement) D90821 D90821 g1742892 Escherichia coli 562 -11535029 300886 b1773 putative aldolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 162 of 400 of the completegenome.) (nt:f278; this 278 aa orf is 44 pct identical (17 gaps)) (le:4389) (re:5225) (di:complement) AE000272 AE000272 g1788072 Escherichia coli 562 -11535029 224251 tagatose-bisphosphate aldolase agay ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o329#10; similar to (swissprot accession) (le:4610) (re:5446) (di:complement) D90821 D90821 g1742892 Escherichia coli 562 -11535029 6500731171 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1773 b1773 Escherichia coli 562 -11535029

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851855	11037	33193	456	151

Description

GTC ORF with score 126 to: (db:genpept-bct1) (de:pseudomonas aeruginosa putative reductase (slfa), putativefmnh2-dependent monooxygenase (slfb), and putative fmnh2-dependentmonooxygenase (slfc) genes, complete cds.) (le:2902) (re:4119) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851873	11038	33194	657	219

Description

6500731172 ydjj:b1774 hypothetical protein:hypothetical zinc-type alcohol dehydrogenase-like protein in ansa-gapa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1774 b1774 Escherichia coli 562 -11535030 4000707542 ydjj (de:intergenic region) (db:swissprot) YDJJ_ECOLI P77280 ESCHERICHIA COLI 562 -11535030 7000687570 probable l-iditol 2-dehydrogenase:b1774:sorbitol dehydrogenase (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.14) (db:pir1.dat) F64937 F64937 Escherichia coli 562 -11535030 224252 sorbitol dehydrogenase ec 1.1.1.14 l-iditol (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o330#1; similar to (swissprot accession) (le:5467) (re:6510) (di:complement) D90821 D90821 g1742893 Escherichia coli 562 -11535030 300894 ydjj putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 162 of 400 of the completegenome.) (nt:f347; this 347 aa orf is 45 pct identical (21 gaps)) (le:5246) (re:6289) (di:complement) AE000272 AE000272 g1788073 Escherichia coli 562 -11535030 5000692486 (de:(ecoli_1731) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1731 ECOLI_1731 Escherichia coli 562 10119827

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851874	11039	33195	753	250

Description

5000692487 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1775 b1775 Escherichia coli 562 -11535031 7000691452 hypothetical protein b1775 (cl:hypothetical protein b1775) (db:pir2.dat) G64937 G64937 Escherichia coli 562 -11535031 7500960057 b1775 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 162 of 400 of the completegenome.) (nt:f459; this 459 aa orf is 32 pct identical (30 gaps)) (le:6306) (re:7685) (di:complement) AE000272 AE000272 g1788074 Escherichia coli 562 -11535031 6500731173 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1775 b1775 Escherichia coli 562 -11535031

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851888	11040	33196	408	135

Description

5000692488 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1776 b1776 Escherichia coli 562 -11535032
7502852254 ydjl (de:intergenic region) (db:swissprot) YDJL_ECOLI P77539
ESCHERICHIA COLI 562 -11535032 7000691453 probable dehydrogenase
(cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology)
(ec:1.-.-.-) (db:pir2.dat) H64937 H64937 Escherichia coli 562 -11535032
224254 threonine 3-dehydrogenase ec 1.1.1.103 . (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.))
(nt:orf_id:o330#3; similar to (swissprot accession) (le:7933) (re:9009)
(di:complement) D90821 D90821 g1742895 Escherichia coli 562 -11535032
300896 b1776 putative oxidoreductase (fn:putative enzyme; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 162 of 400 of the
completegenome.) (nt:f358; residues 252-328 are 36 pct identical to)
(le:7712) (re:8788) (di:complement) AE000272 AE000272 g1788075 Escherichia
coli 562 -11535032 6500731174 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1776 b1776
Escherichia coli 562 -11535032

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851897	11041	33197	1233	410

Description

5000692489 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1777 b1777 Escherichia coli 562 -11535033
7000691454 hypothetical protein b1777 (db:pir2.dat) A64938 A64938
Escherichia coli 562 -11535033 7500960058 b1777 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
162 of 400 of the completegenome.) (nt:f105; this 105 aa orf is 34 pct
identical (18 gaps)) (le:9158) (re:9475) (di:complement) AE000272 AE000272
g1788076 Escherichia coli 562 -11535033 6500731175 hypothetical protein
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1777
b1777 Escherichia coli 562 -11535033

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851914	11042	33198	354	117

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851916	11043	33199	666	221

Description

6500731176 yeaa:b1778 hypothetical protein: hypothetical 15.5 kd protein in ansa-gapa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1778 b1778 Escherichia coli 562 -11535034 111464 yeaa (de: hypothetical 15.5 kd protein in ansa-gapa intergenic region) (db:swissprot) YEAA_ECOLI P39903 ESCHERICHIA COLI 562 -11535034 7000687581 hypothetical protein b1778 (cl: hypothetical protein ycl033c) (db:pir2.dat) B64938 B64938 Escherichia coli 562 -11535034 7500922829 yeaa orf: hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de: escherichia coli k-12 mg1655 section 162 of 400 of the complete genome.) (nt:f137; this 137 aa orf is 56 pct identical (4 gaps)) (le:9472) (re:9885) (di:complement) AE000272 AE000272 g1788077 Escherichia coli 562 -11535034 5000692490 (de: (ecoli_1735) (pn: function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1735 ECOLI_1735 Escherichia coli 562 10123463

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501851922	11044	33200	1407	468

Description

5000692491 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1780 b1780 Escherichia coli 562 -11535035 7000691455 hypothetical protein b1780 (db:pir2.dat) D64938 D64938 Escherichia coli 562 -11535035 7500960059 yead orf: hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de: escherichia coli k-12 mg1655 section 163 of 400 of the complete genome.) (nt:o301; this 301 aa orf is 42 pct identical (38 gaps)) (le:1259) (re:2164) (di:direct) AE000273 AE000273 g1788080 Escherichia coli 562 -11535035 6500731177 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1780 b1780 Escherichia coli 562 -11535035

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851928	11045	33201	1692	563

Description

5000692492 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1781 b1781 Escherichia coli 562 -11535036
7000689027 hypothetical protein b1781 (cl:aldehyde reductase) (db:pir2.dat) E64938 E64938 Escherichia coli 562 -11535036 224263 morphine 6-dehydrogenase ec 1.1.1.218 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.)) (nt:orf_id:o330#8; similar to (swissprot accession) (le:1929) (re:2783) (di:complement) D90822 D90822 g1736409 Escherichia coli 562 -11535036 300905 b1781 putative an aldehyde reductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 163 of 400 of the completegenome.) (nt:f284; residues 72-114 are 46 pct identical to) (le:2212) (re:3066) (di:complement) AE000273 AE000273 g1788081 Escherichia coli 562 -11535036 6500731178 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1781 b1781 Escherichia coli 562 -11535036

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851951	11046	33202	912	303

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851969	11047	33203	234	77

Description

5000692493 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1782 b1782 Escherichia coli 562 -11535037

7500922839 yeaf (de:hypothetical 27.8 kd protein in gapa-rnd intergenic region precursor) (db:swissprot) YEAF_ECOLI P77486 ESCHERICHIA COLI 562 -11535037 7000691456 hypothetical protein b1782 (cl:hypothetical protein b1782) (db:pir2.dat) F64938 F64938 Escherichia coli 562 -11535037 224259 outer membrane protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o330#9; similar to (swissprot accession) (le:13403) (re:14149) (di:complement) D90821 D90821 g1742900 Escherichia coli 562 -11535037 300901 outer membrane protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.)) (nt:orf_id:o330#9; similar to (swissprot accession) (le:2873) (re:3619) (di:complement) D90822 D90822 g1736410 Escherichia coli 562 -11535037 300906 yeaf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 163 of 400 of the completegenome.) (nt:f248; this 248 aa orf is 40 pct identical (6 gaps)) (le:3156) (re:3902) (di:complement) AE000273 AE000273 g1788082 Escherichia coli 562 -11535037 224264 outer membrane protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.)) (nt:orf_id:o330#9; similar to (swissprot accession) (le:13403) (re:14149) (di:complement) D90821 D90821 g1742900 Escherichia coli 562 -11535037 6500731179 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1782 b1782 Escherichia coli 562 -11535037

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851975	11048	33204	669	222

Description

5000692494 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1783 b1783 Escherichia coli 562 -11535038
7500922844 yeag (de:hypothetical 74.5 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAG_ECOLI P77391 ESCHERICHIA COLI 562 -11535038
7000691457 hypothetical protein b1783 (db:pir2.dat) G64938 G64938 Escherichia coli 562 -11535038 224260 prka protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.).) (nt:orf_id:o330#10; similar to (swissprot accession) (le:14585) (re:16519) (di:direct) D90821 D90821 g1742901 Escherichia coli 562 -11535038 300902 prka protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.).) (nt:orf_id:o330#10; similar to (swissprot accession) (le:4055) (re:5989) (di:direct) D90822 D90822 g1736411 Escherichia coli 562 -11535038 300907 yeag orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 163 of 400 of the completegenome.) (nt:o644; this 644 aa orf is 35 pct identical (34 gaps)) (le:4338) (re:6272) (di:direct) AE000273 AE000273 g1788083 Escherichia coli 562 -11535038 224265 prka protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #330(39.9-40.3 min.).) (nt:orf_id:o330#10; similar to (swissprot accession) (le:14585) (re:16519) (di:direct) D90821 D90821 g1742901 Escherichia coli 562 -11535038 6500731180 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1783 b1783 Escherichia coli 562 -11535038

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851993	11049	33205	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851994	11050	33206	1368	455

Description

5000692495 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1784 b1784 Escherichia coli 562 -11535039
7500922846 yeah (de:hypothetical 49.4 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAH_ECOLI P76235 ESCHERICHIA COLI 562 -11535039
7000691458 hypothetical protein b1784 (db:pir2.dat) H64938 H64938
Escherichia coli 562 -11535039 224266 yzdc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.)) (nt:orf_id:o331#1; similar to (swissprot accession) (le:6102) (re:7385) (di:direct) D90822 D90822 g1736412 Escherichia coli 562 -11535039
7500922848 yeah orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 163 of 400 of the completegenome.) (nt:o427; this 427 aa orf is 28 pct identical (43 gaps)) (le:6385) (re:7668) (di:direct) AE000273 AE000273 g1788084 Escherichia coli 562 -11535039 300908 yzdc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.)) (nt:orf_id:o331#1; similar to (swissprot accession) (le:6102) (re:7385) (di:direct) D90822 D90822 g1736412
Escherichia coli 562 -11535039 6500731181 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1784 b1784
Escherichia coli 562 -11535039

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501851999	11051	33207	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852009	11052	33208	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852022	11053	33209	384	127

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852024	11054	33210	216	71

Description

5000692496 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1785 b1785 Escherichia coli 562 -11535040
7500922852 yeai (de:hypothetical 56.1 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAI_ECOLI P76236 ESCHERICHIA COLI 562 -11535040
7000691459 hypothetical protein b1785 (cl:hypothetical protein b1785) (db:pir2.dat) A64939 A64939 Escherichia coli 562 -11535040 224267 yhck (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.)) (nt:orf_id:o331#2; similar to (swissprot accession) (le:7532) (re:9007) (di:direct) D90822 D90822 g1736413 Escherichia coli 562 -11535040
7500922854 yeai orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 163 of 400 of the completegenome.) (nt:o491; this 491 aa orf is 28 pct identical (8 gaps)) (le:7815) (re:9290) (di:direct) AE000273 AE000273 g1788085 Escherichia coli 562 -11535040 300909 yhck (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.)) (nt:orf_id:o331#2; similar to (swissprot accession) (le:7532) (re:9007) (di:direct) D90822 D90822 g1736413 Escherichia coli 562 -11535040 6500731182 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1785 b1785 Escherichia coli 562 -11535040

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852028	11055	33211	1236	411

Description

5000692497 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1786 b1786 Escherichia coli 562 -11535041
7500922857 yeaj (de:hypothetical 63.2 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAJ_ECOLI P76237 ESCHERICHIA COLI 562 -11535041
7000691460 hypothetical protein b1786 (db:pir2.dat) B64939 B64939 Escherichia coli 562 -11535041 7500922859 yeaj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 163 of 400 of the completegenome.) (nt:o556; this 556 aa orf is 27 pct identical (3 gaps)) (le:9291) (re:10961) (di:direct) AE000273 AE000273 g1788086 Escherichia coli 562 -11535041 6500731183 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1786 b1786 Escherichia coli 562 -11535041

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852031	11056	33212	435	144

Description

5000692498 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1787 b1787 Escherichia coli 562 -11535042
7500922860 yeak (de:hypothetical 17.9 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAK_ECOLI P76238 ESCHERICHIA COLI 562 -11535042
7000691461 hypothetical protein b1787 (db:pir2.dat) C64939 C64939 Escherichia coli 562 -11535042 7500922862 yeak orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 163 of 400 of the completegenome.) (nt:o167) (le:11004) (re:11507) (di:direct) AE000273 AE000273 g1788087 Escherichia coli 562 -11535042
6500731184 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1787 b1787 Escherichia coli 562 -11535042

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852040	11057	33213	1389	462

Description

GTC ORF with score 337 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid zk84.) (nt:final exon in repeat region; similar to long tandem) (le:24170:24288:24411:24654) (re:24234:24357:24597:26737) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852060	11058	33214	1701	566

Description

5000692499 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1788 b1788 Escherichia coli 562 -11535043
7000691462 hypothetical protein b1788 (db:pir2.dat) D64939 D64939 Escherichia coli 562 -11535043 7500960060 b1788 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 163 of 400 of the completegenome.) (nt:f50; this 50 aa orf is 38 pct identical (3 gaps)) (le:11508) (re:11660) (di:complement) AE000273 AE000273 g1788088 Escherichia coli 562 -11535043 6500731185 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1788 b1788 Escherichia coli 562 -11535043

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852063	11059	33215	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852089	11060	33216	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852096	11061	33217	810	269

Description

5000692500 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1789 b1789 Escherichia coli 562 -11535044
7500922863 yeal (de:hypothetical 15.3 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAL_ECOLI P76240 ESCHERICHIA COLI 562 -11535044
7000691463 hypothetical protein b1789 (cl:hypothetical protein ytwi) (db:pir2.dat) E64939 E64939 Escherichia coli 562 -11535044 224269 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.)) (nt:orf_id:o331#5; similar to (swissprot accession) (le:11499) (re:11945) (di:direct) D90822 D90822 g1736415 Escherichia coli 562 -11535044 300911 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.)) (nt:orf_id:o331#5; similar to (swissprot accession) (le:548) (re:994) (di:direct) D90823 D90823 g1736418 Escherichia coli 562 -11535044 300913 yeal orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:o148; this 148 aa orf is 53 pct identical (1 gap)) (le:91) (re:537) (di:direct) AE000274 AE000274 g1788090 Escherichia coli 562 -11535044 224271 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.)) (nt:orf_id:o331#5; similar to (swissprot accession) (le:11499) (re:11945) (di:direct) D90822 D90822 g1736415 Escherichia coli 562 -11535044 6500731186 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1789 b1789 Escherichia coli 562 -11535044

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852131	11062	33218	615	204

Description

5000692501 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1790 b1790 Escherichia coli 562 -11535045
 7500922866 yeam (de:hypothetical transcriptional regulator in gapa-rnd intergenic region) (db:swissprot) YEAM_ECOLI P76241 ESCHERICHIA COLI 562 -11535045 7000691464 hypothetical protein b1790 (db:pir2.dat) F64939 F64939 Escherichia coli 562 -11535045 7500922868 yeam putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:f273; this 273 aa orf is 21 pct identical (7 gaps)) (le:494) (re:1315) (di:complement) AE000274 AE000274 g1788091 Escherichia coli 562 -11535045 6500731187 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1790 b1790 Escherichia coli 562 -11535045

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852133	11063	33219	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852135	11064	33220	372	123

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852136	11065	33221	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852166	11066	33222	882	293

Description

5000692502 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1791 b1791 Escherichia coli 562 -11535046
7500922869 yeon (de:hypothetical 41.2 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAN_ECOLI P76242 ESCHERICHIA COLI 562 -11535046
7000691465 hypothetical protein b1791 (cl:cynx protein) (db:pir2.dat) G64939 G64939 Escherichia coli 562 -11535046 224270 cyanate transport protein cynx. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.)) (nt:orf_id:o331#7; similar to (swissprot accession) (le:12820) (re:14001) (di:direct) D90822 D90822 g1736416 Escherichia coli 562 -11535046 300912 cyanate transport protein cynx. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.)) (nt:orf_id:o331#7; similar to (swissprot accession) (le:1869) (re:3050) (di:direct) D90823 D90823 g1736419 Escherichia coli 562 -11535046 300914 yeon putative amino acid/amine transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completengenome.) (nt:o393; this 393 aa orf is 42 pct identical (7 gaps)) (le:1412) (re:2593) (di:direct) AE000274 AE000274 g1788092 Escherichia coli 562 -11535046 224272 cyanate transport protein cynx. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #331(40.1-40.4 min.)) (nt:orf_id:o331#7; similar to (swissprot accession) (le:12820) (re:14001) (di:direct) D90822 D90822 g1736416 Escherichia coli 562 -11535046 6500731188 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1791 b1791 Escherichia coli 562 -11535046

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852170	11067	33223	996	332

Description

5000692503 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1792 b1792 Escherichia coli 562 -11535047
7500922871 yeao (de:hypothetical 14.2 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAO_ECOLI P76243 ESCHERICHIA COLI 562 -11535047
7000691466 hypothetical protein b1792 (db:pir2.dat) H64939 H64939 Escherichia coli 562 -11535047 7500922873 yeao orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completengenome.) (nt:o122; this 122 aa orf is 34 pct identical (5 gaps)) (le:2627) (re:2995) (di:direct) AE000274 AE000274 g1788093 Escherichia coli 562 -11535047 6500731189 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1792 b1792 Escherichia coli 562 -11535047

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852171	11068	33224	492	163

Description

GTC ORF with score 193 to: (fn:required for conidial pigmentation)
(db:genpept-pln2) (de:aspergillus fumigatus polyketide synthase (alb1) gene,
completecds.) (nt:alb1) (le:598:932:1268:4755:5584)
(re:884:1220:4699:5510:7260) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852181	11069	33225	243	80

Description

5000692504 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1793 b1793 Escherichia coli 562 -11535048
7500952077 yoaf (de:hypothetical 8.9 kd protein in gapa-rnd intergenic
region) (db:swissprot) YOAF_ECOLI P76244 ESCHERICHIA COLI 562 -11535048
7000691467 hypothetical protein b1793 (db:pir2.dat) A64940 A64940
Escherichia coli 562 -11535048 7500952079 yoaf orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
164 of 400 of the completegenome.) (nt:f84; this 84 aa orf is 30 pct
identical (6 gaps)) (le:3017) (re:3271) (di:complement) AE000274 AE000274
g1788094 Escherichia coli 562 -11535048 6500731190 hypothetical protein
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1793
b1793 Escherichia coli 562 -11535048

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852182	11070	33226	192	63

Description

5000692505 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1794 b1794 Escherichia coli 562 -11535049
7500922874 yeap (de:hypothetical 43.6 kd protein in gapa-rnd intergenic
region) (db:swissprot) YEAP_ECOLI P76245 ESCHERICHIA COLI 562 -11535049
7000691468 hypothetical protein b1794 (db:pir2.dat) B64940 B64940
Escherichia coli 562 -11535049 7500922876 yeap orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
164 of 400 of the completegenome.) (nt:o384; uug start; this 384 aa orf is
32 pct) (le:3325) (re:4479) (di:direct) AE000274 AE000274 g1788095
Escherichia coli 562 -11535049 6500731191 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1794 b1794
Escherichia coli 562 -11535049

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852198	11071	33227	909	303

Description

5000692506 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1795 b1795 Escherichia coli 562 -11535050
7500922877 yeaq (de:hypothetical 8.7 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAQ_ECOLI P76246 ESCHERICHIA COLI 562 -11535050
7000691469 yeaq transglycosylase-associated protein yeaq (cl:conserved hypothetical protein hi1364) (db:pir2.dat) C64940 C64940 Escherichia coli 562 -11535050 7500922879 yeaq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:f82; this 82 aa orf is 33 pct identical (4 gaps)) (le:4746) (re:4994) (di:complement) AE000274 AE000274 g1788096 Escherichia coli 562 -11535050 6500731192 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1795 b1795 Escherichia coli 562 -11535050

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852215	11072	33228	1425	474

Description

5000692507 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1796 b1796 Escherichia coli 562 -11535051
7500952080 yoag (de:hypothetical 6.6 kd protein in gapa-rnd intergenic region) (db:swissprot) YOAG_ECOLI P76247 ESCHERICHIA COLI 562 -11535051
7000691470 hypothetical protein b1796 (db:pir2.dat) D64940 D64940 Escherichia coli 562 -11535051 7500952082 yoag orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:f60; this 60 aa orf is 33 pct identical (2 gaps)) (le:5142) (re:5324) (di:complement) AE000274 AE000274 g1788097 Escherichia coli 562 -11535051 6500731193 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1796 b1796 Escherichia coli 562 -11535051

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852221	11073	33229	195	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852224	11074	33230	480	159

Description

5000692508 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1797 b1797 Escherichia coli 562 -11535052
7500922880 year (de:hypothetical 13.6 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAR_ECOLI P76248 ESCHERICHIA COLI 562 -11535052
7000691471 hypothetical protein b1797 (db:pir2.dat) E64940 E64940 Escherichia coli 562 -11535052 7500922882 year orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:f119; this 119 aa orf is 22 pct identical (4 gaps)) (le:5328) (re:5687) (di:complement) AE000274 AE000274 g1788098 Escherichia coli 562 -11535052 6500731194 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1797 b1797 Escherichia coli 562 -11535052

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852225	11075	33231	411	136

Description

5000692509 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1798 b1798 Escherichia coli 562 -11535053
7500922883 yeas (de:hypothetical 23.2 kd protein in gapa-rnd intergenic region) (db:swissprot) YEAS_ECOLI P76249 ESCHERICHIA COLI 562 -11535053
7000691472 hypothetical protein b1798 (cl:hypothetical protein b1798) (db:pir2.dat) F64940 F64940 Escherichia coli 562 -11535053 224274 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.)) (nt:orf_id:o332#6; similar to (swissprot accession) (le:6317) (re:6955) (di:complement) D90823 D90823 g1736421 Escherichia coli 562 -11535053 300916 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #333(40.5-40.8 min.)) (nt:orf_id:o332#6; similar to (swissprot accession) (le:1787) (re:2425) (di:complement) D90824 D90824 g1736431 Escherichia coli 562 -11535053 300925 yeas orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:f212; this 212 aa orf is 50 pct identical (4 gaps)) (le:5860) (re:6498) (di:complement) AE000274 AE000274 g1788099 Escherichia coli 562 -11535053 224283 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.)) (nt:orf_id:o332#6; similar to (swissprot accession) (le:6317) (re:6955) (di:complement) D90823 D90823 g1736421 Escherichia coli 562 -11535053 6500731195 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1798 b1798 Escherichia coli 562 -11535053

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852248	11076	33232	501	166

Description

5000692510 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1799 b1799 Escherichia coli 562 -11535054
7000691473 hypothetical protein b1799 (cl:conserved hypothetical protein
hi1364) (db:pir2.dat) G64940 G64940 Escherichia coli 562 -11535054
7500922887 yeast putative transcriptional regulator lysr-type (fn:putative
regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 164 of 400 of the completegenome.) (nt:f314; this 314 aa orf
is 34 pct identical (6 gaps)) (le:6625) (re:7569) (di:complement) AE000274
AE000274 g1788100 Escherichia coli 562 -11535054 7500922885 yeast
(de:hypothetical transcriptional regulator in gapa-rnd intergenic region)
(db:swissprot) YEAT_ECOLI P76250 ESCHERICHIA COLI 562 -11535054 6500731196
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1799 b1799 Escherichia coli 562 -11535054

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852255	11077	33233	828	275

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852269	11078	33234	213	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501852277	11079	33235	1518	505
Description				
5000692511 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1800 b1800 Escherichia coli 562 -11535055				
7500893574 yeau (ec:1.1.1.93) (de:probable tartrate dehydrogenase, (tdh)) (db:swissprot) TTUC_ECOLI P76251 ESCHERICHIA COLI 562 -11535055 7000691474 tartrate dehydrogenase (cl:3-isopropylmalate dehydrogenase) (ec:1.1.1.93) (db:pir2.dat) H64940 H64940 Escherichia coli 562 -11535055 224276 3-isopropylmalate dehydrogenase ec 1.1.1.85 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.)).) (nt:orf_id:o332#8; similar to (swissprot accession) (le:8108) (re:9193) (di:direct) D90823 D90823 g1736423 Escherichia coli 562 -11535055 300918 3-isopropylmalate dehydrogenase ec 1.1.1.85 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #333(40.5-40.8 min.)).) (nt:orf_id:o332#8; similar to (swissprot accession) (le:3578) (re:4663) (di:direct) D90824 D90824 g1736433 Escherichia coli 562 -11535055 300927 yeau putative tartrate dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:o361; this 361 aa orf is 40 pct identical (17 gaps)) (le:7651) (re:8736) (di:direct) AE000274 AE000274 g1788101 Escherichia coli 562 -11535055 224285 3-isopropylmalate dehydrogenase ec 1.1.1.85 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.)).) (nt:orf_id:o332#8; similar to (swissprot accession) (le:8108) (re:9193) (di:direct) D90823 D90823 g1736423 Escherichia coli 562 -11535055 6500731197 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1800 b1800 Escherichia coli 562 -11535055				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852334	11080	33236	411	136

Description

5000692512 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1801 b1801 Escherichia coli 562 -11535056
 7500922888 yeav (de:probable transport protein yeav) (db:swissprot) YEAV_ECOLI P76252 ESCHERICHIA COLI 562 -11535056 7000691475 hypothetical protein b1801 (cl:escherichia coli probable carnitine transport protein) (db:pir2.dat) A64941 A64941 Escherichia coli 562 -11535056 7500922890 yeav putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:o481; uug start; 29 pct identical (3 gaps) to) (le:8927) (re:10372) (di:direct) AE000274 AE000274 g1788102 Escherichia coli 562 -11535056 6500731198 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1801 b1801 Escherichia coli 562 -11535056

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852355	11081	33237	708	235

Description

GTC ORF with score 458 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c1734.) (nt:spbc1734.08, len:373, similarity:saccharomyces) (le:13418:13590:13839:14117) (re:13545:13665:14058:14814) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852356	11082	33238	789	262

Description

5000692513 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1802 b1802 Escherichia coli 562 -11535057
 7500922891 yeav (ec:1.14.1.-) (de:putative dioxygenase alpha subunit yeav,) (db:swissprot) YEAV_ECOLI P76253 ESCHERICHIA COLI 562 -11535057 7000691476 hypothetical protein b1802 (db:pir2.dat) B64941 B64941 Escherichia coli 562 -11535057 7500922893 yeav orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:o374; 29 pct identical (11 gaps) to 258 residues) (le:10404) (re:11528) (di:direct) AE000274 AE000274 g1788103 Escherichia coli 562 -11535057 6500731199 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1802 b1802 Escherichia coli 562 -11535057

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852362	11083	33239	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852366	11084	33240	540	179

Description

5000692514 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1803 b1803 Escherichia coli 562 -11535058
7500922894 yeax (ec:1.-.-.-) (de:putative dioxygenase beta subunit yeax,) (db:swissprot) YEAX_ECOLI P76254 ESCHERICHIA COLI 562 -11535058 7000691477
hypothetical protein b1803 (cl:phthalate dioxygenase reductase:cytochrome-b5 reductase homology:ferredoxin (2fe-2s) homology) (db:pir2.dat) C64941 C64941 Escherichia coli 562 -11535058 224279 vanillate demethylase oxidoreductase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.)) (nt:orf_id:o332#12; similar to (swissprot accession) (le:12041) (re:13006) (di:direct) D90823 D90823 g1736426 Escherichia coli 562 -11535058 300921 vanillate demethylase oxidoreductase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #333(40.5-40.8 min.)) (nt:orf_id:o332#12; similar to (swissprot accession) (le:7511) (re:8476) (di:direct) D90824 D90824 g1736436 Escherichia coli 562 -11535058 300930 yeax putative diogenase beta subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 164 of 400 of the completegenome.) (nt:o321; this 321 aa orf is 39 pct identical (10 gaps)) (le:11584) (re:12549) (di:direct) AE000274 AE000274 g1788104 Escherichia coli 562 -11535058 224288 vanillate demethylase oxidoreductase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #332(40.4-40.7 min.)) (nt:orf_id:o332#12; similar to (swissprot accession) (le:12041) (re:13006) (di:direct) D90823 D90823 g1736426 Escherichia coli 562 -11535058 6500731200 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1803 b1803 Escherichia coli 562 -11535058

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852368	11085	33241	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852371	11086	33242	402	133

Description

5000692515 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1806 b1806 Escherichia coli 562 -11535059
7000691478 rnd rnd protein (cl:rnd protein) (db:pir2.dat) F64941 F64941 Escherichia coli 562 -11535059 224291 outer membrane protein slp precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #333(40.5-40.8 min.)) (nt:orf_id:o333#2; similar to (swissprot accession) (le:11617) (re:12198) (di:complement) D90824 D90824 g1736439 Escherichia coli 562 -11535059 300938 outer membrane protein slp precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.)) (nt:orf_id:o333#2; similar to (swissprot accession) (le:2657) (re:3238) (di:complement) D90825 D90825 g1736445 Escherichia coli 562 -11535059 300933 b1806 putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 165 of 400 of the completegenome.) (nt:f193; this 193 aa orf is 41 pct identical (7 gaps)) (le:1955) (re:2536) (di:complement) AE000275 AE000275 g1788108 Escherichia coli 562 -11535059 224296 outer membrane protein slp precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.)) (nt:orf_id:o333#2; similar to (swissprot accession) (le:2657) (re:3238) (di:complement) D90825 D90825 g1736445 Escherichia coli 562 -11535059 6500731201 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1806 b1806 Escherichia coli 562 -11535059

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852372	11087	33243	339	112

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852374	11088	33244	363	120

Description

5000692516 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1807 b1807 Escherichia coli 562 -11535060
5500686565 yeaz (de:hypothetical 25.2 kd protein in fadd-pabb intergenic region) (db:swissprot) YEAZ_ECOLI P76256 ESCHERICHIA COLI 562 -11535060
7000687586 hypothetical protein b1807 (cl:hypothetical protein hi0388) (db:pir2.dat) G64941 G64941 Escherichia coli 562 -11535060 224292
o-sialoglycoprotein endopeptidase ec 3.4.24.57 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #333(40.5-40.8 min.))
(nt:orf_id:o333#3; similar to (swissprot accession) (le:12238) (re:12933) (di:complement) D90824 D90824 g1736440 Escherichia coli 562 -11535060
300939 o-sialoglycoprotein endopeptidase ec 3.4.24.57 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.))
(nt:orf_id:o333#3; similar to (swissprot accession) (le:3278) (re:3973) (di:complement) D90825 D90825 g1736446 Escherichia coli 562 -11535060
300934 yeaz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 165 of 400 of the completegenome.)
(nt:f231; this 231 aa orf is 45 pct identical (8 gaps)) (le:2576) (re:3271) (di:complement) AE000275 AE000275 g1788109 Escherichia coli 562 -11535060
224297 o-sialoglycoprotein endopeptidase ec 3.4.24.57 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.))
(nt:orf_id:o333#3; similar to (swissprot accession) (le:3278) (re:3973) (di:complement) D90825 D90825 g1736446 Escherichia coli 562 -11535060
6500731202 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1807 b1807 Escherichia coli 562 -11535060

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852375	11089	33245	417	138

Description

GTC ORF with score 241 to: (sr:aspergillus parasiticus (strain wild type) (tissue library) (db:genpept-pln2) (de:aspergillus parasiticus polyketide synthase (pksl1) gene, completecds.) (le:421:773:1134:4909:5526) (re:707:1067:4856:5466:6938) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852404	11090	33246	546	181

Description

5000692517 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1808 b1808 Escherichia coli 562 -11535061
 7500952073 yoaa (de:probable atp-dependent helicase yoaa) (db:swissprot) YOAA_ECOLI P76257 ESCHERICHIA COLI 562 -11535061 7000691479 hypothetical protein b1808 (db:pir2.dat) H64941 H64941 Escherichia coli 562 -11535061
 224298 probable atp-dependent helicase ding homolog. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.)) (nt:orf_id:o334#1; similar to (swissprot accession) (le:4031) (re:5941) (di:complement) D90825 D90825 g1736447 Escherichia coli 562 -11535061
 7500952075 b1808 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 165 of 400 of the completegenome.) (nt:f636; this 636 aa orf is 61 pct identical (3 gaps)) (le:3329) (re:5239) (di:complement) AE000275 AE000275 g1788110 Escherichia coli 562 -11535061 300940 probable atp-dependent helicase ding homolog. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.)) (nt:orf_id:o334#1; similar to (swissprot accession) (le:4031) (re:5941) (di:complement) D90825 D90825 g1736447 Escherichia coli 562 -11535061 6500731203 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1808 b1808 Escherichia coli 562 -11535061

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852410	11091	33247	324	107

Description

5000692518 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1809 b1809 Escherichia coli 562 -11535062
 7000691480 hypothetical protein b1809 (db:pir2.dat) A64942 A64942 Escherichia coli 562 -11535062 7500960061 b1809 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 165 of 400 of the completegenome.) (nt:o130; residues 53-124 are 55 pct identical to) (le:5323) (re:5715) (di:direct) AE000275 AE000275 g1788111 Escherichia coli 562 -11535062 6500731204 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1809 b1809 Escherichia coli 562 -11535062

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852421	11092	33248	291	96

Description

5000692519 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1810 b1810 Escherichia coli 562 -11535063
 7000691481 hypothetical protein b1810 (db:pir2.dat) B64942 B64942
 Escherichia coli 562 -11535063 7500960062 b1810 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 165 of 400 of the completegenome.) (nt:o119; this 119 aa orf is 38 pct identical (2 gaps)) (le:6077) (re:6436) (di:direct) AE000275 AE000275
 g1788112 Escherichia coli 562 -11535063 6500731205 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1810 b1810 Escherichia coli 562 -11535063

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852435	11093	33249	663	220

Description

5000692520 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1811 b1811 Escherichia coli 562 -11535064
 7500952083 yoah (de:hypothetical 6.6 kd protein in fadd-pabb intergenic region) (db:swissprot) YOAH_ECOLI P76260 ESCHERICHIA COLI 562 -11535064
 7000691482 hypothetical protein b1811 (db:pir2.dat) C64942 C64942
 Escherichia coli 562 -11535064 7500952085 b1811 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 165 of 400 of the completegenome.) (nt:f59; this 59 aa orf is 37 pct identical (2 gaps)) (le:6556) (re:6735) (di:complement) AE000275 AE000275
 g1788113 Escherichia coli 562 -11535064 6500731206 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1811 b1811 Escherichia coli 562 -11535064

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852439	11094	33250	507	168

Description

6500731207 yeab:b1813 hypothetical 21.4 kd protein in pabb-sdaa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1813 b1813 Escherichia coli 562 -11535065 111465 yeab (de:hypothetical 21.4 kd protein in pabb-sdaa intergenic region) (db:swissprot) YEAB_ECOLI P43337 ESCHERICHIA COLI 562 -11535065 7000687583 yeab hypothetical 21.4 kd protein in pabb-sdaa intergenic region (db:pir2.dat) E64942 E64942 Escherichia coli 562 -11535065 224301 yeab (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.)) (nt:orf_id:o334#5; similar to (swissprot accession) (le:8876) (re:9454) (di:direct) D90825 D90825 gl736450 Escherichia coli 562 -11535065 300943 yeab orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 165 of 400 of the completegenome.) (nt:o192; 100 pct identical to yeab_ecoli sw: p43337) (le:8174) (re:8752) (di:direct) AE000275 AE000275 gl788115 Escherichia coli 562 -11535065 5000692521 (de:(ecoli_1770) (pn:hypothetical 21) (gn:yeab) (gtcfc:13.7:14.1) (ec:) (yeab_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1770 ECOLI_1770 Escherichia coli 562 10053194

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852447	11095	33251	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852459	11096	33252	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852460	11097	33253	987	329

Description

5000692522 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1815 b1815 Escherichia coli 562 -11535066
7000691483 hypothetical protein b1815 (db:pir2.dat) G64942 G64942
Escherichia coli 562 -11535066 7500960063 b1815 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:o542; uug start; this 542 aa orf is 35 pct) (le:81) (re:1709) (di:direct) AE000276 AE000276 g1788118 Escherichia coli 562 -11535066 6500731208 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1815 b1815 Escherichia coli 562 -11535066

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852469	11098	33254	366	121

Description

6500731209 yoae:b1816 hypothetical protein:hypothetical 56.5 kd protein in sdaa-manx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1816 b1816 Escherichia coli 562 -11535067
1500686258 yoae (de:hypothetical 56.5 kd protein in sdaa-manx intergenic region) (db:swissprot) YOA_ECOLI P76262 ESCHERICHIA COLI 562 -11535067
7000688173 hypothetical protein b1816 (db:pir2.dat) H64942 H64942
Escherichia coli 562 -11535067 224304 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #334(40.6-41.0 min.)) (nt:orf_id:o334#8; similar to (swissprot accession) (le:12735) (re:14291) (di:complement) D90825 D90825 g1736453 Escherichia coli 562 -11535067 300951 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o334#8; similar to (swissprot accession) (le:1193) (re:2749) (di:complement) D90826 D90826 g1736460 Escherichia coli 562 -11535067 300946 yoae putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:f518; this 518 aa orf is 50 pct identical (0 gaps)) (le:1713) (re:3269) (di:complement) AE000276 AE000276 g1788119 Escherichia coli 562 -11535067 224310 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o334#8; similar to (swissprot accession) (le:1193) (re:2749) (di:complement) D90826 D90826 g1736460 Escherichia coli 562 -11535067 5000692523 (de:(ecoli_1773) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1773 ECOLI_1773 Escherichia coli 562 10061008

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852470	11099	33255	276	91

Description

5000692524 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1820 b1820 Escherichia coli 562 -11535068
7000691484 probable membrane protein b1820 (db:pir2.dat) D64943 D64943 Escherichia coli 562 -11535068 7500960064 b1820 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:o152; this 152 aa orf is 36 pct identical (0 gaps)) (le:6485) (re:6943) (di:direct) AE000276 AE000276 g1788123 Escherichia coli 562 -11535068 6500731210 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1820 b1820 Escherichia coli 562 -11535068

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852471	11100	33256	306	101

Description

5000692525 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1821 b1821 Escherichia coli 562 -11535069
7500922926 yebn (de:hypothetical 22.1 kd protein in manz-cspc intergenic region) (db:swissprot) YEBN_ECOLI P76264 ESCHERICHIA COLI 562 -11535069
7000691485 probable membrane protein b1821 (cl:escherichia coli conserved hypothetical protein b1821) (db:pir2.dat) E64943 E64943 Escherichia coli 562 -11535069 224315 ywld (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o335#4; similar to (swissprot accession) (le:6798) (re:7418) (di:direct) D90826 D90826 g1736465 Escherichia coli 562 -11535069 7500922928 b1821 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:o206; this 206 aa orf is 30 pct identical (6 gaps)) (le:7318) (re:7938) (di:direct) AE000276 AE000276 g1788124 Escherichia coli 562 -11535069 300955 ywld (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o335#4; similar to (swissprot accession) (le:6798) (re:7418) (di:direct) D90826 D90826 g1736465 Escherichia coli 562 -11535069 6500731211 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1821 b1821 Escherichia coli 562 -11535069

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852477	11101	33257	1239	412

Description

6500731212 yebh:b1822 hypothetical 30.4 kd protein in manz-cspc intergenic region:orf30 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1822 b1822 Escherichia coli 562 -11535070 111488 rrma (ec:2.1.1.51) (de:methyltransferase)) (db:swissprot) RRMA_ECOLI P36999 ESCHERICHIA COLI 562 -11535070 163491 yebh probable s-adenosylmethionine-dependent methyltransferase yebh (cl:bioc homology) (db:pir2.dat) S49049 S49049 Escherichia coli 562 -11535070 224316 yebh mycinamicin-resistance protein myra. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o335#5; similar to (swissprot accession) (le:7415) (re:8224) (di:complement) D90826 D90826 g1736466 Escherichia coli 562 -11535070 300956 orf30 orf30 (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:escherichia coli cspc (msmb) gene, complete cds.) (le:618) (re:1427) (di:direct) ECOCSPCA D28496 g460699 Escherichia coli 562 -11535070 234066 yebh putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:f269; 100 pct identical to yebh_ecoli sw: p36999;) (le:7935) (re:8744) (di:complement) AE000276 AE000276 g1788125 Escherichia coli 562 -11535070 5000692526 (de:(ecoli_1779) (pn:hypothetical 30) (gn:yebh) (gtcfc:13.7:14.1) (ec:) (yebh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1779 ECOLI_1779 Escherichia coli 562 10053217

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852478	11102	33258	183	60

Description

5000692528 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1824 b1824 Escherichia coli 562 -11535071 7000691486 hypothetical protein b1824 (db:pir2.dat) H64943 H64943 Escherichia coli 562 -11535071 7500960065 b1824 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:f47) (le:9132) (re:9275) (di:complement) AE000276 AE000276 g1788127 Escherichia coli 562 -11535071 6500731213 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1824 b1824 Escherichia coli 562 -11535071

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852479	11103	33259	675	224

Description

5000692529 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1825 b1825 Escherichia coli 562 -11535072
 7000691487 hypothetical protein b1825 precursor (db:pir2.dat) A64944 A64944 Escherichia coli 562 -11535072 7500960066 b1825 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:f95; this 95 aa orf is 33 pct identical (4 gaps)) (le:9945) (re:10232) (di:complement) AE000276 AE000276 g1788128 Escherichia coli 562 -11535072 6500731214 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1825 b1825 Escherichia coli 562 -11535072

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852483	11104	33260	1509	502

Description

GTC ORF with score 877 to: (fn:involved in poly-3-hydroxybutyrate degradation) (db:genpept-bct2) (ec:6.2.1.16) (de:sinorhizobium meliloti acetoacetyl-coa synthetase (acsa) gene,complete cds.) (nt:acetoacetyl-coa ligase; acyl-activating enzyme) (le:548)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852492	11105	33261	291	96

Description

5000692530 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1826 b1826 Escherichia coli 562 -11535073
 7000691488 hypothetical protein b1826 precursor (db:pir2.dat) B64944 B64944 Escherichia coli 562 -11535073 7500960067 b1826 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 167 of 400 of the completegenome.) (nt:f47; this 47 aa orf is 34 pct identical (3 gaps)) (le:68) (re:211) (di:complement) AE000277 AE000277 g1788130 Escherichia coli 562 -11535073 6500731215 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1826 b1826 Escherichia coli 562 -11535073

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852495	11106	33262	492	163

Description

5000692531 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1827 b1827 Escherichia coli 562 -11535074
7500884553 kdgr (de:transcriptional regulator kdgr) (db:swissprot) KDGR_ECOLI P76268 ESCHERICHIA COLI 562 -11535074 7000691489 transcription regulator b1827 (cl:acetate operon repressor) (db:pir2.dat) C64944 C64944 Escherichia coli 562 -11535074 224318 pectin degradation repressor protein kdgr. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o335#8; similar to (swissprot accession) (le:10472) (re:11263) (di:complement) D90826 D90826 g1736468 Escherichia coli 562 -11535074 7500884555 b1827 putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 167 of 400 of the completegenome.) (nt:f263; this 263 aa orf is 90 pct identical (0 gaps)) (le:753) (re:1544) (di:complement) AE000277 AE000277 g1788131 Escherichia coli 562 -11535074 300958 pectin degradation repressor protein kdgr. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o335#8; similar to (swissprot accession) (le:10472) (re:11263) (di:complement) D90826 D90826 g1736468 Escherichia coli 562 -11535074 6500731216 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1827 b1827 Escherichia coli 562 -11535074

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852504	11107	33263	663	220

Description

5000692532 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1828 b1828 Escherichia coli 562 -11535075
7000691490 probable permease b1828 (db:pir2.dat) D64944 D64944 Escherichia coli 562 -11535075 7500960068 b1828 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 167 of 400 of the completegenome.) (nt:o494; this 494 aa orf is 32 pct identical (14 gaps)) (le:1610) (re:3094) (di:direct) AE000277 AE000277 g1788132 Escherichia coli 562 -11535075 6500731217 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1828 b1828 Escherichia coli 562 -11535075

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852512	11108	33264	411	136

Description

6500731218 yebj:b1831 hypothetical 4.2 kd protein in prc
5region:hypothetical 4.2 kd protein in prc-prpa intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1831
b1831 Escherichia coli 562 -11535076 111491 yebj (de:hypothetical 4.2 kd
protein in prc-prpa intergenic region) (db:swissprot) YEBJ_ECOLI P45577
ESCHERICHIA COLI 562 -11535076 7000687592 yebj yebj protein
(cl:hypothetical protein hi1669) (db:pir2.dat) G64944 G64944 Escherichia
coli 562 -11535076 224322 yebj (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o335#12; similar to
(swissprot accession) (le:16000) (re:16119) (di:complement) D90826 D90826
g1736472 Escherichia coli 562 -11535076 224327 yebj (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #336(41.2-41.6 min.))
(nt:orf_id:o335#12; similar to (swissprot accession) (le:1953) (re:2072)
(di:complement) D90827 D90827 g1736478 Escherichia coli 562 -11535076
4000707432 (sr:escherichia coli (strain:k12, sub_strain:w3110) dna)
(db:genpept-bct1) (de:escherichia coli prc gene involved in the c-terminal
processing ofpenicillin-binding protein 3, complete cds.) (nt:similar to
genbank accession number u32840:hi1669) (le:148... ECOPRC D00674 g2251116
Escherichia coli 562 -11535076 300962 yebj orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
167 of 400 of the completegenome.) (nt:f232; 100 pct identical to 38 amino
acids of) (le:6281) (re:6400) (di:complement) AE000277 AE000277 g1788135
Escherichia coli 562 -11535076 300967 (sr:escherichia coli (strain:k12,
sub_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli prc gene
involved in the c-terminal processing ofpenicillin-binding protein 3,
complete cds.) (nt:similar to genbank accession number u32840:hi1669)
(le:148... ECOPRC D00674 g2251116 Escherichia coli 562 -11535076 5000692534
(de:(ecoli_1788) (pn:hypothetical 4) (gn:yebj) (gtcfc:13.7:14.1) (ec:)
(yebj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_1788 ECOLI_1788 Escherichia coli 562 10053220

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852525	11109	33265	546	181

Description

5000692535 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1832 b1832 Escherichia coli 562 -11535077
7502852255 yebr (de:hypothetical 20.3 kd protein in prc-ppha intergenic region) (db:swissprot) YEBR_ECOLI P76270 ESCHERICHIA COLI 562 -11535077
7000691491 probable membrane protein b1832 (cl:hypothetical protein ykl069w) (db:pir2.dat) H64944 H64944 Escherichia coli 562 -11535077 224323 ykl069w: ykl1340 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o335#13; similar to (swissprot accession) (le:16795) (re:17346) (di:complement) D90826 D90826 g1736473 Escherichia coli 562 -11535077 300968 ykl069w: ykl1340 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336(41.2-41.6 min.)) (nt:orf_id:o335#13; similar to (swissprot accession) (le:2748) (re:3299) (di:complement) D90827 D90827 g1736479 Escherichia coli 562 -11535077 300963 b1832 orf: hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 167 of 400 of the complete genome.) (nt:f183; residues 72-127 are 57 pct identical to) (le:7076) (re:7627) (di:complement) AE000277 AE000277 g1788136 Escherichia coli 562 -11535077 224328 ykl069w: ykl1340 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336(41.2-41.6 min.)) (nt:orf_id:o335#13; similar to (swissprot accession) (le:2748) (re:3299) (di:complement) D90827 D90827 g1736479 Escherichia coli 562 -11535077 6500731219 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1832 b1832 Escherichia coli 562 -11535077

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852528	11110	33266	705	235

Description

5000692536 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1833 b1833 Escherichia coli 562 -11535078
7502852256 yebs (de:hypothetical 48.3 kd protein in prc-ppha intergenic region) (db:swissprot) YEBS_ECOLI P76271 ESCHERICHIA COLI 562 -11535078
7000691492 probable membrane protein b1833 (cl:hypothetical protein hi1671) (db:pir2.dat) A64945 A64945 Escherichia coli 562 -11535078 224324
paraquat-inducible protein a. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o335#14; similar to (swissprot accession) (le:17422) (re:18705) (di:direct) D90826 D90826 g1736474 Escherichia coli 562 -11535078 300969 paraquat-inducible protein a. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336(41.2-41.6 min.)) (nt:orf_id:o335#14; similar to (swissprot accession) (le:3375) (re:4658) (di:direct) D90827 D90827 g1736480 Escherichia coli 562 -11535078 300964 b1833 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 167 of 400 of the completegenome.) (nt:o427; 43 pct identical (9 gaps) to 390 residues) (le:7703) (re:8986) (di:direct) AE000277 AE000277 g1788137 Escherichia coli 562 -11535078 224329 paraquat-inducible protein a. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336(41.2-41.6 min.)) (nt:orf_id:o335#14; similar to (swissprot accession) (le:3375) (re:4658) (di:direct) D90827 D90827 g1736480 Escherichia coli 562 -11535078 6500731220 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1833 b1833 Escherichia coli 562 -11535078

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852540	11111	33267	1017	338

Description

GTC ORF with score 141 to: (fn:phosphorylation; shuttling) (sr:rattus norvegicus liver cdna to mrna) (db:genpept-rod) (de:rattus norvegicus nucleolar phosphoprotein of 140kd, noppl40 mrna,complete cds.) (le:804) (re:2915) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852571	11112	33268	261	86

Description

5000692537 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1834 b1834 Escherichia coli 562 -11535079
7000689495 probable membrane protein b1834 (cl:hypothetical protein b1834) (db:pir2.dat) B64945 B64945 Escherichia coli 562 -11535079 7500955795 b1834 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 167 of 400 of the completegenome.) (nt:o879; 42 pct identical (13 gaps) to 877 residues) (le:8949) (re:11588) (di:direct) AE000277 AE000277 g1788138 Escherichia coli 562 -11535079 6500731221 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1834 b1834 Escherichia coli 562 -11535079

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852572	11113	33269	234	77

Description

5000692538 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1835 b1835 Escherichia coli 562 -11535080
7000687597 yebu probable rna methylase yebu (db:pir2.dat) C64945 C64945 Escherichia coli 562 -11535080 224331 proliferating-cell nucleolar antigen p120 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336(41.2-41.6 min.)) (nt:orf_id:o336#2; similar to (swissprot accession) (le:7334) (re:8779) (di:direct) D90827 D90827 g1736482 Escherichia coli 562 -11535080 300971 yebu putative nucleolar proteins (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 168 of 400 of the completegenome.) (nt:o481; this 481 aa orf is 35 pct identical (19 gaps) (le:67) (re:1512) (di:direct) AE000278 AE000278 g1788140 Escherichia coli 562 -11535080 7000687596 yebu (de:hypothetical 53.4 kd protein in prc-prpa intergenic region) (db:swissprot) YEBU_ECOLI P76273 ESCHERICHIA COLI 562 -11535080 6500731222 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1835 b1835 Escherichia coli 562 -11535080

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852573	11114	33270	471	156

Description

5000692539 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1836 b1836 Escherichia coli 562 -11535081
7000691493 hypothetical protein b1836 (db:pir2.dat) D64945 D64945
Escherichia coli 562 -11535081 7500960069 b1836 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 168 of 400 of the completegenome.) (nt:o83; this 83 aa orf is 32 pct identical (4 gaps)) (le:1615) (re:1866) (di:direct) AE000278 AE000278
g1788141 Escherichia coli 562 -11535081 6500731223 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1836 b1836 Escherichia coli 562 -11535081

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852574	11115	33271	540	179

Description

5000692540 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1837 b1837 Escherichia coli 562 -11535082
7502852257 yebw (de:hypothetical 10.4 kd protein in prc-hole intergenic region) (db:swissprot) YEBW_ECOLI P76275 ESCHERICHIA COLI 562 -11535082
7000691494 probable membrane protein b1837 (db:pir2.dat) E64945 E64945
Escherichia coli 562 -11535082 7500960070 b1837 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 168 of 400 of the completegenome.) (nt:o91; this 91 aa orf is 38 pct identical (1 gap)) (le:1887) (re:2162) (di:direct) AE000278 AE000278
g1788142 Escherichia coli 562 -11535082 6500731224 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1837 b1837 Escherichia coli 562 -11535082

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852579	11116	33272	855	284

Description

6500731225 prpa:b1838 hypothetical protein:serine/threonine protein phosphatase prpa (gtcfc:14.1) (ec:3.1.3.16) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1838 b1838 Escherichia coli 562 -11535083
7000691495 ppha:prpa phosphoprotein phosphatase:1:serine/threonine specific (cl:phage lambda phosphoprotein phosphatase:phosphoesterase core homology) (ec:3.1.3.16) (db:pir1.dat) F64945 F64945 Escherichia coli 562 -11535083
224332 serine/threonine protein phosphatase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336(41.2-41.6 min.)) (nt:orf_id:o336#5; similar to (swissprot accession) (le:9430) (re:10089) (di:complement) D90827 D90827 g1736483 Escherichia coli 562 -11535083
300972 ppha protein phosphatase 1 modulates phosphoproteins (fn:regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 168 of 400 of the completegenome.) (nt:f219; uug start; this 219 aa orf is 49 pct) (le:2163) (re:2822) (di:complement) AE000278 AE000278 g1788143 Escherichia coli 562 -11535083 5000692541 (de:(ecoli_1795) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1795 ECOLI_1795 Escherichia coli 562 10119869

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852584	11117	33273	426	141

Description

5000692542 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1839 b1839 Escherichia coli 562 -11535084
7000691496 hypothetical protein b1839 precursor (db:pir2.dat) G64945 G64945 Escherichia coli 562 -11535084 7500960071 b1839 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 168 of 400 of the completegenome.) (nt:f113; this 113 aa orf is 29 pct identical (2 gaps)) (le:3215) (re:3556) (di:complement) AE000278 AE000278 g1788144 Escherichia coli 562 -11535084 6500731226 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1839 b1839 Escherichia coli 562 -11535084

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852589	11118	33274	957	318

Description

5000692543 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1840 b1840 Escherichia coli 562 -11535085
 7000691497 probable membrane protein b1840 (db:pir2.dat) H64945 H64945 Escherichia coli 562 -11535085 7500960072 b1840 putative resistance protein (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 168 of 400 of the completegenome.) (nt:f290; this 290 aa orf is 31 pct identical (19 gaps)) (le:3569) (re:4441) (di:complement) AE000278 AE000278 g1788145 Escherichia coli 562 -11535085
 6500731227 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1840 b1840 Escherichia coli 562 -11535085

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852600	11119	33275	555	184

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852604	11120	33276	426	141

Description

5000692544 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1841 b1841 Escherichia coli 562 -11535086
 7000691498 hypothetical protein b1841 (cl:copper resistance protein pcoc) (db:pir2.dat) A64946 A64946 Escherichia coli 562 -11535086 7500960073 b1841 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 168 of 400 of the completegenome.) (nt:f124; this 124 aa orf is 39 pct identical (6 gaps)) (le:4445) (re:4819) (di:complement) AE000278 AE000278 g1788146 Escherichia coli 562 -11535086 6500731228 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1841 b1841 Escherichia coli 562 -11535086

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852611	11121	33277	1032	343

Description

5000692545 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1843 b1843 Escherichia coli 562 -11535087
7000691499 hypothetical protein b1843 (db:pir2.dat) C64946 C64946
Escherichia coli 562 -11535087 7500960074 b1843 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 168 of 400 of the completegenome.) (nt:o218; this 218 aa orf is 24 pct identical (2 gaps)) (le:5290) (re:5946) (di:direct) AE000278 AE000278
g1788148 Escherichia coli 562 -11535087 6500731229 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1843 b1843 Escherichia coli 562 -11535087

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852618	11122	33278	1764	587

Description

5000692546 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1844 b1844 Escherichia coli 562 -11535088
7000691500 probable dna polymerase iii epsilon chain (db:pir2.dat) D64946 D64946 Escherichia coli 562 -11535088 7500960075 b1844 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 168 of 400 of the completegenome.) (nt:o220; this 220 aa orf is 32 pct identical (20 gaps)) (le:5970) (re:6632) (di:direct) AE000278 AE000278
g1788149 Escherichia coli 562 -11535088 6500731230 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1844 b1844 Escherichia coli 562 -11535088

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852619	11123	33279	351	117

Description

6500731231 yebe:b1846 hypothetical 23.7 kd protein in purt
5region:hypothetical 23.7 kd protein in ptrb-purt intergenic region:orf153
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1846
b1846 Escherichia coli 562 -11535089 111484 yebe (de:hypothetical 23.7 kd
protein in ptrb-purt intergenic region (orf153)) (db:swissprot) YEBE_ECOLI
P33218 ESCHERICHIA COLI 562 -11535089 7000687588 yebe yebe protein
(db:pir2.dat) F64946 F64946 Escherichia coli 562 -11535089 224335 yebe
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336(41.2-41.6
min.)) (nt:orf_id:o336#13; similar to (swissprot accession) (le:16165)
(re:16824) (di:complement) D90827 D90827 g1736486 Escherichia coli 562
-11535089 300975 yebe orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 168 of 400 of the
completegenome.) (nt:f219; 100 pct identical to yebe_ecoli sw: p33218;)
(le:8898) (re:9557) (di:complement) AE000278 AE000278 g1788151 Escherichia
coli 562 -11535089 5000692547 (de:(ecoli_1803) (pn:hypothetical 23)
(gn:yebe) (gtcfc:13.7:14.1) (ec:) (yebe_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_1803 ECOLI_1803 Escherichia coli 562
10053213

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852639	11124	33280	951	316

Description

GTC ORF with score 1248 to: (db:genpept-pln1) (de:neurospora crassa vacuolar
atpase 41 kda subunit (vma6) gene,ribosome-associated protein (rap-1) gene,
complete cds.) (le:1400:1488:1653:2603) (re:1431:1576:2542:2686)
(di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852641	11125	33281	735	245

Description

6500731232 yebf:b1847 hypothetical 13.5 kd lipoprotein in purt
5region:hypothetical 13.5 kd lipoprotein in ptrb-purt intergenic region
precursor:orf122 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1847 b1847 Escherichia coli 562 -11535090 111486
yebf (de:precursor (orf122)) (db:swissprot) YEBF_ECOLI P33219 ESCHERICHIA
COLI 562 -11535090 7000687589 yebf lipoprotein yebf precursor (db:pir2.dat)
G64946 G64946 Escherichia coli 562 -11535090 224336 yebf (sr:escherichia
coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #336(41.2-41.6 min.))
(nt:orf_id:o336#14; similar to (swissprot accession) (le:17151) (re:17519)
(di:complement) D90827 D90827 g1736487 Escherichia coli 562 -11535090
300976 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1)
(de:escherichia coli glycinamide ribonucleotide transformylase (purt)gene,
2-keto-3-deoxy-6-phosphogluconate aldolase (eda) gene,6-phosphogluconate
dehydratase (edd) gene, complete cds's.) (nt:p... ECOGARA L20897 g304885
Escherichia coli 562 -11535090 234460 yebf orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
168 of 400 of the completegenome.) (nt:f122; 100 pct identical to yebf_ecoli
sw: p33219;) (le:9884) (re:10252) (di:complement) AE000278 AE000278 g1788152
Escherichia coli 562 -11535090 5000692548 (de:(ecoli_1804) (pn:hypothetical
13) (gn:yebf) (gtcfc:13.7:14.1) (ec:) (yebf_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1804 ECOLI_1804 Escherichia
coli 562 10053215

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852663	11126	33282	405	134

Description

6500731233 yebg:b1848 hypothetical 10.7 kd protein in purt
5region:hypothetical 10.7 kd protein in ptrb-purt intergenic region:orf96
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1848
b1848 Escherichia coli 562 -11535091 111487 yebg (de:hypothetical 10.7 kd
protein in ptrb-purt intergenic region (orf96)) (db:swissprot) YEBG_ECOLI
P33220 ESCHERICHIA COLI 562 -11535091 7000687590 yebg yebg protein
(db:pir2.dat) H64946 H64946 Escherichia coli 562 -11535091 224337 yebg
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336(41.2-41.6
min.)) (nt:orf_id:o336#15; similar to (swissprot accession) (le:17574)
(re:17864) (di:complement) D90827 D90827 g1736488 Escherichia coli 562
-11535091 300977 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1)
(de:escherichia coli glycinamide ribonucleotide transformylase (purt)gene,
2-keto-3-deoxy-6-phosphogluconate aldolase (eda) gene,6-phosphogluconate
dehydratase (edd) gene, complete cds's.) (nt:p... ECOGARA L20897 g304886
Escherichia coli 562 -11535091 234461 yebg orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
168 of 400 of the completegenome.) (nt:f96; 100 pct identical to yebg_ecoli
sw: p33220) (le:10307) (re:10597) (di:complement) AE000278 AE000278 g1788153
Escherichia coli 562 -11535091 5000692549 (de:(ecoli_1805) (pn:hypothetical
10) (gn:yebg) (gtcfc:13.7:14.1) (ec:) (yebg_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1805 ECOLI_1805 Escherichia
coli 562 10053216

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852666	11127	33283	1023	341

Description

GTC ORF with score 99 to: (sr:tomato (l.esculentum breeding line t3) dna
(library o) (db:genpept-pln1) (de:tomato cell wall hrgp (hydroxproline-rich
glycoprotein) gene,partial cds.) (nt:cell wall hydroxyproline-rich
glycoprotein) (le:<1) (re:279) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852668	11128	33284	183	60

Description

6500731234 yebk:b1853 hypothetical 32.0 kd protein in pyka-zwf intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1853 b1853 Escherichia coli 562 -11535092 111493 yebk (de:hypothetical 32.0 kd protein in pyka-zwf intergenic region) (db:swissprot) YEBK_ECOLI P46118 ESCHERICHIA COLI 562 -11535092 7000687593 yebk yebk protein (cl:hypothetical protein ybbh) (db:pir2.dat) E64947 E64947 Escherichia coli 562 -11535092 224344 yebk rpir protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336gap(41.6-41.9 min.)) (nt:orf_id:o336gap#6; similar to (swissprot accession) (le:6178) (re:7047) (di:direct) D90828 D90828 g1736496 Escherichia coli 562 -11535092 300984 yebk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 169 of 400 of the completgenome.) (nt:o289; 97 pct identical to yebk_ecoli sw: p46118) (le:5868) (re:6737) (di:direct) AE000279 AE000279 g1788159 Escherichia coli 562 -11535092 5000692550 (de:(ecoli_1810) (pn:hypothetical 32) (gn:yebk) (gtcfc:13.7:14.1) (ec:) (yebk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1810 ECOLI_1810 Escherichia coli 562 10119874

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852674	11129	33285	237	79

Description

6500731235 yeba:b1856 hypothetical 46.7 kd protein in msbb-ruvb intergenic region:orfu (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1856 b1856 Escherichia coli 562 -11535093 5000692552 yeba (de:hypothetical 46.7 kd protein in msbb-ruvb intergenic region (orfu)) (db:swissprot) YEBA_ECOLI P24204 ESCHERICHIA COLI 562 -11535093 7000690947 yeba membrane protein yeba (cl:hypothetical protein hi0409) (db:pir2.dat) H64947 H64947 Escherichia coli 562 -11535093 224347 yeba lysostaphin precursor ec 3.5.1.-. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336gap(41.6-41.9 min.)) (nt:orf_id:o336gap#9; similar to (swissprot accession) (le:9839) (re:11098) (di:complement) D90828 D90828 g1736499 Escherichia coli 562 -11535093 300987 yeba orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 169 of 400 of the completgenome.) (nt:f419; 99 pct identical to yeba_ecoli sw: p24204;) (le:9529) (re:10788) (di:complement) AE000279 AE000279 g1788162 Escherichia coli 562 -11535093

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852681	11130	33286	1590	530

Description

6500731236 yebm:b1858 hypothetical protein:hypothetical abc transporter
atp-binding protein in msbb-ruvb intergenic region (gtcfc:12.6)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1858 b1858
Escherichia coli 562 -11535094 111495 znuc (de:high-affinity zinc uptake
system atp-binding protein znuc) (db:swissprot) ZNUC_ECOLI P52648
ESCHERICHIA COLI 562 -11535094 7000687595 yebm probable abc transport
system atp-binding protein yebm (cl:unassigned atp-binding cassette
proteins:atp-binding cassette homology) (db:pir2.dat) B64948 B64948
Escherichia coli 562 -11535094 224349 yebm sulfate transport atp-binding
protein cysa. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#336gap(41.6-41.9 min.)) (nt:orf_id:o336gap#11; similar to (swissprot
accession) (le:12188) (re:12943) (di:direct) D90828 D90828 g1736501
Escherichia coli 562 -11535094 300989 yebm putative atp-binding component
of a transport (fn:putative transport; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.)
(nt:o251; this 251 aa orf is 54 pct identical (0 gaps)) (le:1081) (re:1836)
(di:direct) AE000280 AE000280 g1788165 Escherichia coli 562 -11535094
5000692554 (de:(ecoli_1815) (pn:function not assigned) (gtcfc:13.7:14.1)
(ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1815
ECOLI_1815 Escherichia coli 562 10119877

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852688	11131	33287	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852690	11132	33288	279	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852720	11133	33289	3183	1060

Description

6500731237 yebi:b1859 hypothetical 27.8 kd protein in msbb-ruvb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1859 b1859 Escherichia coli 562 -11535095 111489 znuB (de:high-affinity zinc uptake system membrane protein znuB) (db:swissprot) ZNUB_ECOLI P39832 ESCHERICHIA COLI 562 -11535095 7000687591 yebi probable membrane protein yebi (db:pir2.dat) C64948 C64948 Escherichia coli 562 -11535095 224350 yebi (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336gap(41.6-41.9 min.)) (nt:orf_id:o336gap#12; similar to (swissprot accession) (le:12940) (re:13725) (di:direct) D90828 D90828 g1736502 Escherichia coli 562 -11535095 300993 yebi (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf_id:o336gap#12; similar to (swissprot accession) (le:216) (re:1001) (di:direct) D90829 D90829 g1736506 Escherichia coli 562 -11535095 300990 yebi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:o261; 99 pct identical to yebi_ecoli sw: p39832) (le:1833) (re:2618) (di:direct) AE000280 AE000280 g1788166 Escherichia coli 562 -11535095 224353 yebi (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf_id:o336gap#12; similar to (swissprot accession) (le:216) (re:1001) (di:direct) D90829 D90829 g1736506 Escherichia coli 562 -11535095 5000692555 (de:(ecoli_1816) (pn:hypothetical 27) (gn:yebi) (gtcfc:13.7:14.1) (ec:) (yebi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1816 ECOLI_1816 Escherichia coli 562 10119878

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852727	11134	33290	516	171

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852728	11135	33291	231	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852742	11136	33292	2088	695

Description

6500731238 yebb:b1862 hypothetical 26.8 kd protein in ruva-ruvc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1862 b1862 Escherichia coli 562 -11535096 111481 yebb (de:hypothetical 26.8 kd protein in ruva-ruvc intergenic region) (db:swissprot) YEBB_ECOLI P24238 ESCHERICHIA COLI 562 -11535096 7000687587 yebb hypothetical 26.8 kd protein ruva-ruvc intergenic region (db:pir2.dat) F64948 F64948 Escherichia coli 562 -11535096 224356 yebb (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf_id:o337#3; similar to (swissprot accession) (le:2954) (re:3655) (di:direct) D90829 D90829 g1736509 Escherichia coli 562 -11535096 300996 yebb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completgenome.) (nt:o233; 100 pct identical to yebb_ecoli sw: p24238;) (le:4571) (re:5272) (di:direct) AE000280 AE000280 g1788169 Escherichia coli 562 -11535096 5000692556 (de:(ecoli_1819) (pn:hypothetical 26) (gn:yebb) (gtcfc:13.7:14.1) (ec:) (yebb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1819 ECOLI_1819 Escherichia coli 562 10053210

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852756	11137	33293	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852778	11138	33294	1461	486

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852782	11139	33295	1110	369

Description

6500731239 yebc:b1864 hypothetical 26.4 kd protein in ruvc-asps intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1864 b1864 Escherichia coli 562 -11535097 235947 yebc (de:hypothetical 26.4 kd protein in ruvc-asps intergenic region) (db:swissprot) YEBC_ECOLI P24237 ESCHERICHIA COLI 562 -11535097 162605 yebc hypothetical 26.4k protein ruvc-asps intergenic region (cl:hypothetical protein mg332) (db:pir2.dat) C38113 C38113 Escherichia coli 562 -11535097 224358 yebc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf_id:o337#5; similar to (pir accession number) (le:4213) (re:4953) (di:complement) D90829 D90829 g1736511 Escherichia coli 562 -11535097 5000692557 orf246 (db:genpept-bct1) (de:e.coli orf150, orf246, orf11 and ruvc gene for resolvase ofholliday junction intermediates.) (le:499) (re:1239) (di:direct) ECORFRUFC X59551 g42173 Escherichia coli 562 -11535097 300998 orf26 (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e. coli dna for orf17, orf26, ruvc and orf23 genes.) (le:992) (re:1732) (di:direct) ECORUVC D10165 g216652 Escherichia coli 562 -11535097 235775 yebc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:f246; 100 pct identical to yebc_ecoli sw: p24237;) (le:5830) (re:6570) (di:complement) AE000280 AE000280 g1788171 Escherichia coli 562 -11535097 111482 yebc (de:hypothetical 26.4 kd protein in ruvc-asps intergenic region) (db:swissprot) YEBC_ECOLI P24237 ESCHERICHIA COLI 562 -11535097

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852786	11140	33296	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852794	11141	33297	753	250

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852801	11142	33298	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852809	11143	33299	888	295

Description

6500731240 yecd:b1867 hypothetical 21.8 kd protein in asps 5region:hypothetical 21.7 kd protein in asps-bisz intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1867 b1867 Escherichia coli 562 -11535098 111507 yecd (de:hypothetical 21.7 kd protein in asps-bisz intergenic region) (db:swissprot) YECD_ECOLI P37347 ESCHERICHIA COLI 562 -11535098 7000687600 yecd hypothetical 21.8 kd protein in asps 5region (cl:hypothetical protein b1011) (db:pir2.dat) C64949 C64949 Escherichia coli 562 -11535098 7500922933 yecd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:o199; residues 12-190 are 100 pct identical) (le:9218) (re:9817) (di:direct) AE000280 AE000280 g1788174 Escherichia coli 562 -11535098 5000692558 (de:(ecoli_1824) (pn:hypothetical 21) (gn:yecd) (gtcfc:13.7:14.1) (ec:) (yecd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1824 ECOLI_1824 Escherichia coli 562 10123495

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852814	11144	33300	225	74

Description

6500731241 yece:b1868 hypothetical protein in asps 5region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1868 b1868 Escherichia coli 562 -11535099 7000691826 yece hypothetical protein in asps 5region (db:pir2.dat) D64949 D64949 Escherichia coli 562 -11535099 7500960343 yece orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:o272; residues 16-156 are 98 pct identical to) (le:9814) (re:10632) (di:direct) AE000280 AE000280 g1788175 Escherichia coli 562 -11535099 5000692559 (de:(ecoli_1825) (pn:hypothetical protein in asps 5"region:fragment) (gn:yece) (gtcfc:13.7:14.1) (ec:) (yece_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1825 ECOLI_1825 Escherichia coli 562 10123496

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852816	11145	33301	267	88

Description

5000692560 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1869 b1869 Escherichia coli 562 -11535100
 7000691501 hypothetical protein b1869 (db:pir2.dat) E64949 E64949
 Escherichia coli 562 -11535100 7500922945 yecn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:o141; 29 pct identical (2 gaps) to 79 residues from) (le:10655) (re:11080) (di:direct) AE000280 AE000280 g1788176 Escherichia coli 562 -11535100 7500922943 yecn (de:hypothetical 16.2 kd protein in asps-bisz intergenic region) (db:swissprot) YECN_ECOLI P76289 ESCHERICHIA COLI 562 -11535100 6500731242 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1869 b1869 Escherichia coli 562 -11535100

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852819	11146	33302	321	106

Description

5000692561 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1870 b1870 Escherichia coli 562 -11535101
 7500922946 yeco (de:hypothetical 27.8 kd protein in asps-bisz intergenic region) (db:swissprot) YECO_ECOLI P76290 ESCHERICHIA COLI 562 -11535101
 7000691502 hypothetical protein b1870 (cl:conserved hypothetical protein hi0319) (db:pir2.dat) F64949 F64949 Escherichia coli 562 -11535101 224363 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf_id:o337#11; similar to (swissprot accession) (le:9504) (re:10247) (di:direct) D90829 D90829 g1736516 Escherichia coli 562 -11535101 7500922948 yeco orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:o247; residues 5-237 are 71 pct identical to) (le:11121) (re:11864) (di:direct) AE000280 AE000280 g1788177 Escherichia coli 562 -11535101 301003 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3min.)) (nt:orf_id:o337#11; similar to (swissprot accession) (le:9504) (re:10247) (di:direct) D90829 D90829 g1736516 Escherichia coli 562 -11535101 6500731243 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1870 b1870 Escherichia coli 562 -11535101

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852821	11147	33303	759	252

Description

GTC ORF with score 200 to: (or:Mus musculus) (sr:mouse (strain cd-1) dna, library of o.smithies, clone pump-3 hb) (db:genpept-rod) (de:mouse prp gene encoding proline-rich protein mp-3, exon 2.) (nt:proline-rich protein mp-3) (le:<1) (re:893) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852825	11148	33304	273	90

Description

5000692562 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1871 b1871 Escherichia coli 562 -11535102
7500922950 yecp (de:hypothetical 37.0 kd protein in asps-bisz intergenic region) (db:swissprot) YECP_ECOLI P76291 ESCHERICHIA COLI 562 -11535102
7000691503 hypothetical protein b1871 (cl:conserved hypothetical protein hp0419:bioc homology) (db:pir2.dat) G64949 G64949 Escherichia coli 562 -11535102 224364 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf_id:o337#12; similar to (swissprot accession) (le:10244) (re:11215) (di:direct) D90829 D90829 g1736517 Escherichia coli 562 -11535102 7500922952 yecp putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:o323; this 323 aa orf is 65 pct identical (1 gap)) (le:11861) (re:12832) (di:direct) AE000280 AE000280 g1788178 Escherichia coli 562 -11535102 301004 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf_id:o337#12; similar to (swissprot accession) (le:10244) (re:11215) (di:direct) D90829 D90829 g1736517 Escherichia coli 562 -11535102 6500731244 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1871 b1871 Escherichia coli 562 -11535102

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852826	11149	33305	471	157

Description

6500731245 yeck:b1873 hypothetical protein:probable cytochrome c-type protein in bisz-cutc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1873 b1873 Escherichia coli 562 -11535103 111514 yeck (de:probable cytochrome c-type protein in bisz-cutc intergenic region) (db:swissprot) YECK_ECOLI P52005 ESCHERICHIA COLI 562 -11535103 7000687603 hypothetical protein b1873 (cl:membrane-bound cytochrome torc:nirt homology) (db:pir2.dat) A64950 A64950 Escherichia coli 562 -11535103 224366 torc cytochrome c-type protein torc. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf_id:o337#14; similar to (swissprot accession) (le:13834) (re:14934) (di:complement) D90829 D90829 g1736519 Escherichia coli 562 -11535103 301013 torc cytochrome c-type protein torc. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf_id:o337#14; similar to (swissprot accession) (le:1399) (re:2499) (di:complement) D90830 D90830 g1736527 Escherichia coli 562 -11535103 301006 yeck putative cytochrome c-type protein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 171 of 400 of the completegenome.) (nt:f366; this 366 aa orf is 42 pct identical (7 gaps)) (le:2567) (re:3667) (di:complement) AE000281 AE000281 g1788181 Escherichia coli 562 -11535103 224373 torc cytochrome c-type protein torc. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf_id:o337#14; similar to (swissprot accession) (le:1399) (re:2499) (di:complement) D90830 D90830 g1736527 Escherichia coli 562 -11535103 5000692564 (de:(ecoli_1830) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1830 ECOLI_1830 Escherichia coli 562 10119887

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852840	11150	33306	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852844	11151	33307	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852847	11152	33308	237	79

Description

6500731246 yecm:b1875 hypothetical protein:hypothetical 21.4 kd protein in cutc-args intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1875 b1875 Escherichia coli 562 -11535104 7000687604 hypothetical protein b1875 (cl:hypothetical protein b1875) (db:pir2.dat) C64950 C64950 Escherichia coli 562 -11535104 7500960077 yecm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 171 of 400 of the completegenome.) (nt:f190; this 190 aa orf is 38 pct identical (3 gaps)) (le:4815) (re:5387) (di:complement) AE000281 AE000281 g1788183 Escherichia coli 562 -11535104 111518 yecm_ecoli (de:hypothetical protein in cutc 5'region (fragment).) P52007 P52007 Escherichia coli 562 -11535104 5000692566 (de:(ecoli_1832) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1832 ECOLI_1832 Escherichia coli 562 10123500

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852849	11153	33309	288	95

Description

5000692567 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1877 b1877 Escherichia coli 562 -11535105 7000691504 hypothetical protein b1877 (db:pir2.dat) E64950 E64950 Escherichia coli 562 -11535105 7500960078 yect orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 171 of 400 of the completegenome.) (nt:o169; uug start; this 169 aa orf is 30 pct) (le:7486) (re:7995) (di:direct) AE000281 AE000281 g1788185 Escherichia coli 562 -11535105 6500731247 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1877 b1877 Escherichia coli 562 -11535105

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852852	11154	33310	273	90

Description

6500731248 flhe:b1878 hypothetical protein:flagellar protein flhe precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1878 b1878 Escherichia coli 562 -11535106 118246 flhe (de:flagellar protein flhe precursor) (db:swissprot) FLHE_ECOLI P76297 ESCHERICHIA COLI 562 -11535106 7000685280 hypothetical protein b1878 (cl:flhe protein) (db:pir2.dat) F64950 F64950 Escherichia coli 562 -11535106 224370 flagellar protein flhe precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #337(41.9-42.3 min.)) (nt:orf_id:o337#18; similar to (swissprot accession) (le:19382) (re:19774) (di:complement) D90829 D90829 g1736523 Escherichia coli 562 -11535106 224377 flagellar protein flhe precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf_id:o337#18; similar to (swissprot accession) (le:6947) (re:7339) (di:complement) D90830 D90830 g1736531 Escherichia coli 562 -11535106 301017 flhe flagellar protein flhe (fn:flagellar basal body formation) (db:genpept-bct1) (de:escherichia coli flagellar proteins flhb (flhb), flha (flha) and flhe (flhe) genes, complete cds.) (le:3495) (re:3887) (di:direct) ECU88319 U88319 g3169256 Escherichia coli 562 -11535106 301010 flhe flagellar protein (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 171 of 400 of the complete genome.) (nt:f130; 75 pct identical to flagellar) (le:8115) (re:8507) (di:complement) AE000281 AE000281 g1788186 Escherichia coli 562 -11535106 5000692568 (de:(ecoli_1835) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1835 ECOLI_1835 Escherichia coli 562 10060351

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852853	11155	33311	324	107

Description

6500731249 flhb:b1880 hypothetical protein:flagellar biosynthetic protein flhb (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1880 b1880 Escherichia coli 562 -11535107 118243 flhb (de:flagellar biosynthetic protein flhb) (db:swissprot) FLHB_ECOLI P76299 ESCHERICHIA COLI 562 -11535107 7000685278 hypothetical protein b1880 (cl:flagellar biosynthetic protein flhb) (db:pir2.dat) H64950 H64950 Escherichia coli 562 -11535107 224379 flagellar biosynthetic protein flhb. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #338(42.1-42.5 min.)) (nt:orf_id:o338#2; similar to (swissprot accession) (le:9410) (re:10558) (di:complement) D90830 D90830 g1736533 Escherichia coli 562 -11535107 301019 flhb putative part of export apparatus for flagellar (fn:structural component; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 171 of 400 of the completegenome.) (nt:f382; 90 pct identical (1 gap) to flhb_salty) (le:10578) (re:11726) (di:complement) AE000281 AE000281 g1788188 Escherichia coli 562 -11535107 5000692569 (de:(ecoli_1837) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1837 ECOLI_1837 Escherichia coli 562 10060347

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852856	11156	33312	288	95

Description

6500731250 yecg:b1895 hypothetical 17.1 kd protein in flhd-otsa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1895 b1895 Escherichia coli 562 -11535108 111510 yecg (de:hypothetical 17.1 kd protein in flhd-otsa intergenic region) (db:swissprot) YECG_ECOLI P46888 ESCHERICHIA COLI 562 -11535108 7000687601 yecg hypothetical 17.1 kd protein in flhd-otsa intergenic region (cl:universal stress protein a) (db:pir2.dat) G64952 G64952 Escherichia coli 562 -11535108 224399 yecg universal stress protein a (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #339(42.4-42.8 min.)) (nt:orf_id:o339#10; similar to (pir accession number) (le:11493) (re:11921) (di:direct) D90831 D90831 g1736554 Escherichia coli 562 -11535108 301039 yecg (db:genpept-bct1) (de:escherichia coli trehalose-6-phosphate synthase (otsa) gene,partial cds, and universal stress protein a homolog (yecg) gene,complete cds.) (nt:similar to escherichia coli universal stress) (le:549) (re:977) (di:direct) ECU27211 U27211 g862972 Escherichia coli 562 -11535108 239059 yecg putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:o142; 100 pct identical to yecg_ecoli sw: p46888) (le:2581) (re:3009) (di:direct) AE000283 AE000283 g1788205 Escherichia coli 562 -11535108 5000692570 (de:(ecoli_1852) (pn:hypothetical 17) (gn:yecg) (gtcfc:13.7:14.1) (ec:) (yecg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1852 ECOLI_1852 Escherichia coli 562 10053239

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852866	11157	33313	240	79

Description

5000692571 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1899 b1899 Escherichia coli 562 -11535109 7500974862 arah_1 high-affinity l-arabinose transport system (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:f234; frameshift in arah relative to arah_ecoli sw:) (le:5666) (re:6370) (di:complement) AE000283 AE000283 g1788209 Escherichia coli 562 -11535109 6500731251 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1899 b1899 Escherichia coli 562 -11535109

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852881	11158	33314	582	193

Description

5000692573 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1903 b1903 Escherichia coli 562 -11535110
 7000691505 hypothetical protein b1903 (db:pir2.dat) G64953 G64953
 Escherichia coli 562 -11535110 7500960079 b1903 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:o112; this 112 aa orf is 29 pct identical (8 gaps)) (le:10271) (re:10609) (di:direct) AE000283 AE000283 g1788213 Escherichia coli 562 -11535110 6500731252 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1903 b1903 Escherichia coli 562 -11535110

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852882	11159	33315	801	266

Description

5000692574 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1904 b1904 Escherichia coli 562 -11535111
 7000691506 hypothetical protein b1904 (db:pir2.dat) H64953 H64953
 Escherichia coli 562 -11535111 7500960080 b1904 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:o107; this 107 aa orf is 36 pct identical (5 gaps)) (le:250) (re:573) (di:direct) AE000284 AE000284 g1788215 Escherichia coli 562 -11535111 6500731253 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1904 b1904 Escherichia coli 562 -11535111

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852883	11160	33316	402	133

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852893	11161	33317	684	227

Description

6500731254 yech:b1906 hypothetical 7.3 kd protein in tyrp-rsga intergenic region:hypothetical 8.6 kd protein in ftn-tyrp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1906 b1906 Escherichia coli 562 -11535112 111511 yech (de:hypothetical 8.6 kd protein in ftn-tyrp intergenic region) (db:swissprot) YECH_ECOLI P46887 ESCHERICHIA COLI 562 -11535112 7000687602 yech hypothetical 7.3 kd protein in tyrp-rsga intergenic region (db:pir2.dat) B64954 B64954 Escherichia coli 562 -11535112 224412 yech (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf_id:o341#6; similar to (swissprot accession) (le:5781) (re:6020) (di:complement) D90832 D90832 g1736568 Escherichia coli 562 -11535112 301052 yech orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:f79; 100 pct identical yech_ecoli sw: p46887 (67) (le:1279) (re:1518) (di:complement) AE000284 AE000284 g1788217 Escherichia coli 562 -11535112 5000692575 (de:(ecoli_1863) (pn:hypothetical 8) (gn:yech) (gtcfc:13.7:14.1) (ec:) (yech_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1863 ECOLI_1863 Escherichia coli 562 10053240

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852894	11162	33318	447	148

Description

6500731255 yecc:b1917 hypothetical protein:hypothetical abc transporter atp-binding protein in sdia-fliy intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1917 b1917 Escherichia coli 562 -11535113 111506 yecc (de:hypothetical amino-acid abc transporter atp-binding protein yecc) (db:swissprot) YECC_ECOLI P37774 ESCHERICHIA COLI 562 -11535113 7000687599 yecc abc-type transport protein yecc (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) B64955 B64955 Escherichia coli 562 -11535113 224420 yecc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf_id:o341#14; similar to (swissprot accession) (le:13592) (re:14344) (di:complement) D90832 D90832 g1736576 Escherichia coli 562 -11535113 301060 yecc putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:f250; cg site no. 30919; this 250 aa orf is 57 pct) (le:9090) (re:9842) (di:complement) AE000284 AE000284 g1788225 Escherichia coli 562 -11535113 5000692579 (de:(ecoli_1871) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1871 ECOLI_1871 Escherichia coli 562 10119909

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852896	11163	33319	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852897	11164	33320	417	139

Description

5000692581 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1919 b1919 Escherichia coli 562 -11535114
7500876072 yedo (ec:4.1.99.4) (de:(acc deaminase)) (db:swissprot)
1A1D_ECOLI P76316 ESCHERICHIA COLI 562 -11535114 7000691507 hypothetical protein b1919 (cl:1-aminocyclopropane-1-carboxylate deaminase) (db:pir2.dat) D64955 D64955 Escherichia coli 562 -11535114 224422
1-aminocyclopropane-1-carboxylate deaminase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.).)
(nt:orf_id:o341#16; similar to (swissprot accession) (le:15024) (re:16106) (di:complement) D90832 D90832 g1736578 Escherichia coli 562 -11535114 301062 1-aminocyclopropane-1-carboxylate deaminase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.).)
(nt:orf_id:o341#16; similar to (swissprot accession) (le:237) (re:1319) (di:complement) D90833 D90833 g1736586 Escherichia coli 562 -11535114 301069 yedo putative 1-aminocyclopropane-1-carboxylate (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:f360; this 360 aa orf is 39 pct identical (12 gaps)) (le:10522) (re:11604) (di:complement) AE000284 AE000284 g1788227 Escherichia coli 562 -11535114 224429
1-aminocyclopropane-1-carboxylate deaminase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.).)
(nt:orf_id:o341#16; similar to (swissprot accession) (le:15024) (re:16106) (di:complement) D90832 D90832 g1736578 Escherichia coli 562 -11535114 6500731256 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1919 b1919 Escherichia coli 562 -11535114

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852908	11165	33321	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852913	11166	33322	891	297

Description

6500731257 yedd:b1928 hypothetical 15.0 kd protein in amya-flie intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1928 b1928 Escherichia coli 562 -11535115 111524 yedd (de:hypothetical 15.0 kd protein in amya-flie intergenic region) (db:swissprot) YEDD_ECOLI P31063 ESCHERICHIA COLI 562 -11535115 7000687605 yedd hypothetical 15.0 kd protein in amya-flie intergenic region (db:pir2.dat) E64956 E64956 Escherichia coli 562 -11535115 224439 yedd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min..)) (nt:orf_id:o342#7; similar to (swissprot accession) (le:9420) (re:9833) (di:complement) D90833 D90833 g1736596 Escherichia coli 562 -11535115 301079 orf15 (sr:escherichia coli (strain jall) dna) (db:genpept-bct1) (de:e.coli alpha-amylase (amya) gene, 3' end; orf15, orf48, orf9, orf8,complete cds; and flagellar basal body protein (flie) gene, 3' end.) (le:101) (re:514) (di:complement) ECOAMYAP L13279 g290413 Escherichia coli 562 -11535115 233795 yedd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 175 of 400 of the completegenome.) (nt:f137; 100 pct identical to yedd_ecoli sw: p31063;) (le:7278) (re:7691) (di:complement) AE000285 AE000285 g1788237 Escherichia coli 562 -11535115 5000692584 (de:(ecoli_1882) (pn:hypothetical 15) (gn:yedd) (gtcfc:13.7:14.1) (ec:) (yedd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1882 ECOLI_1882 Escherichia coli 562 10053253

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852930	11167	33323	432	143

Description

6500731258 yede:b1929 hypothetical 44.4 kd protein in amya-flie intergenic region:orf 48 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1929 b1929 Escherichia coli 562 -11535116 111526 yede (de:hypothetical 44.4 kd protein in amya-flie intergenic region (orf 48)) (db:swissprot) YEDE_ECOLI P31064 ESCHERICHIA COLI 562 -11535116 7000687606 yede hypothetical 44.4 kd protein in amya-flie intergenic region (db:pir2.dat) F64956 F64956 Escherichia coli 562 -11535116 224440 yede (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.)) (nt:orf_id:o342#8; similar to (swissprot accession) (le:10020) (re:11225) (di:direct) D90833 D90833 g1736597 Escherichia coli 562 -11535116 301080 orf48 (sr:escherichia coli (strain:jall) dna) (db:genpept-bct1) (de:e.coli alpha-amylase (amya) gene, 3' end; orf15, orf48, orf9, orf8,complete cds; and flagellar basal body protein (flie) gene, 3' end.) (nt:level of amino acid identity between e. coli and s... ECOAMYAP L13279 g290414 Escherichia coli 562 -11535116 233796 yede putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 175 of 400 of the completegenome.) (nt:o401; 100 pct identical to yede_ecoli sw: p31064;) (le:7878) (re:9083) (di:direct) AE000285 AE000285 g1788238 Escherichia coli 562 -11535116 5000692585 (de:(ecoli_1883) (pn:hypothetical 44) (gn:yede) (gtcfc:13.7:14.1) (ec:) (yede_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1883 ECOLI_1883 Escherichia coli 562 10053255

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852932	11168	33324	666	221

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501852933	11169	33325	534	177

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501852935	11170	33326	624	207

Description

6500731259 yedf:b1930 hypothetical 8.6 kd protein in amya-flie intergenic region:orf 9 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1930 b1930 Escherichia coli 562 -11535117 111529 yedf (de:hypothetical 8.6 kd protein in amya-flie intergenic region (orf 9)) (db:swissprot) YEDF_ECOLI P31065 ESCHERICHIA COLI 562 -11535117 7502852258 yedf (de:hypothetical 8.6 kd protein in amya-flie intergenic region (orf 9)) (db:swissprot) YEDF_ECOLI P31065 SALMONELLA TYPHIMURIUM 602 -11535117 7000687607 yedf hypothetical 8.6 kd protein in amya-flie intergenic region (cl:conserved hypothetical protein hi0721) (db:pir2.dat) G64956 G64956 Escherichia coli 562 -11535117 301081 yedf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min..)) (nt:orf_id:o342#9; similar to (swissprot accession) (le:11222) (re:11455) (di:direct) D90833 D90833 g1736598 Escherichia coli 562 -11535117 233797 orf9 (sr:escherichia coli (strain jall) dna) (db:genpept-bct1) (de:e.coli alpha-amylase (amya) gene, 3' end; orf15, orf48, orf9, orf8,complete cds; and flagellar basal body protein (flie) gene, 3' end.) (nt:level of amino acid identity between e. coli and s... ECOAMYAP L13279 g290415 Escherichia coli 562 -11535117 264085 (sr:salmonella typhimurium (strain sjw1103) dna) (db:genpept-bct1) (de:salmonella typhimurium alpha-amylase (amya) gene, 3' end; orf 15,orf 48, orf9, orf8 complete cds's; and flagellar basal body protein(flie) gene, 3'end.) (nt:level of amino acid iden... STYAMYA L13280 g295197 Salmonella typhimurium 602 -11535117 224441 yedf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 175 of 400 of the completegenome.) (nt:o77; 100 pct identical to yedf_ecoli sw: p31065;) (le:9080) (re:9313) (di:direct) AE000285 AE000285 g1788239 Escherichia coli 562 -11535117 111528 yedf (de:hypothetical 8.6 kd protein in amya-flie intergenic region (orf 9)) (db:swissprot) YEDF_ECOLI P31065 ESCHERICHIA COLI 562 -11535117 7502852259 yedf (de:hypothetical 8.6 kd protein in amya-flie intergenic region (orf 9)) (db:swissprot) YEDF_ECOLI P31065 SALMONELLA TYPHIMURIUM 602 -11535117 5000692586 (de:(ecoli_1884) (pn:hypothetical 8) (gn:yedf) (gtcfc:13.7:14.1) (ec:) (yedf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1884 ECOLI_1884 Escherichia coli 562 10053257

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852960	11171	33327	2154	717

Description

6500731260 yedl:b1932 hypothetical protein:hypothetical 17.9 kd protein in amya-flie intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1932 b1932 Escherichia coli 562 -11535118
 1500686260 yedl (de:hypothetical 17.9 kd protein in amya-flie intergenic region) (db:swissprot) YEDL_ECOLI P76319 ESCHERICHIA COLI 562 -11535118
 7000687611 hypothetical protein b1932 (db:pir2.dat) A64957 A64957 Escherichia coli 562 -11535118 7500922962 yedl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:ol59; this 159 aa orf is 33 pct identical (5 gaps)) (le:93) (re:572) (di:direct) AE000286 AE000286 g1788242 Escherichia coli 562 -11535118 5000692588 (de:(ecoli_1886) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1886 ECOLI_1886 Escherichia coli 562 10061010

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852961	11172	33328	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852968	11173	33329	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501852978	11174	33330	2121	706

Description

5000692589 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1933 b1933 Escherichia coli 562 -11535119
 7000691508 hypothetical protein b1933 (db:pir2.dat) B64957 B64957 Escherichia coli 562 -11535119 7500960081 b1933 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:f63; this 63 aa orf is 33 pct identical (2 gaps)) (le:841) (re:1032) (di:complement) AE000286 AE000286 g1788243 Escherichia coli 562 -11535119 6500731261 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1933 b1933 Escherichia coli 562 -11535119

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853002	11175	33331	867	288

Description

GTC ORF with score 231 to: (fn:uteroglobin promoter binding protein) (sr:european rabbit) (db:genpept-mam) (de:oryctolagus cuniculus rush-1beta mrna, complete cds.) (nt:progesterone-dependent splice variant of) (le:171) (re:2681) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853003	11176	33332	213	70

Description

GTC ORF with score 150 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana chromosome 1 bac t7a14 sequence, completesequence.) (nt:similar to the end of dna repair protein gb|x74615) (le:<2:140:316:480) (re:46:228:396:552) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853006	11177	33333	234	77

Description

5000692590 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1934 b1934 Escherichia coli 562 -11535120
7000691509 hypothetical protein b1934 (db:pir2.dat) C64957 C64957
Escherichia coli 562 -11535120 7500960082 yedn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:f106; this 106 aa orf is 32 pct identical (1 gap)) (le:1042) (re:1362) (di:complement) AE000286 AE000286
g1788244 Escherichia coli 562 -11535120 6500731262 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1934 b1934 Escherichia coli 562 -11535120

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853007	11178	33334	396	131

Description

6500731263 yedm:b1935 hypothetical protein:hypothetical 13.4 kd protein in amya-flie intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1935 b1935 Escherichia coli 562 -11535121
 1500686261 yedm (de:hypothetical 13.4 kd protein in amya-flie intergenic region) (db:swissprot) YEDM_ECOLI P76322 ESCHERICHIA COLI 562 -11535121
 7000687612 hypothetical protein b1935 (db:pir2.dat) D64957 D64957
 Escherichia coli 562 -11535121 7500922963 yedm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:f116; this 116 aa orf is 38 pct identical (0 gaps)) (le:1494) (re:1844) (di:complement) AE000286 AE000286 g1788245 Escherichia coli 562 -11535121 5000692591 (de:(ecoli_1889) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1889 ECOLI_1889 Escherichia coli 562 10061011

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853013	11179	33335	423	141

Description

5000692592 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1936 b1936 Escherichia coli 562 -11535122
 7000691510 hypothetical protein b1936 (db:pir2.dat) E64957 E64957
 Escherichia coli 562 -11535122 7500960083 b1936 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 176 of 400 of the completegenome.) (nt:o92; this 92 aa orf is 47 pct identical (4 gaps)) (le:1995) (re:2273) (di:direct) AE000286 AE000286 g1788246 Escherichia coli 562 -11535122 6500731264 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1936 b1936 Escherichia coli 562 -11535122

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853032	11180	33336	498	165

Description

5000692594 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1953 b1953 Escherichia coli 562 -11535123
 7000691511 hypothetical protein b1953 (db:pir2.dat) F64959 F64959
 Escherichia coli 562 -11535123 7500960084 b1953 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 177 of 400 of the completegenome.) (nt:o80; uug start; this 80 aa orf is 30 pct identical) (le:3469) (re:3711) (di:direct) AE000287 AE000287 g1788264 Escherichia coli 562 -11535123 6500731265 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1953 b1953 Escherichia coli 562 -11535123

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853042	11181	33337	444	147

Description

GTC ORF with score 111 to: (or:Homo sapiens) (sr:human) (db:genpept-pri2)
(de:homo sapiens chromosome 19, cosmid f23858, complete sequence.)
(nt:hypothetical human protein; similar to novel) (le:1275:1574:2361)
(re:1301:1703:2506) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853051	11182	33338	714	237

Description

5000692595 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1955 b1955 Escherichia coli 562 -11535124
7500922964 yedp (de:hypothetical 30.4 kd protein in dsrb-vsr intergenic
region) (db:swissprot) YEDP_ECOLI P76329 ESCHERICHIA COLI 562 -11535124
7000691512 hypothetical protein b1955 (db:pir2.dat) G64959 G64959
Escherichia coli 562 -11535124 7500922966 b1955 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
177 of 400 of the completegenome.) (nt:o271; this 271 aa orf is 25 pct
identical (2 gaps)) (le:4009) (re:4824) (di:direct) AE000287 AE000287
g1788265 Escherichia coli 562 -11535124 6500731266 hypothetical protein
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1955
b1955 Escherichia coli 562 -11535124

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853053	11183	33339	249	82

Description

5000692596 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b1956 b1956 Escherichia coli 562 -11535125
7000691513 hypothetical protein b1956 (db:pir2.dat) H64959 H64959
Escherichia coli 562 -11535125 7500960085 b1956 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
177 of 400 of the completegenome.) (nt:f569; uug start; this 569 aa orf is
34 pct) (le:4821) (re:6530) (di:complement) AE000287 AE000287 g1788266
Escherichia coli 562 -11535125 6500731267 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1956 b1956
Escherichia coli 562 -11535125

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853054	11184	33340	435	144

Description

5000692597 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b1957 b1957 Escherichia coli
562 -11535126 7000691514 hypothetical protein b1957 (db:pir2.dat) A64960
A64960 Escherichia coli 562 -11535126 7500960086 b1957 orf:hypothetical
protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
section 177 of 400 of the completegenome.) (nt:f60) (le:6686) (re:6868)
(di:complement) AE000287 AE000287 g1788267 Escherichia coli 562 -11535126
6500731268 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b1957 b1957 Escherichia coli
562 -11535126

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853060	11185	33341	609	202

Description

6500731269 yedi:b1958 hypothetical protein in vsr 5region:hypothetical 32.2
kd protein in dsrb-vsr intergenic region (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b1958 b1958 Escherichia coli 562
-11535127 111531 yedi (de:hypothetical 32.2 kd protein in dsrb-vsr
intergenic region) (db:swissprot) YEDI_ECOLI P46125 ESCHERICHIA COLI 562
-11535127 7000687608 yedi hypothetical protein in vsr 5region (db:pir2.dat)
B64960 B64960 Escherichia coli 562 -11535127 224468 yedi (sr:escherichia
coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.).)
(nt:orf_id:o344#4; similar to (swissprot accession) (le:6854) (re:7771)
(di:complement) D90835 D90835 g1736627 Escherichia coli 562 -11535127
301108 yedi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 177 of 400 of the completegenome.)
(nt:f305; 100 pct identical to fragment yedi_ecoli) (le:6947) (re:7864)
(di:complement) AE000287 AE000287 g1788268 Escherichia coli 562 -11535127
5000692598 (de:(ecoli_1911) (pn:hypothetical protein in vsr
5"region:fragment) (gn:yedi) (gtcfc:13.7:14.1) (ec:) (yedi_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1911
ECOLI_1911 Escherichia coli 562 10119925

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853070	11186	33342	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853086	11187	33343	492	164

Description

6500731270 yeda:b1959 hypothetical 32.2 kd protein in vsr
5region:hypothetical 32.2 kd protein in dsra-vsr intergenic region:orf 4
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1959
b1959 Escherichia coli 562 -11535128 301109 yeda (de:hypothetical 32.2 kd
protein in dsra-vsr intergenic region (orf 4)) (db:swissprot) YEDA_ECOLI
P09185 ESCHERICHIA COLI 562 -11535128 163269 yeda hypothetical 32.2k
protein dcm-vsr intergenic region (db:pir2.dat) JS0266 JS0266 Escherichia
coli 562 -11535128 224469 yeda (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #344(43.5-43.9 min.)) (nt:orf_id:o344#5; similar to (pir
accession number) (le:7944) (re:8864) (di:direct) D90835 D90835 g1736628
Escherichia coli 562 -11535128 5000692599 (db:genpept-bct1) (de:e. coli dcm
gene for dna-cytosine methyltransferase and 3 orfs.) (nt:orf 4 (aa 1 - 306))
(le:2156) (re:3076) (di:complement) ECDCM X13330 g41242 Escherichia coli 562
-11535128 232650 yeda putative transmembrane subunit (fn:putative membrane;
not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
177 of 400 of the completegenome.) (nt:o306; 100 pct identical to yeda_ecoli
sw: p09185) (le:8037) (re:8957) (di:direct) AE000287 AE000287 g1788269
Escherichia coli 562 -11535128 111523 yeda (de:hypothetical 32.2 kd protein
in dsra-vsr intergenic region (orf 4)) (db:swissprot) YEDA_ECOLI P09185
ESCHERICHIA COLI 562 -11535128

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853091	11188	33344	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853092	11189	33345	225	74

Description

6500731271 yedj:b1962 hypothetical protein in seru-dcm intergenic region:hypothetical 25.9 kd protein in dcm-seru intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1962 b1962 Escherichia coli 562 -11535129 111532 yedj (de:hypothetical 25.9 kd protein in dcm-seru intergenic region) (db:swissprot) YEDJ_ECOLI P46144 ESCHERICHIA COLI 562 -11535129 7000687609 yedj hypothetical protein in seru-dcm intergenic region (cl:conserved hypothetical protein af0994) (db:pir2.dat) F64960 F64960 Escherichia coli 562 -11535129 224473 yedj (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf_id:o344#10; similar to (swissprot accession) (le:10789) (re:11484) (di:complement) D90835 D90835 g1736632 Escherichia coli 562 -11535129 301113 yedj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:f231; 100 pct identical to fragment yedj_ecoli) (le:64) (re:759) (di:complement) AE000288 AE000288 g1788273 Escherichia coli 562 -11535129 5000692600 (de:(ecoli_1915) (pn:hypothetical protein in seru-dcm intergenic region:fragment) (gn:yedj) (gtcfc:13.7:14.1) (ec:) (yedj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1915 ECOLI_1915 Escherichia coli 562 10119926

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853093	11190	33346	339	112

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853094	11191	33347	402	133

Description

5000692601 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1963 b1963 Escherichia coli 562 -11535130 7000691515 hypothetical protein b1963 (db:pir2.dat) G64960 G64960 Escherichia coli 562 -11535130 7500960087 b1963 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:f127; uug start; this 127 aa orf is 30 pct) (le:799) (re:1182) (di:complement) AE000288 AE000288 g1788274 Escherichia coli 562 -11535130 6500731272 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1963 b1963 Escherichia coli 562 -11535130

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853102	11192	33348	936	312

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853103	11193	33349	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853111	11194	33350	561	187

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853124	11195	33351	3087	1029

Description

5000692602 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1964 b1964 Escherichia coli 562 -11535131
7000691516 outer membrane porin homolog b1964 precursor:truncated (db:pir2.dat) H64960 H64960 Escherichia coli 562 -11535131 224474 outer membrane pore protein e precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.)) (nt:orf_id:o344#12; similar to (swissprot accession) (le:12426) (re:12941) (di:direct) D90835 D90835 g1736633 Escherichia coli 562 -11535131 301114 b1964 putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:o171; this 171 aa orf is 73 pct identical (2 gaps)) (le:1701) (re:2216) (di:direct) AE000288 AE000288 g1788275 Escherichia coli 562 -11535131
6500731273 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1964 b1964 Escherichia coli 562 -11535131

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853131	11196	33352	834	277

Description

5000692603 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1965 b1965 Escherichia coli 562 -11535132
7000691517 hypothetical protein b1965 (db:pir2.dat) A64961 A64961
Escherichia coli 562 -11535132 7500960088 b1965 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:o69; this 69 aa orf is 48 pct identical (7 gaps)) (le:2226) (re:2435) (di:direct) AE000288 AE000288 g1788276 Escherichia coli 562 -11535132 6500731274 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1965 b1965 Escherichia coli 562 -11535132

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853148	11197	33353	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853149	11198	33354	465	154

Description

5000692604 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1966 b1966 Escherichia coli 562 -11535133
7000691518 hypothetical protein b1966 (db:pir2.dat) B64961 B64961
Escherichia coli 562 -11535133 7500960089 b1966 putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:o134; this 134 aa orf is 64 pct identical (6 gaps)) (le:2519) (re:2923) (di:direct) AE000288 AE000288 g1788277 Escherichia coli 562 -11535133 6500731275 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1966 b1966 Escherichia coli 562 -11535133

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853151	11199	33355	1185	395

Description

6500731276 yedu:b1967 hypothetical protein:31.1 kd protein in dcm-seru intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1967 b1967 Escherichia coli 562 -11535134 7000690840 30k h-ns-repressed protein (db:pir2.dat) C64961 C64961 Escherichia coli 562 -11535134 7500959667 yedu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:o283; this 283 aa orf is 23 pct identical (18 gaps)) (le:3515) (re:4366) (di:direct) AE000288 AE000288 g1788278 Escherichia coli 562 -11535134 5000692605 (de:(ecoli_1920) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1920 ECOLI_1920 Escherichia coli 562 10123521

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853154	11200	33356	414	137

Description

6500731277 yedv:b1968 hypothetical protein:probable sensor protein yedv (gtcfc:14.1) (ec:2.7.3.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1968 b1968 Escherichia coli 562 -11535135 4000709730 yedv (ec:2.7.3.-) (de:probable sensor protein yedv,) (db:swissprot) YEDV_ECOLI P76339 ESCHERICHIA COLI 562 -11535135 7000687613 hypothetical protein b1968 (db:pir2.dat) D64961 D64961 Escherichia coli 562 -11535135 224478 sensor protein cops ec 2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #344(43.5-43.9 min.).) (nt:orf_id:o344#17; similar to (swissprot accession) (le:15200) (re:16558) (di:complement) D90835 D90835 g1736637 Escherichia coli 562 -11535135 301118 yedv putative 2-component sensor protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:f452; this 452 aa orf is 26 pct identical (16 gaps)) (le:4474) (re:5832) (di:complement) AE000288 AE000288 g1788279 Escherichia coli 562 -11535135 5000692606 (de:(ecoli_1921) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1921 ECOLI_1921 Escherichia coli 562 10119931

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853157	11201	33357	408	135

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853164	11202	33358	183	60

Description

6500731278 yedw:b1969 hypothetical protein:probable transcriptional regulatory protein yedw (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1969 b1969 Escherichia coli 562 -11535136
 4000709724 yedw (de:probable transcriptional regulatory protein yedw) (db:swissprot) YEDW_ECOLI P76340 ESCHERICHIA COLI 562 -11535136 7000687614 yedw probable transcription regulator yedw (cl:ompr protein:response regulator homology) (db:pir2.dat) E64961 E64961 Escherichia coli 562 -11535136 7500922967 yedw putative 2-component transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:f239; this 239 aa orf is 53 pct identical (3 gaps)) (le:5832) (re:6551) (di:complement) AE000288 AE000288 g1788280 Escherichia coli 562 -11535136 5000692607 (de:(ecoli_1922) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1922 ECOLI_1922 Escherichia coli 562 10123522

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853170	11203	33359	609	202

Description

5000692608 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1970 b1970 Escherichia coli 562 -11535137
 7502852260 yedx (de:hypothetical transthyretin-like protein precursor) (db:swissprot) YEDX_ECOLI P76341 ESCHERICHIA COLI 562 -11535137 7000691519 hypothetical protein b1970 (cl:escherichia coli hypothetical protein b1970) (db:pir2.dat) F64961 F64961 Escherichia coli 562 -11535137 7500960090 b1970 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:o137; this 137 aa orf is 39 pct identical (2 gaps)) (le:6636) (re:7049) (di:direct) AE000288 AE000288 g1788281 Escherichia coli 562 -11535137 6500731279 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1970 b1970 Escherichia coli 562 -11535137

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853179	11204	33360	342	113

Description

5000692609 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1971 b1971 Escherichia coli 562 -11535138
 7000691520 hypothetical protein b1971 (db:pir2.dat) G64961 G64961
 Escherichia coli 562 -11535138 7500960091 b1971 putative reductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:o334; this 334 aa orf is 30 pct identical (13 gaps)) (le:7158) (re:8162) (di:direct) AE000288 AE000288 g1788282 Escherichia coli 562 -11535138 6500731280 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1971 b1971 Escherichia coli 562 -11535138

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853189	11205	33361	330	109

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853190	11206	33362	456	151

Description

5000692610 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1972 b1972 Escherichia coli 562 -11535139
 7000691521 hypothetical protein b1972 (db:pir2.dat) H64961 H64961
 Escherichia coli 562 -11535139 7500960092 b1972 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:o211; this 211 aa orf is 22 pct identical (7 gaps)) (le:8163) (re:8798) (di:direct) AE000288 AE000288 g1788283 Escherichia coli 562 -11535139 6500731281 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1972 b1972 Escherichia coli 562 -11535139

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853226	11207	33363	2856	951

Description

5000692611 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1973 b1973 Escherichia coli 562 -11535140
 7502852261 yoda (de:hypothetical 24.8 kd protein in dcm-shia intergenic region) (db:swissprot) YODA_ECOLI P76344 ESCHERICHIA COLI 562 -11535140
 7000691522 hypothetical protein b1973 (cl:hypothetical protein yrpe) (db:pir2.dat) A64962 A64962 Escherichia coli 562 -11535140 7500955902 b1973 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 178 of 400 of the completegenome.) (nt:o216; uug start; this 216 aa orf is 36 pct) (le:9055) (re:9705) (di:direct) AE000288 AE000288 g1788284 Escherichia coli 562 -11535140 6500731282 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1973 b1973 Escherichia coli 562 -11535140

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853227	11208	33364	348	115

Description

5000692612 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1974 b1974 Escherichia coli 562 -11535141
 7000691523 probable cytochrome b:hypothetical protein b1974 (cl:cytochrome b561) (db:pir2.dat) B64962 B64962 Escherichia coli 562 -11535141 7500960093 yodb putative cytochrome (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 179 of 400 of the completegenome.) (nt:o186; uug start; this 186 aa orf is 35 pct) (le:187) (re:747) (di:direct) AE000289 AE000289 g1788286 Escherichia coli 562 -11535141 6500731283 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1974 b1974 Escherichia coli 562 -11535141

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853241	11209	33365	1212	403

Description

GTC ORF with score 242 to: (db:genpept-pln2) (de:emerella nidulans sterigmatocystin biosynthetic gene cluster:(stca), (stcb), (stcc), (stce), (aflr), (stcf), (stci), (stcj), (stck), (stcl), (stco), (stcq), (stcs), (stct), (stcu), (stcv) and(stcw) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853248	11210	33366	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853249	11211	33367	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853257	11212	33368	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853258	11213	33369	1086	361

Description

5000692613 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1976 b1976 Escherichia coli 562 -11535142
7000691524 hypothetical protein b1976 (db:pir2.dat) C64962 C64962
Escherichia coli 562 -11535142 7500960094 b1976 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 179 of 400 of the completegenome.) (nt:o278; this 278 aa orf is 31 pct identical (6 gaps)) (le:1461) (re:2297) (di:direct) AE000289 AE000289 g1788287 Escherichia coli 562 -11535142 6500731284 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1976 b1976 Escherichia coli 562 -11535142

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853293	11214	33370	780	259

Description

5000692614 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1978 b1978 Escherichia coli 562 -11535143
7000691525 hypothetical protein b1978 (db:pir2.dat) D64962 D64962
Escherichia coli 562 -11535143 7500960095 b1978 putative factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 179 of 400 of the completegenome.) (nt:o2383; residues 205-383 are 61 pct identical) (le:2712) (re:9863) (di:direct) AE000289 AE000289 g1788288 Escherichia coli 562 -11535143 6500731285 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1978 b1978 Escherichia coli 562 -11535143

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853297	11215	33371	438	145

Description

5000692615 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1979 b1979 Escherichia coli 562 -11535144
 7000691526 hypothetical protein b1979 (db:pir2.dat) E64962 E64962
 Escherichia coli 562 -11535144 7500960096 b1979 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 180 of 400 of the completegenome.) (nt:f108; this 108 aa orf is 24 pct identical (2 gaps)) (le:161) (re:487) (di:complement) AE000290 AE000290 g1788290 Escherichia coli 562 -11535144 6500731286 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1979 b1979 Escherichia coli 562 -11535144

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853298	11216	33372	453	150

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853340	11217	33373	1485	494

Description

5000692616 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1980 b1980 Escherichia coli 562 -11535145
 7000691527 hypothetical protein b1980 (db:pir2.dat) F64962 F64962
 Escherichia coli 562 -11535145 7500960097 b1980 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 180 of 400 of the completegenome.) (nt:f234; this 234 aa orf is 23 pct identical (15 gaps)) (le:509) (re:1213) (di:complement) AE000290 AE000290 g1788291 Escherichia coli 562 -11535145 6500731287 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1980 b1980 Escherichia coli 562 -11535145

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853350	11218	33374	231	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853358	11219	33375	810	269
<u>Description</u>				
6500731288 shia:b1981 hypothetical protein:shikimate transporter (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1981 b1981 Escherichia coli 562 -11535146 1500687379 shia (de:shikimate transporter) (db:swissprot) SHIA_ECOLI P76350 ESCHERICHIA COLI 562 -11535146 7000686598 hypothetical protein b1981 (cl:citrate utilization determinant) (db:pir2.dat) G64962 G64962 Escherichia coli 562 -11535146 224484 proline/betaine transporter proline porter ii (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #347(44.2-44.5 min.)) (nt:orf_id:o347#2; similar to (swissprot accession) (le:2431) (re:3747) (di:direct) D90837 D90837 g1736645 Escherichia coli 562 -11535146 296050 shia putative transport protein:shikimate (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 180 of 400 of the completegenome.) (nt:o438; this 438 aa orf is 36 pct identical (10 gaps)) (le:1528) (re:2844) (di:direct) AE000290 AE000290 g1788292 Escherichia coli 562 -11535146 301124 shia shikimate transport protein (db:genpept-bct2) (de:escherichia coli shikimate transport protein (shia) gene, completecds, and amp nucleosidase (amn) gene, partial cds.) (le:373) (re:1689) (di:direct) ECU88529 U88529 g1850982 Escherichia coli 562 -11535146 5000692617 (de:(ecoli_1932) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1932 ECOLI_1932 Escherichia coli 562 10064847				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853362	11220	33376	327	108
<u>Description</u>				
5000692618 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1983 b1983 Escherichia coli 562 -11535147 7000691528 hypothetical protein b1983 (cl:hypothetical protein mg332) (db:pir2.dat) A64963 A64963 Escherichia coli 562 -11535147 7500960098 b1983 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 180 of 400 of the completegenome.) (nt:o238; this 238 aa orf is 40 pct identical (5 gaps)) (le:4743) (re:5459) (di:direct) AE000290 AE000290 g1788294 Escherichia coli 562 -11535147 6500731289 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1983 b1983 Escherichia coli 562 -11535147				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853365	11221	33377	471	156

Description

6500731290 yeoo:b1985 hypothetical protein:hypothetical 60.1 kd protein in amn-cbl intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1985 b1985 Escherichia coli 562 -11535148
 1500687484 yeoo (de:hypothetical 60.1 kd protein in amn-cbl intergenic region) (db:swissprot) YEEO_ECOLI P76352 ESCHERICHIA COLI 562 -11535148
 7000687619 hypothetical protein b1985 (db:pir2.dat) B64963 B64963 Escherichia coli 562 -11535148 7500922968 yeoo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 180 of 400 of the completegenome.) (nt:f547; this 547 aa orf is 24 pct identical (21 gaps)) (le:6088) (re:7731) (di:complement) AE000290 AE000290 g2367126 Escherichia coli 562 -11535148

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853382	11222	33378	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853397	11223	33379	1407	468

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853402	11224	33380	657	218
<u>Description</u>				
6500731291 yi52_6:b1994 insertion element is5 hypothetical 39.3 kd protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1994 b1994 Escherichia coli 562 -11535149 7000689460 yi52_6 probable transposase:39k (db:pir2.dat) A64964 A64964 Escherichia coli 562 -11535149 224494 is5 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #347(44.2-44.5 min.)) (nt:orf_id:o347#12; similar to (pir accession number) (le:15093) (re:16109) (di:complement) D90837 D90837 g1736655 Escherichia coli 562 -11535149 301139 is5 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o347#12; similar to (pir accession number) (le:1871) (re:2887) (di:complement) D90838 D90838 g1736661 Escherichia coli 562 -11535149 301134 trs5_6 is5 transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 181 of 400 of the completgenome.) (nt:f338; 99 pct identical to yi52_ecoli sw: p03837) (le:4239) (re:5255) (di:complement) AE000291 AE000291 g1788303 Escherichia coli 562 -11535149 224499 is5 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o347#12; similar to (pir accession number) (le:1871) (re:2887) (di:complement) D90838 D90838 g1736661 Escherichia coli 562 -11535149 5000692626 (de:(ecoli_1942) (pn:insertion element is5 hypothetical 39) (gn:yi52_6) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1942 ECOLI_1942 Escherichia coli 562 10119943				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853425	11225	33381	204	67
<u>Description</u>				
5000692627 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1995 b1995 Escherichia coli 562 -11535150 7000691529 probable membrane protein b1995 (db:pir2.dat) B64964 B64964 Escherichia coli 562 -11535150 7500960099 b1995 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 181 of 400 of the completgenome.) (nt:ol39; this 139 aa orf is 33 pct identical (4 gaps)) (le:6542) (re:6961) (di:direct) AE000291 AE000291 g1788304 Escherichia coli 562 -11535150 6500731292 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1995 b1995 Escherichia coli 562 -11535150				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853432	11226	33382	1269	422

Description

GTC ORF with score 832 to: (sr:baker's yeast strain=ab972) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xvi left arm from mnn9 topho85.) (nt:ypl042c: also called ume5, srb10 and gig2;) (le:12384) (re:14051) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853438	11227	33383	948	315

Description

6500731293 yi21_3:b1997 insertion sequence is2 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1997 b1997 Escherichia coli 562 -11535151 7000691852 yi21_3 hypothetical protein (cl:agrobacterium tumefaciens insertion sequence is1312 hypothetical protein) (db:pir2.dat) D64964 D64964 Escherichia coli 562 -11535151 7500960370 yi21_3 is2 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 181 of 400 of the completegenome.) (nt:f136; 99 pct identical to gb: ecu28377_14 accession) (le:7749) (re:8159) (di:complement) AE000291 AE000291 g1788306 Escherichia coli 562 -11535151 5000692628 (de:(ecoli_1945) (pn:insertion sequence is2 hypothetical protein) (gn:yi21_3) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1945 ECOLI_1945 Escherichia coli 562 10123534

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853451	11228	33384	1113	370

Description

5000692629 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1998 b1998 Escherichia coli 562 -11535152 7000691530 hypothetical protein b1998 (cl:tonb-dependent receptor amino-terminal homology) (db:pir2.dat) E64964 E64964 Escherichia coli 562 -11535152 7500960100 b1998 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 181 of 400 of the completegenome.) (nt:o86; this 86 aa orf is 46 pct identical (6 gaps)) (le:8178) (re:8438) (di:direct) AE000291 AE000291 g1788307 Escherichia coli 562 -11535152 6500731294 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1998 b1998 Escherichia coli 562 -11535152

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853459	11229	33385	621	206

Description

6500731295 yeep:b1999 hypothetical protein:hypothetical 27.1 kd protein in cobu-sbmc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b1999 b1999 Escherichia coli 562 -11535153
 5500686566 yeep (de:hypothetical 27.1 kd protein in cobu-sbmc intergenic region) (db:swissprot) YEPEP_ECOLI P76359 ESCHERICHIA COLI 562 -11535153
 7000687620 hypothetical protein b1999 (cl:ykfa protein:translation elongation factor tu homology) (db:pir2.dat) F64964 F64964 Escherichia coli 562 -11535153 7500922969 yeep putative histone (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 181 of 400 of the completegenome.) (nt:o236; this 236 aa orf is 33 pct identical (5 gaps)) (le:8435) (re:9145) (di:direct) AE000291 AE000291 g1788308 Escherichia coli 562 -11535153 5000692630 (de:(ecoli_1947) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1947 ECOLI_1947 Escherichia coli 562 10123536

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853462	11230	33386	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853489	11231	33387	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853500	11232	33388	630	209

Description

5000692631 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2000 b2000 Escherichia coli 562 -11535154
 7000691531 hypothetical protein b2000 (db:pir2.dat) G64964 G64964 Escherichia coli 562 -11535154 7500960101 flu outer membrane fluffing protein:similar to (fn:membrane; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 181 of 400 of the completegenome.) (nt:o1091; this 1091 aa orf is 27 pct identical) (le:9317) (re:12592) (di:direct) AE000291 AE000291 g1788309 Escherichia coli 562 -11535154 6500731296 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2000 b2000 Escherichia coli 562 -11535154

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853504	11233	33389	627	208

Description

5000692632 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2001 b2001 Escherichia coli 562 -11535155
7000691532 hypothetical protein b2001 (db:pir2.dat) H64964 H64964
Escherichia coli 562 -11535155 7500960102 b2001 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
182 of 400 of the completegenome.) (nt:o512; this 512 aa orf is 35 pct
identical (7 gaps)) (le:88) (re:1626) (di:direct) AE000292 AE000292 g1788311
Escherichia coli 562 -11535155 6500731297 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2001 b2001
Escherichia coli 562 -11535155

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853508	11234	33390	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853509	11235	33391	207	68
<u>Description</u>				
5000692633 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2002 b2002 Escherichia coli 562 -11535156				
7500922970 yeess (de:hypothetical 16.6 kd protein in cobu-sbmc intergenic region) (db:swissprot) YEES_ECOLI P76362 ESCHERICHIA COLI 562 -11535156				
7000691533 hypothetical protein b2002 (db:pir2.dat) A64965 A64965 Escherichia coli 562 -11535156 224509 dna repair protein radc. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o348#13; similar to (swissprot accession) (le:11874) (re:12320) (di:direct) D90838 D90838 g1736671 Escherichia coli 562 -11535156 301149 dna repair protein radc. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #349(44.6-45.0 min.)) (nt:orf_id:o348#13; similar to (swissprot accession) (le:4960) (re:5406) (di:direct) D90839 D90839 g1736679 Escherichia coli 562 -11535156 301156 yeess putative dna repair protein:radc family (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 182 of 400 of the completegenome.) (nt:o148; this 148 aa orf is 48 pct identical (0 gaps)) (le:1623) (re:2069) (di:direct) AE000292 AE000292 g1788312 Escherichia coli 562 -11535156 224516 dna repair protein radc. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o348#13; similar to (swissprot accession) (le:11874) (re:12320) (di:direct) D90838 D90838 g1736671 Escherichia coli 562 -11535156 6500731298 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2002 b2002 Escherichia coli 562 -11535156				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853512	11236	33392	447	148
<u>Description</u>				
5000692634 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2003 b2003 Escherichia coli 562 -11535157				
7500922972 yeet (de:hypothetical 8.4 kd protein in cobu-sbmc intergenic region) (db:swissprot) YEET_ECOLI P76363 ESCHERICHIA COLI 562 -11535157				
7000691534 hypothetical protein b2003 (db:pir2.dat) B64965 B64965 Escherichia coli 562 -11535157 7500922974 yeet orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 182 of 400 of the completegenome.) (nt:o73; this 73 aa orf is 46 pct identical (0 gaps) to) (le:2132) (re:2353) (di:direct) AE000292 AE000292 g1788313 Escherichia coli 562 -11535157 6500731299 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2003 b2003 Escherichia coli 562 -11535157				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853536	11237	33393	324	107

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853537	11238	33394	327	108

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853559	11239	33395	372	123

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853563	11240	33396	897	299

Description

GTC ORF with score 114 to: (sr:caenorhabditis elegans strain=bristol n2)
(db:genpept-inv) (de:caenorhabditis elegans cosmid f59e12.) (nt:coded for by
c. elegans cdna yk144h11.5) (le:23003:23302:24192) (re:23229:24108:25067)
(di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853572	11241	33397	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853575	11242	33398	477	158

Description

5000692635 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2004 b2004 Escherichia coli 562 -11535158
7500922975 yeeu (de:hypothetical 13.7 kd protein in cobu-sbmc intergenic region) (db:swissprot) YEEU_ECOLI P76364 ESCHERICHIA COLI 562 -11535158
7000691535 hypothetical protein b2004 (db:pir2.dat) C64965 C64965 Escherichia coli 562 -11535158 224510 yfjz (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o348#15; similar to (swissprot accession) (le:12678) (re:13046) (di:direct) D90838 D90838 g1736672 Escherichia coli 562 -11535158 301150 yfjz (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #349(44.6-45.0 min.)) (nt:orf_id:o348#15; similar to (swissprot accession) (le:5764) (re:6132) (di:direct) D90839 D90839 g1736680 Escherichia coli 562 -11535158 301157 yeeu putative structural protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 182 of 400 of the completegenome.) (nt:o122; residues 20-117 are 66 pct identical to) (le:2427) (re:2795) (di:direct) AE000292 AE000292 g1788314 Escherichia coli 562 -11535158 224517 yfjz (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o348#15; similar to (swissprot accession) (le:12678) (re:13046) (di:direct) D90838 D90838 g1736672 Escherichia coli 562 -11535158 6500731300 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2004 b2004 Escherichia coli 562 -11535158

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853576	11243	33399	483	160

Description

5000692636 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2005 b2005 Escherichia coli 562 -11535159
7500922977 yeev (de:hypothetical 13.9 kd protein in cobu-sbmc intergenic region) (db:swissprot) YEEV_ECOLI P76365 ESCHERICHIA COLI 562 -11535159
7000691536 hypothetical protein b2005 (db:pir2.dat) D64965 D64965 Escherichia coli 562 -11535159 7500922979 yeev orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 182 of 400 of the completegenome.) (nt:o124) (le:2884) (re:3258) (di:direct) AE000292 AE000292 g1788315 Escherichia coli 562 -11535159 6500731301 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2005 b2005 Escherichia coli 562 -11535159

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853577	11244	33400	426	141

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853585	11245	33401	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853590	11246	33402	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853593	11247	33403	411	136

Description

5000692637 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2006 b2006 Escherichia coli 562 -11535160
 7500922980 yeew (de:hypothetical 7.0 kd protein in cobu-sbmc intergenic region) (db:swissprot) YREW_ECOLI P76366 ESCHERICHIA COLI 562 -11535160
 7000691537 hypothetical protein b2006 (db:pir2.dat) E64965 E64965 Escherichia coli 562 -11535160 7500922982 yeew orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 182 of 400 of the completegenome.) (nt:o64; residues 1-30 are 43 pct identical to 30 aa of) (le:3255) (re:3449) (di:direct) AE000292 AE000292 g1788316 Escherichia coli 562 -11535160 6500731302 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2006 b2006 Escherichia coli 562 -11535160

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853597	11248	33404	261	87

Description

GTC ORF with score 130 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone 1750.) (nt:similar to s.pombe swiss_prot hypothetical protein) (le:19195) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853600	11249	33405	456	151

Description

5000692638 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2007 b2007 Escherichia coli 562 -11535161
7500922983 yeex (de:hypothetical 15.1 kd protein in cobu-sbmc intergenic region) (db:swissprot) YEEX_ECOLI P76367 ESCHERICHIA COLI 562 -11535161
7000691538 hypothetical protein b2007 (db:pir2.dat) F64965 F64965 Escherichia coli 562 -11535161 224511 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o348#19; similar to (swissprot accession) (le:14598) (re:14993) (di:complement) D90838 D90838 g1736673 Escherichia coli 562 -11535161 301151 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #349(44.6-45.0 min.)) (nt:orf_id:o348#19; similar to (swissprot accession) (le:7684) (re:8079) (di:complement) D90839 D90839 g1736681 Escherichia coli 562 -11535161 301158 yeex putative alpha helix protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 182 of 400 of the completegenome.) (nt:f131; residues 29-113 are 62 pct identical to) (le:4347) (re:4742) (di:complement) AE000292 AE000292 g1788317 Escherichia coli 562 -11535161 224518 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o348#19; similar to (swissprot accession) (le:14598) (re:14993) (di:complement) D90838 D90838 g1736673 Escherichia coli 562 -11535161 6500731303 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2007 b2007 Escherichia coli 562 -11535161

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853604	11250	33406	1020	339

Description

6500731304 yeed:b2012 hypothetical 8.1 kd protein in sbcb
3region:hypothetical 8.1 kd protein in sbcb-hisl intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2012
b2012 Escherichia coli 562 -11535162 111534 yeed (de:hypothetical 8.1 kd
protein in sbcb-hisl intergenic region) (db:swissprot) YEED_ECOLI P33014
ESCHERICHIA COLI 562 -11535162 7000687616 yeed hypothetical 8.1 kd protein
in sbcb 3region (cl:conserved hypothetical protein hi0721) (db:pir2.dat)
C64966 C64966 Escherichia coli 562 -11535162 224523 yeed (sr:escherichia
coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #349(44.6-45.0 min.))
(nt:orf_id:o349#3; similar to (swissprot accession) (le:12878) (re:13105)
(di:complement) D90839 D90839 g1736686 Escherichia coli 562 -11535162
301168 yeed (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#350(44.9-45.2 min.)) (nt:orf_id:o349#3; similar to (swissprot accession)
(le:1569) (re:1796) (di:complement) D90840 D90840 g1736692 Escherichia coli
562 -11535162 301163 yeed (sr:escherichia coli k12 bhb2600)
(db:genpept-bct1) (de:sbcb region of e.coli k12 bhb2600.) (nt:similar to orf
in flie-amyia intergenic region) (le:4083) (re:4310) (di:complement) ECOHU43
U00009 g405955 Escherichia coli 562 -11535162 234714 yeed orf:hypothetical
protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
section 182 of 400 of the completegenome.) (nt:f75; 100 pct identical to
yeed_ecoli sw: p33014) (le:9541) (re:9768) (di:complement) AE000292 AE000292
g1788322 Escherichia coli 562 -11535162 224528 yeed (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #350(44.9-45.2 min.))
(nt:orf_id:o349#3; similar to (swissprot accession) (le:1569) (re:1796)
(di:complement) D90840 D90840 g1736692 Escherichia coli 562 -11535162
5000692641 (de:(ecoli_1960) (pn:hypothetical 8) (gn:yeed) (gtcfc:13.7:14.1)
(ec:) (yeed_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_1960 ECOLI_1960 Escherichia coli 562 10053262

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853605	11251	33407	444	147

Description

6500731305 yeee:b2013 hypothetical 38.1 kd protein in sbcb
3region:hypothetical 38.1 kd protein in sbcb-hisl intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2013
b2013 Escherichia coli 562 -11535163 111535 yeee (de:hypothetical 38.1 kd
protein in sbcb-hisl intergenic region) (db:swissprot) YEEE_ECOLI P33015
ESCHERICHIA COLI 562 -11535163 7000687617 yeee hypothetical 38.1 kd protein
in sbcb 3region (db:pir2.dat) D64966 D64966 Escherichia coli 562 -11535163
224524 yeee (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#349(44.6-45.0 min.)) (nt:orf_id:o349#4; similar to (swissprot accession)
(le:13119) (re:14177) (di:complement) D90839 D90839 g1736687 Escherichia
coli 562 -11535163 301169 yeee (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #350(44.9-45.2 min.)) (nt:orf_id:o349#4; similar to (swissprot
accession) (le:1810) (re:2868) (di:complement) D90840 D90840 g1736693
Escherichia coli 562 -11535163 301164 yeee (sr:escherichia coli k12
bhb2600) (db:genpept-bct1) (de:sbcb region of e.coli k12 bhb2600.)
(nt:similar to orf in flie-amyia intergenic region) (le:4324) (re:5382)
(di:complement) ECOHU43 U00009 g405956 Escherichia coli 562 -11535163
234715 yeee putative transport system permease protein (fn:putative
transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 182 of 400 of the completegenome.) (nt:f352; 100 pct
identical to yeee_ecoli sw: p33015) (le:9782) (re:10840) (di:complement)
AE000292 AE000292 g1788323 Escherichia coli 562 -11535163 224529 yeee
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #350(44.9-45.2
min.)) (nt:orf_id:o349#4; similar to (swissprot accession) (le:1810)
(re:2868) (di:complement) D90840 D90840 g1736693 Escherichia coli 562
-11535163 5000692642 (de:(ecoli_1961) (pn:hypothetical 38) (gn:yeee)
(gtcfc:13.7:14.1) (ec:) (yeee_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_1961 ECOLI_1961 Escherichia coli 562
10053263

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853606	11252	33408	597	199

Description

GTC ORF with score 284 to: (db:genpept-inv) (de:caenorhabditis elegans
cosmid f27d4, complete sequence.) (nt:similarity to human 2-oxoisovalerate
dehydrogenase) (le:24796:25241:26050:26200) (re:25194:25714:26136:26340)
(di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853623	11253	33409	609	202

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853625	11254	33410	258	85

Description

6500731306 yeef:b2014 hypothetical 49.8 kd transport protein in sbcb
3region: hypothetical 49.8 kd transport protein in sbcb-hisI intergenic
region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)
b2014 b2014 Escherichia coli 562 -11535164 111536 yeef (de: hypothetical
49.8 kd transport protein in sbcb-hisI intergenic region) (db:swissprot)
YEUF_ECOLI P33016 ESCHERICHIA COLI 562 -11535164 7000687618 yeef probable
amino acid permease yeef (db:pir2.dat) E64966 E64966 Escherichia coli 562
-11535164 224525 yeef proline transport protein (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #349(44.6-45.0 min.))
(nt:orf_id:o349#5; similar to (pir accession number) (le:14356) (re:15720)
(di:complement) D90839 D90839 g1736688 Escherichia coli 562 -11535164
301170 yeef proline transport protein (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #350(44.9-45.2 min.)) (nt:orf_id:o349#5; similar to (pir
accession number) (le:3047) (re:4411) (di:complement) D90840 D90840 g1736694
Escherichia coli 562 -11535164 301165 yeef (sr:escherichia coli k12
bhb2600) (db:genpept-bct1) (de:sbcb region of e.coli k12 bhb2600.)
(nt:probable permease, perhaps of amino acids.) (le:5561) (re:6925)
(di:complement) ECOHU43 U00009 g405957 Escherichia coli 562 -11535164
234716 yeef putative amino acid/amine transport protein (fn:putative
transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 183 of 400 of the complete genome.) (nt:f454; 100 pct
identical to yeef_ecoli sw: p33016) (le:120) (re:1484) (di:complement)
AE000293 AE000293 g1788325 Escherichia coli 562 -11535164 224530 yeef
proline transport protein (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #350(44.9-45.2 min.)) (nt:orf_id:o349#5; similar to (pir
accession number) (le:3047) (re:4411) (di:complement) D90840 D90840 g1736694
Escherichia coli 562 -11535164 5000692643 (de:(ecoli_1962) (pn: hypothetical
49) (gn:yeef) (gtcfc:13.7:14.1) (ec:) (yeef_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) ECOLI_1962 ECOLI_1962 Escherichia
coli 562 10053264

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853628	11255	33411	636	211

Description

5000692644 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2015 b2015 Escherichia coli 562 -11535165
7500922986 yeey (de:hypothetical transcriptional regulator in sbcb-his1 intergenic region) (db:swissprot) YEEY_ECOLI P76369 ESCHERICHIA COLI 562 -11535165 7000691539 hypothetical protein b2015 (cl:hypothetical protein b2015) (db:pir2.dat) F64966 F64966 Escherichia coli 562 -11535165 224531 transcriptional activator protein metr. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #350(44.9-45.2 min.)) (nt:orf_id:o350#1; similar to (swissprot accession) (le:4672) (re:5622) (di:complement) D90840 D90840 g1736695 Escherichia coli 562 -11535165 7500922988 yeey putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 183 of 400 of the completegenome.) (nt:f316; this 316 aa orf is 38 pct identical (4 gaps)) (le:1745) (re:2695) (di:complement) AE000293 AE000293 g1788326 Escherichia coli 562 -11535165 301171 transcriptional activator protein metr. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #350(44.9-45.2 min.)) (nt:orf_id:o350#1; similar to (swissprot accession) (le:4672) (re:5622) (di:complement) D90840 D90840 g1736695 Escherichia coli 562 -11535165 6500731307 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2015 b2015 Escherichia coli 562 -11535165

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853633	11256	33412	537	178

Description

5000692645 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2016 b2016 Escherichia coli 562 -11535166
7502852262 yeez (de:hypothetical 29.7 kd protein in sbcb-his1 intergenic region precursor) (db:swissprot) YEEZ_ECOLI P76370 ESCHERICHIA COLI 562 -11535166 7000691540 hypothetical protein b2016 (db:pir2.dat) G64966 G64966 Escherichia coli 562 -11535166 7500960103 b2016 putative enzyme of sugar metabolism (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 183 of 400 of the completegenome.) (nt:f274; this 274 aa orf is 26 pct identical (18 gaps)) (le:2720) (re:3544) (di:complement) AE000293 AE000293 g1788327 Escherichia coli 562 -11535166 6500731308 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2016 b2016 Escherichia coli 562 -11535166

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853637	11257	33413	306	101
<u>Description</u>				
5000692647 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2027 b2027 Escherichia coli 562 -11535167				
7000691541 hypothetical protein b2027 (db:pir2.dat) B64968 B64968 Escherichia coli 562 -11535167 7500960104 wzzb regulator of length of o-antigen component of (fn:regulator; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 184 of 400 of the completegenome.) (nt:f338; this 338 aa orf is 97 pct identical (1 gap)) (le:78) (re:1094) (di:complement) AE000294 AE000294 g1788339 Escherichia coli 562 -11535167 6500731309 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2027 b2027 Escherichia coli 562 -11535167				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853640	11258	33414	843	280
<u>Description</u>				
6500731310 yefj:b2031 hypothetical protein in gnd-rfc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2031 b2031 Escherichia coli 562 -11535168 7000691830 yefj hypothetical protein in gnd-rfc intergenic region (db:pir2.dat) F64968 F64968 Escherichia coli 562 -11535168 224556 yefj (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf_id:o351#7; similar to (swissprot accession) (le:9216) (re:9689) (di:complement) D90841 D90841 g1736721 Escherichia coli 562 -11535168 301208 yefj (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#7; similar to (swissprot accession) (le:5) (re:478) (di:complement) D90842 D90842 g1736734 Escherichia coli 562 -11535168 301196 yefj putative creatinase ec 3.5.- (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 184 of 400 of the completegenome.) (nt:f157; 100 pct identical to 148 aa from) (le:5673) (re:6146) (di:complement) AE000294 AE000294 g1788343 Escherichia coli 562 -11535168 224568 yefj (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#7; similar to (swissprot accession) (le:5) (re:478) (di:complement) D90842 D90842 g1736734 Escherichia coli 562 -11535168 5000692649 (de:(ecoli_1979) (pn:hypothetical 31) (gn:yefj) (gtcfc:13.7:14.1) (ec:) (yefj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1979 ECOLI_1979 Escherichia coli 562 10119966				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501853644	11259	33415	639	212

Description

6500731311 yefi:b2032 hypothetical 43.2 kd protein in gnd-rfc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2032 b2032 Escherichia coli 562 -11535169 111552 yefi (de:hypothetical 43.2 kd protein in gnd-rfc intergenic region) (db:swissprot) YEFI_ECOLI P37751 ESCHERICHIA COLI 562 -11535169 163139 yefi glycosyltransferase:hypothetical 43.2k protein gnd-rfc intergenic region (db:pir2.dat) (mp:45 min) I69647 I69647 Escherichia coli 562 -11535169 224557 yefi (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf_id:o351#8; similar to (swissprot accession) (le:9691) (re:10809) (di:complement) D90841 D90841 g1736722 Escherichia coli 562 -11535169 301209 yefi (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#8; similar to (swissprot accession) (le:480) (re:1598) (di:complement) D90842 D90842 g1736735 Escherichia coli 562 -11535169 238057 wbbk putative glucose transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 184 of 400 of the completegenome.) (nt:f372; formerly designated yefi) (le:6148) (re:7266) (di:complement) AE000294 AE000294 g1788344 Escherichia coli 562 -11535169 301197 wbbk glycosyltransferase (db:genpept-bct2) (de:escherichia coli k12 glucose-1-phosphate thymidyltransferase (rmla)gene, partial cds; dtdp-6-deoxy-1-xylo-4-hexulose 4-reductase(rmlc), membrane protein (wzx), dehydrogenase (glf), o-antigenpolymerase (wbbh), nucleotide sugar synt... ECRFBA U03041 g510257 Escherichia coli 562 -11535169 224569 yefi (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#8; similar to (swissprot accession) (le:480) (re:1598) (di:complement) D90842 D90842 g1736735 Escherichia coli 562 -11535169 5000692650 (de:(ecoli_1980) (pn:hypothetical 43) (gn:yefi) (gtcfc:13.7:14.1) (ec:) (yefi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1980 ECOLI_1980 Escherichia coli 562 10053280

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501853645	11260	33416	1686	561

Description

6500731312 yefg:b2034 hypothetical 37.8 kd protein in gnd-rfc intergenic region:galf transferase (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2034 b2034 Escherichia coli 562 -11535170 111550 yefg (de:transferase)) (db:swissprot) YEFG_ECOLI P37749 ESCHERICHIA COLI 562 -11535170 164392 yefg probable nucleotide sugar synthetase:hypothetical 37.8k protein gnd-rfc intergenic region (db:pir2.dat) I69645 I69645 Escherichia coli 562 -11535170 301199 yefg (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf_id:o351#10; similar to (swissprot accession) (le:11365) (re:12357) (di:complement) D90841 D90841 g1736724 Escherichia coli 562 -11535170 301211 yefg (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#10; similar to (swissprot accession) (le:2154) (re:3146) (di:complement) D90842 D90842 g1736737 Escherichia coli 562 -11535170 238585 wbbi putative galf transferase (db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose 4,6-dehydratase (rmlb),dtdp-6-deoxy-1-mannose-dehydrogenase (rmla), dtdp-6-deoxy-d-glucose-3,5 epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876 g508244 Escherichia coli 562 -11535170 238055 wbbi putative galf transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 184 of 400 of the completegenome.) (nt:f330; formerly designated yefg) (le:7822) (re:8814) (di:complement) AE000294 AE000294 g1788346 Escherichia coli 562 -11535170 297658 wbbi nucleotide sugar synthetase (db:genpept-bct2) (de:escherichia coli k12 glucose-1-phosphate thymidyltransferase (rmla)gene, partial cds; dtdp-6-deoxy-1-xylo-4-hexulose 4-reductase(rmlc), membrane protein (wzx), dehydrogenase (glf), o-antigenpolymerase (wbbh), nucleotide sugar synt... ECRFBA U03041 g510255 Escherichia coli 562 -11535170 224559 yefg (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf_id:o351#10; similar to (swissprot accession) (le:11365) (re:12357) (di:complement) D90841 D90841 g1736724 Escherichia coli 562 -11535170 224571 yefg (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#10; similar to (swissprot accession) (le:2154) (re:3146) (di:complement) D90842 D90842 g1736737 Escherichia coli 562 -11535170 5000692652 (de:(ecoli_1982) (pn:hypothetical 37) (gn:yefg) (gtcfc:13.7:14.1) (ec:) (yefg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1982 ECOLI_1982 Escherichia coli 562 10053278

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853653	11261	33417	420	139

Description

6500731313 yefe:b2036 hypothetical 43.0 kd protein in rfc-rfbx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2036 b2036 Escherichia coli 562 -11535171 111549 glf (ec:5.4.99.9) (de:udp-galactopyranose mutase,) (db:swissprot) GLF_ECOLI P37747 ESCHERICHIA COLI 562 -11535171 163342 yefe hypothetical 43k protein rfc-rfbx intergenic region (cl:methanobacterium thermoautotrophicum udp-galactopyranose mutase) (db:pir2.dat) (mp:45 min) I69653 I69653 Escherichia coli 562 -11535171 301201 yefe (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf_id:o351#12; similar to (swissprot accession) (le:13526) (re:14629) (di:complement) D90841 D90841 g1736726 Escherichia coli 562 -11535171 301213 yefe (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#12; similar to (swissprot accession) (le:4315) (re:5418) (di:complement) D90842 D90842 g1736739 Escherichia coli 562 -11535171 238583 glf galf synthesis pathway protein (db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose 4,6-dehydratase (rmlb), dtdp-6-deoxy-1-mannose-dehydrogenase (rmld), glucose-1-phosphatethymidyltransferase (rmla), dtdp-6-deoxy-d-glucose-3,5 epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876 g508242 Escherichia coli 562 -11535171 238053 glf udp-galactopyranose mutase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 184 of 400 of the completegenome.) (nt:f367; formerly designated yefe) (le:9983) (re:11086) (di:complement) AE000294 AE000294 g1788348 Escherichia coli 562 -11535171 297656 glf dehydrogenase (fn:fad carrying enzyme) (db:genpept-bct2) (de:escherichia coli k12 glucose-1-phosphate thymidyltransferase (rmla)gene, partial cds; dtdp-6-deoxy-1-xylo-4-hexulose 4-reductase(rmlc), membrane protein (wzx), dehydrogenase (glf), o-antigenpolymerase (wbb... ECRFBA U03041 g510253 Escherichia coli 562 -11535171 224561 yefe (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf_id:o351#12; similar to (swissprot accession) (le:13526) (re:14629) (di:complement) D90841 D90841 g1736726 Escherichia coli 562 -11535171 224573 yefe (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#12; similar to (swissprot accession) (le:4315) (re:5418) (di:complement) D90842 D90842 g1736739 Escherichia coli 562 -11535171 5000692654 (de:(ecoli_1984) (pn:hypothetical 43) (gn:yefe) (gtcfc:13.7:14.1) (ec:) (yefe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1984 ECOLI_1984 Escherichia coli 562 10053277

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853656	11262	33418	309	102

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853662	11263	33419	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853666	11264	33420	873	290

Description

6500731314 wcam:b2043 hypothetical protein:colanic acid biosynthesis protein
 wcam (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)
 b2043 b2043 Escherichia coli 562 -11535172 1500686875 wcam (de:colanic acid
 biosynthesis protein wcam) (db:swissprot) WCAM_ECOLI P71244 ESCHERICHIA COLI
 562 -11535172 7000687015 hypothetical protein b2043 (db:pir2.dat) B64970
 B64970 Escherichia coli 562 -11535172 224580 yefk (sr:escherichia coli
 (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
 (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min..))
 (nt:orf_id:o352#2; similar to (swissprot accession) (le:11591) (re:12985)
 (di:complement) D90842 D90842 g1736746 Escherichia coli 562 -11535172
 301220 wcam orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
 (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.)
 (nt:f464; this 464 aa orf is 77 pct identical (7 gaps)) (le:1285) (re:2679)
 (di:complement) AE000295 AE000295 g1788356 Escherichia coli 562 -11535172
 7000687016 wcam unknown (db:genpept-bct2) (de:escherichia coli k-12 wca
 gene cluster.) (nt:previously referred to as orf1.3) (le:21077) (re:22471)
 (di:direct) ECU38473 U38473 g3041818 Escherichia coli 562 -11535172
 5000692655 (de:(ecoli_1991) (pn:function not assigned) (gtcfc:13.7:14.1)
 (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1991
 ECOLI_1991 Escherichia coli 562 10062883

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853669	11265	33421	771	256

Description

6500731315 wcal:b2044 hypothetical protein:putative colanic acid biosynthesis glycosyl transferase wcal (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2044 b2044 Escherichia coli 562 -11535173 1500686874 wcal (de:putative colanic acid biosynthesis glycosyl transferase wcal) (db:swissprot) WCAL_ECOLI P71243 ESCHERICHIA COLI 562 -11535173 7000687014 hypothetical protein b2044 (db:pir2.dat) C64970 C64970 Escherichia coli 562 -11535173 224581 yefl (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o352#3; similar to (pir accession number) (le:12996) (re:14216) (di:complement) D90842 D90842 g1736747 Escherichia coli 562 -11535173 301221 wcal putative colanic acid biosynthesis glycosyl (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f406; 85 pct identical to yefl_salty sw: p26388) (le:2690) (re:3910) (di:complement) AE000295 AE000295 g1788357 Escherichia coli 562 -11535173 5000692656 (de:(ecoli_1992) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1992 ECOLI_1992 Escherichia coli 562 10062882

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853672	11266	33422	783	260

Description

6500731316 wcal:b2045 hypothetical protein:colanic acid biosynthesis protein wcal (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2045 b2045 Escherichia coli 562 -11535174 1500686873 wcal (de:colanic acid biosynthesis protein wcal) (db:swissprot) WCAK_ECOLI P71242 ESCHERICHIA COLI 562 -11535174 7000687013 hypothetical protein b2045 (db:pir2.dat) D64970 D64970 Escherichia coli 562 -11535174 7500894371 wcal putative galactokinase ec 2.7.1.6 . (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f426; this 426 aa orf is 21 pct identical (13 gaps)) (le:3907) (re:5187) (di:complement) AE000295 AE000295 g1788358 Escherichia coli 562 -11535174 5000692657 (de:(ecoli_1993) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1993 ECOLI_1993 Escherichia coli 562 10062881

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853679	11267	33423	819	273

Description

5000692658 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2046 b2046 Escherichia coli 562 -11535175
7500894420 wzxc:wzx (de:lipopolysaccharide biosynthesis protein wzxc) (db:swissprot) WZXC_ECOLI P77377 ESCHERICHIA COLI 562 -11535175 7000691542 hypothetical protein b2046 (cl:hypothetical protein b2046) (db:pir2.dat) E64970 E64970 Escherichia coli 562 -11535175 224582 succinoglycan biosynthesis transport protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o352#5; similar to (swissprot accession) (le:15769) (re:17247) (di:complement) D90842 D90842 g1736748 Escherichia coli 562 -11535175 301225 succinoglycan biosynthesis transport protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.)) (nt:orf_id:o352#5; similar to (swissprot accession) (le:448) (re:1926) (di:complement) D90843 D90843 g1736752 Escherichia coli 562 -11535175 296207 wzxc probable export protein (fn:putative transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f492; this 492 aa orf is 21 pct identical (7 gaps)) (le:5463) (re:6941) (di:complement) AE000295 AE000295 g1788359 Escherichia coli 562 -11535175 301222 wxs putative export protein (db:genpept-bct2) (de:escherichia coli k-12 wca gene cluster.) (le:16815) (re:18293) (di:direct) ECU38473 U38473 g1407619 Escherichia coli 562 -11535175 224585 succinoglycan biosynthesis transport protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o352#5; similar to (swissprot accession) (le:15769) (re:17247) (di:complement) D90842 D90842 g1736748 Escherichia coli 562 -11535175 239548 succinoglycan biosynthesis transport protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.)) (nt:orf_id:o352#5; similar to (swissprot accession) (le:448) (re:1926) (di:complement) D90843 D90843 g1736752 Escherichia coli 562 -11535175 6500731317 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2046 b2046 Escherichia coli 562 -11535175

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853683	11268	33424	858	286

Description

6500731318 wcaj:b2047 hypothetical protein:putative colanic biosynthesis
 udp-glucose lipid carrier transferase (gtcfc:11.2:7.2:12.2) (keggfc:14.2)
 (rileyfc:5.7.0) (db:gtc-escherichia coli) b2047 b2047 Escherichia coli 562
 -11535176 1500686872 wcaj (de:putative colanic biosynthesis udp-glucose
 lipid carrier transferase) (db:swissprot) WCAJ_ECOLI P71241 ESCHERICHIA COLI
 562 -11535176 7000687012 hypothetical protein b2047 (cl:xps2a protein)
 (db:pir2.dat) F64970 F64970 Escherichia coli 562 -11535176 224583
 exopolysaccharide production protein pss. (sr:escherichia coli (strain:k12)
 dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
 dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o352#6; similar to
 (swissprot accession) (le:17249) (re:18643) (di:complement) D90842 D90842
 g1736749 Escherichia coli 562 -11535176 301226 exopolysaccharide production
 protein pss. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
 minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
 #353(45.6-46.0 min.)) (nt:orf_id:o352#6; similar to (swissprot accession)
 (le:1928) (re:3322) (di:complement) D90843 D90843 g1736753 Escherichia coli
 562 -11535176 301223 wcaj putative colanic acid biosynthesis udp-glucose
 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli
 k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f464; this 464 aa
 orf is 49 pct identical (4 gaps)) (le:6943) (re:8337) (di:complement)
 AE000295 AE000295 g1788360 Escherichia coli 562 -11535176 224586
 exopolysaccharide production protein pss. (sr:escherichia coli (strain:k12)
 dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
 dna, kohara clone #353(45.6-46.0 min.)) (nt:orf_id:o352#6; similar to
 (swissprot accession) (le:1928) (re:3322) (di:complement) D90843 D90843
 g1736753 Escherichia coli 562 -11535176 5000692659 (de:(ecoli_1995)
 (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2)
 (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1995 ECOLI_1995 Escherichia
 coli 562 10062880

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853685	11269	33425	1074	357

Description

6500731319 yefd:wcai:b2050 hypothetical 44.9 kd protein in cpsb
5region:putative colanic acid biosynthesis glycosyl transferase wcai
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2050
b2050 Escherichia coli 562 -11535177 111548 wcai (de:putative colanic acid
biosynthesis glycosyl transferase wcai) (db:swissprot) WCAI_ECOLI P32057
ESCHERICHIA COLI 562 -11535177 162866 yefd hypothetical 44.9k protein cpsb
5region (db:pir2.dat) F55239 F55239 Escherichia coli 562 -11535177 301229
yefd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0
min.)) (nt:orf_id:o353#3; similar to (swissprot accession) (le:6291)
(re:7514) (di:complement) D90843 D90843 g1736756 Escherichia coli 562
-11535177 239544 wcai putative colanic biosynthesis glycosyl (fn:putative
enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
section 185 of 400 of the completegenome.) (nt:f407; formerly designated
yefd) (le:11306) (re:12529) (di:complement) AE000295 AE000295 g1788363
Escherichia coli 562 -11535177 296203 wcai putative glycosyl transferase
(db:genpept-bct2) (de:escherichia coli k-12 wca gene cluster.) (nt:referred
to as orf2.4 in reference (2)) (le:11227) (re:12450) (di:direct) ECU38473
U38473 g1407615 Escherichia coli 562 -11535177 224589 yefd (sr:escherichia
coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.))
(nt:orf_id:o353#3; similar to (swissprot accession) (le:6291) (re:7514)
(di:complement) D90843 D90843 g1736756 Escherichia coli 562 -11535177
5000692660 (de:(ecoli_1998) (pn:hypothetical 44) (gn:yefd)
(gtcfc:13.7:14.1) (ec:) (yefd_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_1998 ECOLI_1998 Escherichia coli 562
10053276

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853686	11270	33426	831	277

Description

6500731320 yefc:wcah:b2051 hypothetical 18.4 kd protein in cpsb
5region:colanic acid biosynthesis protein wcah (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b2051 b2051 Escherichia coli 562
-11535178 111547 wcah (de:colanic acid biosynthesis protein wcah)
(db:swissprot) WCAH_ECOLI P32056 ESCHERICHIA COLI 562 -11535178 162865 yefc
hypothetical 18.4k protein cpsb 5region (cl:mutt domain homology)
(db:pir2.dat) E55239 E55239 Escherichia coli 562 -11535178 301230 yefc
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0
min.)) (nt:orf_id:o353#4; similar to (swissprot accession) (le:7511)
(re:7993) (di:complement) D90843 D90843 g1736757 Escherichia coli 562
-11535178 239543 wcah gdp-mannose mannosyl hydrolase (fn:enzyme; central
intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
section 185 of 400 of the completegenome.) (nt:f160; formerly designated
yefc) (le:12526) (re:13008) (di:complement) AE000295 AE000295 g1788364
Escherichia coli 562 -11535178 296202 gmm gdp-mannose mannosyl hydrolase
(db:genpept-bct2) (de:escherichia coli k-12 wca gene cluster.) (nt:referred
to as orf1.9 in reference (2) and wcah) (le:10748) (re:11230) (di:direct)
ECU38473 U38473 g1407614 Escherichia coli 562 -11535178 224590 yefc
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0
min.)) (nt:orf_id:o353#4; similar to (swissprot accession) (le:7511)
(re:7993) (di:complement) D90843 D90843 g1736757 Escherichia coli 562
-11535178 5000692661 (de:(ecoli_1999) (pn:hypothetical 18) (gn:yefc)
(gtcfc:13.7:14.1) (ec:) (yefc_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_1999 ECOLI_1999 Escherichia coli 562
10053275

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853689	11271	33427	231	76

Description

6500731321 yefb:wcag:b2052 hypothetical 36.1 kd protein in cpsb 5region:colanic acid biosynthesis protein wcag (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2052 b2052 Escherichia coli 562 -11535179 111546 fcl:wcag (de:fucose synthetase) (db:swissprot) FCL_ECOLI P32055 ESCHERICHIA COLI 562 -11535179 7000687011 yefb hypothetical 36.1 kd protein in cpsb 5region:cpsb 5-region hypothetical protein 2 (cl:hypothetical protein sll1213) (db:pir2.dat) C64971 C64971 Escherichia coli 562 -11535179 224591 yefb nodulation protein nolk. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.).) (nt:orf_id:o353#5; similar to (swissprot accession) (le:7993) (re:8958) (di:complement) D90843 D90843 g1736758 Escherichia coli 562 -11535179 301231 wcag putative nucleotide di-p-sugar epimerase or (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f321; formerly designated yefb) (le:13008) (re:13973) (di:complement) AE000295 AE000295 g1788365 Escherichia coli 562 -11535179 5000692662 (de:(ecoli_2000) (pn:hypothetical 36) (gn:yefb) (gtcfc:13.7:14.1) (ec:) (yefb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2000 ECOLI_2000 Escherichia coli 562 10119977

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853692	11272	33428	576	191

Description

6500731322 wcae:b2055 hypothetical protein:putative colanic acid biosynthesis glycosyl transferase wcae (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2055 b2055 Escherichia coli 562 -11535180 1500686870 wcae (de:putative colanic acid biosynthesis glycosyl transferase wcae) (db:swissprot) WCAE_ECOLI P71239 ESCHERICHIA COLI 562 -11535180 7000687008 hypothetical protein b2055 (db:pir2.dat) F64971 F64971 Escherichia coli 562 -11535180 7000687009 wcae putative colanic acid biosynthesis glycosyl (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f248; this 248 aa orf is 27 pct identical (12 gaps)) (le:15687) (re:16433) (di:complement) AE000295 AE000295 g1788368 Escherichia coli 562 -11535180 7500894370 wcae putative glycosyl transferase (db:genpept-bct2) (de:escherichia coli k-12 wca gene cluster.) (le:7323) (re:8069) (di:direct) ECU38473 U38473 g3041814 Escherichia coli 562 -11535180 5000692665 (de:(ecoli_2003) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2003 ECOLI_2003 Escherichia coli 562 10062878

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853696	11273	33429	318	105

Description

6500731323 wcad:b2056 hypothetical protein:putative colanic acid polymerase (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2056 b2056 Escherichia coli 562 -11535181 1500686869 wcad (de:putative colanic acid polymerase) (db:swissprot) WCAD_ECOLI P71238 ESCHERICHIA COLI 562 -11535181 7000687007 hypothetical protein b2056 (db:pir2.dat) G64971 G64971 Escherichia coli 562 -11535181 7500894369 wcad putative colanic acid polymerase (fn:putative enzyme; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f405; 24 pct identical (23 gaps) to 269 residues) (le:16444) (re:17661) (di:complement) AE000295 AE000295 g1788369 Escherichia coli 562 -11535181 5000692666 (de:(ecoli_2004) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2004 ECOLI_2004 Escherichia coli 562 10062877

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853698	11274	33430	651	216

Description

6500731324 wcac:b2057 hypothetical protein:putative colanic acid biosynthesis glycosyl transferase wcac (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2057 b2057 Escherichia coli 562 -11535182 1500686868 wcac (de:putative colanic acid biosynthesis glycosyl transferase wcac) (db:swissprot) WCAC_ECOLI P71237 ESCHERICHIA COLI 562 -11535182 7000687006 hypothetical protein b2057 (db:pir2.dat) H64971 H64971 Escherichia coli 562 -11535182 7500894368 wcac putative glycosyl transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f405; 34 pct identical (4 gaps) to 73 residues) (le:17636) (re:18853) (di:complement) AE000295 AE000295 g1788370 Escherichia coli 562 -11535182 5000692667 (de:(ecoli_2005) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2005 ECOLI_2005 Escherichia coli 562 10062876

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853708	11275	33431	258	85

Description

6500731325 wcaa:b2059 hypothetical protein:putative colanic acid biosynthesis glycosyl transferase wcaa (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2059 b2059 Escherichia coli 562 -11535183 1500686866 wcaa (de:putative colanic acid biosynthesis glycosyl transferase wcaa) (db:swissprot) WCAA_ECOLI P77414 ESCHERICHIA COLI 562 -11535183 7000687004 hypothetical protein b2059 (db:pir2.dat) B64972 B64972 Escherichia coli 562 -11535183 301235 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.)) (nt:orf_id:o353#12; similar to (swissprot accession) (le:14326) (re:15165) (di:complement) D90843 D90843 g1736762 Escherichia coli 562 -11535183 239535 wcaa putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 185 of 400 of the completegenome.) (nt:f279; this 279 aa orf is 29 pct identical (15 gaps)) (le:19341) (re:20180) (di:complement) AE000295 AE000295 g1788372 Escherichia coli 562 -11535183 296194 wcaa putative glycosyl transferase (db:genpept-bct2) (de:escherichia coli k-12 wca gene cluster.) (le:3576) (re:4415) (di:direct) ECU38473 U38473 g1407606 Escherichia coli 562 -11535183 224595 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #353(45.6-46.0 min.)) (nt:orf_id:o353#12; similar to (swissprot accession) (le:14326) (re:15165) (di:complement) D90843 D90843 g1736762 Escherichia coli 562 -11535183 5000692669 (de:(ecoli_2007) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2007 ECOLI_2007 Escherichia coli 562 10062874

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853709	11276	33432	510	169

Description

5000692670 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2060 b2060 Escherichia coli 562 -11535184 7000691543 probable atpase (db:pir2.dat) C64972 C64972 Escherichia coli 562 -11535184 7500960105 b2060 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 186 of 400 of the completegenome.) (nt:f732; this 732 aa orf is 31 pct identical (2 gaps)) (le:77) (re:2275) (di:complement) AE000296 AE000296 g1788374 Escherichia coli 562 -11535184 6500731326 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2060 b2060 Escherichia coli 562 -11535184

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853718	11277	33433	1062	353

Description

6500731327 wzb:b2061 hypothetical protein:probable low molecular weight protein-tyrosine-phosphatase (gtcfc:14.1) (ec:3.1.3.48) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2061 b2061 Escherichia coli 562 -11535185 4000709416 wzb (ec:3.1.3.48) (de:(ec 3.1.3.48)) (db:swissprot) WZB_ECOLI P77153 ESCHERICHIA COLI 562 -11535185 7000687018 wzb probable protein-tyrosine-phosphatase:wzb:low molecular weight (cl:protein-tyrosine-phosphatase, low molecular weight) (ec:3.1.3.48) (db:pir2.dat) D64972 D64972 Escherichia coli 562 -11535185 239533 wzb probable protein-tyrosine-phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 186 of 400 of the completegenome.) (nt:f147; this 147 aa orf is 33 pct identical (13 gaps)) (le:2242) (re:2685) (di:complement) AE000296 AE000296 g1788375 Escherichia coli 562 -11535185 296192 wzb putative acid phosphatase (db:genpept-bct2) (de:escherichia coli k-12 wca gene cluster.) (le:876) (re:1319) (di:direct) ECU38473 U38473 g1407604 Escherichia coli 562 -11535185 5000692671 (de:(ecoli_2009) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2009 ECOLI_2009 Escherichia coli 562 10123550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853719	11278	33434	441	146

Description

6500731328 wza:b2062 hypothetical protein:putative polysaccharide export protein precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2062 b2062 Escherichia coli 562 -11535186 4000709439 wza (de:putative polysaccharide export protein wza precursor) (db:swissprot) WZA_ECOLI P76388 ESCHERICHIA COLI 562 -11535186 7000687017 wza probable polysaccharide export protein wza precursor (db:pir2.dat) E64972 E64972 Escherichia coli 562 -11535186 7500894417 wza putative polysaccharide export protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 186 of 400 of the completegenome.) (nt:f379; this 379 aa orf is 28 pct identical (27 gaps)) (le:2691) (re:3830) (di:complement) AE000296 AE000296 g1788376 Escherichia coli 562 -11535186 5000692672 (de:(ecoli_2010) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2010 ECOLI_2010 Escherichia coli 562 10123551

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853728	11279	33435	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853731	11280	33436	801	266

Description

5000692673 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2063 b2063 Escherichia coli 562 -11535187
7000691544 hypothetical protein b2063 (db:pir2.dat) F64972 F64972
Escherichia coli 562 -11535187 7500960106 yegh putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 186 of 400 of the completegenome.) (nt:o549; this 549 aa orf is 50 pct identical (0 gaps)) (le:4423) (re:6072) (di:direct)
AE000296 AE000296 g1788377 Escherichia coli 562 -11535187 6500731329
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2063 b2063 Escherichia coli 562 -11535187

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853732	11281	33437	1266	421

Description

5000692677 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2070 b2070 Escherichia coli 562 -11535188
7000691545 hypothetical protein b2070 (db:pir2.dat) E64973 E64973
Escherichia coli 562 -11535188 7500960107 putative chaperonin (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 187 of 400 of the completegenome.) (nt:f648) (le:2432) (re:4378) (di:complement) AE000297 AE000297 g1788385 Escherichia coli 562 -11535188 6500731330 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2070 b2070 Escherichia coli 562 -11535188

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853750	11282	33438	2199	732

Description

5000692678 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2071 b2071 Escherichia coli 562 -11535189
7000691546 hypothetical protein b2071 (db:pir2.dat) F64973 F64973
Escherichia coli 562 -11535189 7500960108 b2071 orf: hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 187 of 400 of the completegenome.) (nt:o153) (le:4578) (re:5039) (di:direct)
AE000297 AE000297 g1788386 Escherichia coli 562 -11535189 6500731331
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2071 b2071 Escherichia coli 562 -11535189

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853754	11283	33439	1629	542

Description

5000692679 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2072 b2072 Escherichia coli 562 -11535190
 7000691547 hypothetical protein b2072 (db:pir2.dat) G64973 G64973
 Escherichia coli 562 -11535190 7500960109 b2072 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 187 of 400 of the completegenome.) (nt:f253; 26 pct identical (6 gaps) to 141 residues of) (le:5104) (re:5865) (di:complement) AE000297 AE000297
 g1788387 Escherichia coli 562 -11535190 6500731332 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2072 b2072 Escherichia coli 562 -11535190

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853769	11284	33440	255	84

Description

5000692680 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2073 b2073 Escherichia coli 562 -11535191
 7000691548 hypothetical protein b2073 (db:pir2.dat) H64973 H64973
 Escherichia coli 562 -11535191 7500960110 b2073 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 187 of 400 of the completegenome.) (nt:f219; this 219 aa orf is 25 pct identical (7 gaps)) (le:5862) (re:6521) (di:complement) AE000297 AE000297
 g1788388 Escherichia coli 562 -11535191 6500731333 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2073 b2073 Escherichia coli 562 -11535191

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853779	11285	33441	1092	363

Description

5000692681 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2074 b2074 Escherichia coli 562 -11535192
 7000691549 hypothetical protein b2074 (db:pir2.dat) A64974 A64974
 Escherichia coli 562 -11535192 7500960111 b2074 putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 187 of 400 of the completegenome.) (nt:o464; this 464 aa orf is 33 pct identical (9 gaps)) (le:7262) (re:8656) (di:direct) AE000297 AE000297 g1788389 Escherichia coli 562 -11535192 6500731334 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2074 b2074 Escherichia coli 562 -11535192

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853782	11286	33442	210	69

Description

5000692682 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2075 b2075 Escherichia coli 562 -11535193
7500923001 yegn (de:hypothetical 112.1 kd protein in alka-baes intergenic region) (db:swissprot) YEGN_ECOLI P76398 ESCHERICHIA COLI 562 -11535193
7000691550 hypothetical protein b2075 (cl:hypothetical protein b2075) (db:pir2.dat) B64974 B64974 Escherichia coli 562 -11535193 224612
acriflavin resistance protein d. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #356(46.1-46.5 min.)) (nt:orf_id:o356#9; similar to (swissprot accession) (le:13984) (re:17106) (di:direct) D90845 D90845 g1736781 Escherichia coli 562 -11535193 7500923003 yegn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 187 of 400 of the completgenome.) (nt:o1040; this 1040 aa orf is 30 pct identical) (le:8656) (re:11778) (di:direct) AE000297 AE000297 g1788390 Escherichia coli 562 -11535193 301252 acriflavin resistance protein d. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #356(46.1-46.5 min.)) (nt:orf_id:o356#9; similar to (swissprot accession) (le:13984) (re:17106) (di:direct) D90845 D90845 g1736781 Escherichia coli 562 -11535193 6500731335 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2075 b2075 Escherichia coli 562 -11535193

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853783	11287	33443	885	294

Description

5000692683 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2076 b2076 Escherichia coli 562 -11535194
7500923004 yego (de:hypothetical 111.0 kd protein in alka-baes intergenic region) (db:swissprot) YEGO_ECOLI P76399 ESCHERICHIA COLI 562 -11535194
7000691551 hypothetical protein b2076 (cl:hypothetical protein b2075) (db:pir2.dat) C64974 C64974 Escherichia coli 562 -11535194 224615
acriflavin resistance protein f envd protein . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #357(46.5-46.8 min.)) (nt:orf_id:o357#1; similar to (swissprot accession) (le:1138) (re:4215) (di:direct) D90846 D90846 g1736785 Escherichia coli 562 -11535194
7500923006 yego orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 187 of 400 of the completegenome.) (nt:o1025; this 1025 aa orf is 29 pct identical) (le:11779) (re:14856) (di:direct) AE000297 AE000297 g1788391 Escherichia coli 562 -11535194 301255 acriflavin resistance protein f envd protein . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #357(46.5-46.8 min.)) (nt:orf_id:o357#1; similar to (swissprot accession) (le:1138) (re:4215) (di:direct) D90846 D90846 g1736785 Escherichia coli 562 -11535194
6500731336 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2076 b2076 Escherichia coli 562 -11535194

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853798	11288	33444	360	119

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853812	11289	33445	864	287

Description

6500731337 yegb:b2077 hypothetical protein:hypothetical 50.9 kd protein in alka-baes intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2077 b2077 Escherichia coli 562 -11535195 111563 yegb (de:hypothetical 50.9 kd protein in alka-baes intergenic region) (db:swissprot) YEGB_ECOLI P36554 ESCHERICHIA COLI 562 -11535195 7000687621 hypothetical protein b2077 (cl:multidrug-efflux transporter) (db:pir2.dat) D64974 D64974 Escherichia coli 562 -11535195 224616 yegb methylenomycin a resistance protein mmr (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #357(46.5-46.8 min.)) (nt:orf_id:o357#2; similar to (swissprot accession) (le:4216) (re:5631) (di:direct) D90846 D90846 g1736786 Escherichia coli 562 -11535195 301256 yegb putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 187 of 400 of the completegenome.) (nt:o471; this 471 aa orf is 46 pct identical (11 gaps)) (le:14857) (re:16272) (di:direct) AE000297 AE000297 g1788392 Escherichia coli 562 -11535195 5000692684 (de:(ecoli_2025) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2025 ECOLI_2025 Escherichia coli 562 10119992

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853815	11290	33446	1194	397

Description

5000692685 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2080 b2080 Escherichia coli 562 -11535196 7000691552 hypothetical protein b2080 (db:pir2.dat) G64974 G64974 Escherichia coli 562 -11535196 7500960112 b2080 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.) (nt:o123) (le:106) (re:477) (di:direct) AE000298 AE000298 g1788396 Escherichia coli 562 -11535196 6500731338 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2080 b2080 Escherichia coli 562 -11535196

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853816	11291	33447	345	114

Description

5000692687 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2083 b2083 Escherichia coli 562 -11535197
 7000691553 hypothetical protein b2083 (db:pir2.dat) B64975 B64975
 Escherichia coli 562 -11535197 7500960113 b2083 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.) (nt:f48; this 48 aa orf is 72 pct identical (0 gaps)) (le:2558) (re:2704) (di:complement) AE000298 AE000298 g1788399 Escherichia coli 562 -11535197 6500731339 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2083 b2083 Escherichia coli 562 -11535197

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853822	11292	33448	663	220

Description

5000692688 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2084 b2084 Escherichia coli 562 -11535198
 7000691554 hypothetical protein b2084 (db:pir2.dat) C64975 C64975
 Escherichia coli 562 -11535198 7500960114 b2084 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.) (nt:f88; this 88 aa orf is 26 pct identical (2 gaps)) (le:2691) (re:2957) (di:complement) AE000298 AE000298 g1788400 Escherichia coli 562 -11535198 6500731340 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2084 b2084 Escherichia coli 562 -11535198

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853835	11293	33449	2211	736

Description

5000692689 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2085 b2085 Escherichia coli 562 -11535199
 7000691555 hypothetical protein b2085 (db:pir2.dat) D64975 D64975
 Escherichia coli 562 -11535199 7500960115 b2085 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.) (nt:f125) (le:2945) (re:3322) (di:complement) AE000298 AE000298 g1788401 Escherichia coli 562 -11535199 6500731341 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2085 b2085 Escherichia coli 562 -11535199

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853852	11294	33450	300	99

Description

GTC ORF with score 313 to: (fn:gtp binding protein) (sr:schizosaccharomyces pombe (strain:jy450) cdna to mrna) (db:genpept-pln1) (de:fission yeast mrna for gtp binding protein rho 2, complete cds,clone gp23.) (le:166) (re:768) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853853	11295	33451	324	107

Description

GTC ORF with score 300 to: (fn:gtp binding protein) (sr:schizosaccharomyces pombe (strain:jy450) cdna to mrna) (db:genpept-pln1) (de:fission yeast mrna for gtp binding protein rho 2, complete cds,clone gp23.) (le:166) (re:768) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853860	11296	33452	342	113

Description

6500731342 yegs:b2086 hypothetical protein:hypothetical 32.0 kd protein in ogrk-gatr intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2086 b2086 Escherichia coli 562 -11535200
4000708205 yegs (de:hypothetical 32.0 kd protein in ogrk-gatr intergenic region) (db:swissprot) YEGS_ECOLI P76407 ESCHERICHIA COLI 562 -11535200
7000687624 hypothetical protein b2086 (db:pir2.dat) E64975 E64975 Escherichia coli 562 -11535200 224622 bmru protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #357(46.5-46.8 min.)) (nt:orf_id:o357#9; similar to (swissprot accession) (le:11464) (re:12363) (di:direct) D90846 D90846 g1736792 Escherichia coli 562 -11535200 301273 bmru protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.)) (nt:orf_id:o357#9; similar to (swissprot accession) (le:6109) (re:7008) (di:direct) D90847 D90847 g1736804 Escherichia coli 562 -11535200 301262 b2086 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl1655 section 188 of 400 of the completegenome.) (nt:o299; this 299 aa orf is 29 pct identical (17 gaps)) (le:3668) (re:4567) (di:direct) AE000298 AE000298 g1788402 Escherichia coli 562 -11535200 224633 bmru protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9 min.)) (nt:orf_id:o357#9; similar to (swissprot accession) (le:6109) (re:7008) (di:direct) D90847 D90847 g1736804 Escherichia coli 562 -11535200 5000692690 (de:(ecoli_2034) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2034 ECOLI_2034 Escherichia coli 562 10119996

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853864	11297	33453	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853868	11298	33454	654	217

Description

5000692691 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2097 b2097 Escherichia coli 562 -11535201
 7000691556 hypothetical protein b2097 (db:pir2.dat) H64976 H64976
 Escherichia coli 562 -11535201 7500960116 b2097 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 189 of 400 of the completegenome.) (nt:f374; this 374 aa orf is 30 pct identical (9 gaps)) (le:181) (re:1305) (di:complement) AE000299 AE000299 g1788414 Escherichia coli 562 -11535201 6500731343 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2097 b2097 Escherichia coli 562 -11535201

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853884	11299	33455	192	63

Description

GTC ORF with score 262 to: (sr:humicola grisea var. thermoidea (sub_species:ifo9854) dna) (db:genpept) (de:humicola grisea var. thermoidea bgl4 gene for beta-glucosidase,complete cds.) (le:289:437) (re:332:1823) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853886	11300	33456	336	111

Description

GTC ORF with score 183 to: (sr:humicola grisea var. thermoidea (sub_species:ifo9854) dna) (db:genpept) (de:humicola grisea var. thermoidea bgl4 gene for beta-glucosidase,complete cds.) (le:289:437) (re:332:1823) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853889	11301	33457	252	83

Description

GTC ORF with score 289 to: (sr:humicola grisea var. thermoidea (sub_species:ifo9854) dna) (db:genpept) (de:humicola grisea var. thermoidea bgl4 gene for beta-glucosidase,complete cds.) (le:289:437) (re:332:1823) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853892	11302	33458	669	222

Description

GTC ORF with score 779 to: (sr:humicola grisea var. thermoidea (sub_species:ifo9854) dna) (db:genpept) (de:humicola grisea var. thermoidea bgl4 gene for beta-glucosidase,complete cds.) (le:289:437) (re:332:1823) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853897	11303	33459	468	155

Description

GTC ORF with score 407 to: (sr:humicola grisea var. thermoidea (sub_species:ifo9854) dna) (db:genpept) (de:humicola grisea var. thermoidea bgl4 gene for beta-glucosidase,complete cds.) (le:289:437) (re:332:1823) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853906	11304	33460	1260	419

Description

5000692692 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2098 b2098 Escherichia coli 562 -11535202
7500923008 yegt (de:putative nucleoside transporter yegt) (db:swissprot) YEGT_ECOLI P76417 ESCHERICHIA COLI 562 -11535202 7000691557 hypothetical protein b2098 (db:pir2.dat) A64977 A64977 Escherichia coli 562 -11535202
224651 nucleoside permease nupg nucleoside-transport (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf_id:o359#8; similar to (swissprot accession) (le:6744) (re:8021) (di:direct) D90848 D90848 g1736823 Escherichia coli 562 -11535202
7500923010 yegt putative nucleoside permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 189 of 400 of the completegenome.) (nt:o425; this 425 aa orf is 32 pct identical (30 gaps)) (le:1490) (re:2767) (di:direct) AE000299 AE000299 g1788415 Escherichia coli 562 -11535202 301291 nucleoside permease nupg nucleoside-transport (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf_id:o359#8; similar to (swissprot accession) (le:6744) (re:8021) (di:direct) D90848 D90848 g1736823 Escherichia coli 562 -11535202 6500731344 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2098 b2098 Escherichia coli 562 -11535202

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853909	11305	33461	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853919	11306	33462	264	87

Description

5000692693 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2099 b2099 Escherichia coli 562 -11535203
7000691558 hypothetical protein b2099 (db:pir2.dat) B64977 B64977
Escherichia coli 562 -11535203 7500960117 b2099 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 189 of 400 of the completegenome.) (nt:o334; this 334 aa orf is 27 pct identical (16 gaps)) (le:2764) (re:3768) (di:direct) AE000299 AE000299 g1788416 Escherichia coli 562 -11535203 6500731345 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2099 b2099 Escherichia coli 562 -11535203

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853922	11307	33463	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853933	11308	33464	807	268

Description

5000692694 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2100 b2100 Escherichia coli 562 -11535204
7000691559 hypothetical protein b2100 (db:pir2.dat) C64977 C64977
Escherichia coli 562 -11535204 7500960118 b2100 putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 189 of 400 of the completegenome.) (nt:o321; this 321 aa orf is 26 pct identical (15 gaps)) (le:3765) (re:4730) (di:direct) AE000299 AE000299 g1788417 Escherichia coli 562 -11535204 6500731346 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2100 b2100 Escherichia coli 562 -11535204

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853935	11309	33465	273	90

Description

5000692695 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2101 b2101 Escherichia coli 562 -11535205
7500923011 yegw (de:hypothetical transcriptional regulator in fbab-thid intergenic region) (db:swissprot) YEGW_ECOLI P76420 ESCHERICHIA COLI 562 -11535205 7000691560 hypothetical protein b2101 (db:pir2.dat) D64977 D64977 Escherichia coli 562 -11535205 224653 fatty acyl responsive regulator p30 protein . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf_id:o359#13; similar to (swissprot accession) (le:9956) (re:10702) (di:complement) D90848 D90848 g1736825 Escherichia coli 562 -11535205 7500923013 yegw putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 189 of 400 of the completegenome.) (nt:f248; this 248 aa orf is 30 pct identical (14 gaps)) (le:4704) (re:5450) (di:complement) AE000299 AE000299 g1788418 Escherichia coli 562 -11535205 301293 fatty acyl responsive regulator p30 protein . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf_id:o359#13; similar to (swissprot accession) (le:9956) (re:10702) (di:complement) D90848 D90848 g1736825 Escherichia coli 562 -11535205 6500731347 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2101 b2101 Escherichia coli 562 -11535205

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853947	11310	33466	381	126

Description

5000692696 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2102 b2102 Escherichia coli 562 -11535206
7500923014 yegx (de:hypothetical 32.0 kd protein in fbab-thid intergenic region) (db:swissprot) YEGX_ECOLI P76421 ESCHERICHIA COLI 562 -11535206
7000691561 hypothetical protein b2102 (db:pir2.dat) E64977 E64977 Escherichia coli 562 -11535206 224654 lysozyme m1 precursor ec 3.2.1.17 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf_id:o359#14; similar to (swissprot accession) (le:10754) (re:11581) (di:complement) D90848 D90848 g1736826 Escherichia coli 562 -11535206 7500923016 yegx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 189 of 400 of the completegenome.) (nt:f275; this 275 aa orf is 36 pct identical (21 gaps)) (le:5502) (re:6329) (di:complement) AE000299 AE000299 g1788419 Escherichia coli 562 -11535206 301294 lysozyme m1 precursor ec 3.2.1.17 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf_id:o359#14; similar to (swissprot accession) (le:10754) (re:11581) (di:complement) D90848 D90848 g1736826 Escherichia coli 562 -11535206 6500731348 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2102 b2102 Escherichia coli 562 -11535206

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501853954	11311	33467	204	67

Description

6500731349 yohl:b2105 hypothetical protein:hypothetical 10.1 kd protein in thim-mrp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2105 b2105 Escherichia coli 562 -11535207
500684973 yohl (de:hypothetical 10.1 kd protein in thim-mrp intergenic region) (db:swissprot) YOHL_ECOLI P76424 ESCHERICHIA COLI 562 -11535207
7000688182 hypothetical protein b2105 (cl:hypothetical protein b2105) (db:pir2.dat) H64977 H64977 Escherichia coli 562 -11535207 7500952108 yohl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 189 of 400 of the completegenome.) (nt:f90; this 90 aa orf is 27 pct identical (2 gaps)) (le:8193) (re:8465) (di:complement) AE000299 AE000299 g1788422 Escherichia coli 562 -11535207 5000692699 (de:(ecoli_2053) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2053 ECOLI_2053 Escherichia coli 562 10061014

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853966	11312	33468	1593	530

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853986	11313	33469	630	209

Description

5000692700 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2106 b2106 Escherichia coli 562 -11535208
7500952109 yohm (de:hypothetical 30.4 kd protein in thim-mrp intergenic region) (db:swissprot) YOHEM_ECOLI P76425 ESCHERICHIA COLI 562 -11535208
7000691562 hypothetical protein b2106 (db:pir2.dat) A64978 A64978 Escherichia coli 562 -11535208 224657 histidine-rich glycoprotein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf_id:o359#18; similar to (swissprot accession) (le:13838) (re:14662) (di:direct) D90848 D90848 g1736829 Escherichia coli 562 -11535208 7500952111 yohm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 189 of 400 of the completegenome.) (nt:o274; this 274 aa orf is 55 pct identical (1 gap)) (le:8586) (re:9410) (di:direct) AE000299 AE000299 g1788423 Escherichia coli 562 -11535208 301297 histidine-rich glycoprotein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf_id:o359#18; similar to (swissprot accession) (le:13838) (re:14662) (di:direct) D90848 D90848 g1736829 Escherichia coli 562 -11535208 6500731350 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2106 b2106 Escherichia coli 562 -11535208

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501853995	11314	33470	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854002	11315	33471	414	137

Description

5000692701 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2107 b2107 Escherichia coli 562 -11535209
7000691563 hypothetical protein b2107 (db:pir2.dat) B64978 B64978
Escherichia coli 562 -11535209 7500960119 b2107 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 189 of 400 of the completegenome.) (nt:ol72; this 172 aa orf is 25 pct identical (2 gaps)) (le:9449) (re:9967) (di:direct) AE000299 AE000299 g1788424 Escherichia coli 562 -11535209 6500731351 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2107 b2107 Escherichia coli 562 -11535209

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854003	11316	33472	396	131

Description

GTC ORF with score 111 to: (sr:streptococcus mutans (strain ng5) dna) (db:genpept-bct1) (ec:1.2.1.9) (de:streptococcus mutans non-phosphorylating nadp-dependentglyceraldehyde-3-phosphate dehydrogenase (gapn) gene, complete cds.) (le:233) (re:1660) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854019	11317	33473	1284	427

Description

6500731352 yeha:b2108 hypothetical 36.9 kd protein in mrp 5region precursor:hypothetical 36.9 kd protein in gaty-mrp intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2108 b2108 Escherichia coli 562 -11535210 111571 yeha (de:hypothetical 36.9 kd protein in gaty-mrp intergenic region precursor) (db:swissprot) YEHA_ECOLI P33340 ESCHERICHIA COLI 562 -11535210 7000687625 yeha hypothetical 36.9 kd protein in mrp 5region precursor (db:pir2.dat) C64978 C64978 Escherichia coli 562 -11535210 224658 yeha (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #359(46.8-47.2 min.)) (nt:orf_id:o359#20; similar to (swissprot accession) (le:15301) (re:16335) (di:complement) D90848 D90848 g1736830 Escherichia coli 562 -11535210 301298 yeha (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:148) (re:1182) (di:complement) ECOHU47 U00007 g405837 Escherichia coli 562 -11535210 234717 yeha putative type-1 fimbrial protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 190 of 400 of the completegenome.) (nt:f344; 100 pct identical to yeha_ecoli sw: p33340) (le:71) (re:1105) (di:complement) AE000300 AE000300 g1788426 Escherichia coli 562 -11535210 5000692702 (de:(ecoli_2056) (pn:hypothetical 36) (gn:yeha) (gtcfc:13.7:14.1) (ec:) (yeha_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2056 ECOLI_2056 Escherichia coli 562 10053299

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854039	11318	33474	498	165

Description

6500731353 yehb:b2109 hypothetical outer membrane usher protein in mrp 5region:hypothetical outer membrane usher protein in gaty-mrp intergenic region precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2109 b2109 Escherichia coli 562 -11535211 111572 yehb (de:region precursor) (db:swissprot) YEHB_ECOLI P33341 ESCHERICHIA COLI 562 -11535211 7000687626 yehb probable outer membrane usher protein precursor mrp 5 region (cl:outer membrane usher protein fimd) (db:pir2.dat) D64978 D64978 Escherichia coli 562 -11535211 7500923020 yehb (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:probable fimbrial protein.) (le:1198) (re:3678) (di:complement) ECOHU47 U00007 g405838 Escherichia coli 562 -11535211 234718 yehb putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 190 of 400 of the completegenome.) (nt:f826; 100 pct identical to yehb_ecoli sw: p33341) (le:1121) (re:3601) (di:complement) AE000300 AE000300 g1788427 Escherichia coli 562 -11535211 5000692703 (de:(ecoli_2057) (pn:hypothetical outer membrane usher protein in mrp 5"region precursor) (gn:yehb) (gtcfc:13.7:14.1) (ec:) (yehb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2057 ECOLI_2057 Escherichia coli 562 10053300

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854050	11319	33475	444	147

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854057	11320	33476	972	323

Description

6500731354 yehc:b2110 hypothetical 26.6 kd fimbrial chaperone in mrp 5region:hypothetical 26.6 kd fimbrial chaperone in gaty-mrp intergenic region precursor (gtcfc:12.7) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2110 b2110 Escherichia coli 562 -11535212 111573 yehc (de:precursor) (db:swissprot) YEHC_ECOLI P33342 ESCHERICHIA COLI 562 -11535212 7000687627 yehc hypothetical 26.6 kd fimbrial chaperone in mrp 5region (cl:chaperone protein papd) (db:pir2.dat) E64978 E64978 Escherichia coli 562 -11535212 7500923021 yehc (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:probable fimbrial chaperone protein.) (le:3694) (re:4413) (di:complement) ECOHU47 U00007 g405839 Escherichia coli 562 -11535212 234719 yehc putative chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 190 of 400 of the completegenome.) (nt:f239; 100 pct identical to yehc_ecoli sw: p33342) (le:3617) (re:4336) (di:complement) AE000300 AE000300 g1788428 Escherichia coli 562 -11535212 5000692704 (de:(ecoli_2058) (pn:hypothetical 26) (gn:yehc) (gtcfc:13.7:14.1) (ec:) (yehc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2058 ECOLI_2058 Escherichia coli 562 10053301

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854062	11321	33477	258	85

Description

6500731355 yehd:b2111 hypothetical 19.1 kd protein in mrp 5region precursor:hypothetical 19.1 kd protein in gaty-mrp intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2111 b2111 Escherichia coli 562 -11535213 111574 yehd (de:hypothetical 19.1 kd protein in gaty-mrp intergenic region precursor) (db:swissprot) YEHD_ECOLI P33343 ESCHERICHIA COLI 562 -11535213 7000687628 yehd hypothetical 19.1 kd protein in mrp 5region precursor (db:pir2.dat) F64978 F64978 Escherichia coli 562 -11535213 7500923022 yehd (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:4448) (re:4990) (di:complement) ECOHU47 U00007 g405840 Escherichia coli 562 -11535213 234720 yehd putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 190 of 400 of the completegenome.) (nt:f180; 100 pct identical yehd_ecoli sw: p33343) (le:4371) (re:4913) (di:complement) AE000300 AE000300 g1788429 Escherichia coli 562 -11535213 5000692705 (de:(ecoli_2059) (pn:hypothetical 19) (gn:yehd) (gtcfc:13.7:14.1) (ec:) (yehd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2059 ECOLI_2059 Escherichia coli 562 10053302

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854078	11322	33478	1470	489

Description

6500731356 yehe:b2112 hypothetical 10.1 kd protein in mrp 5 region precursor:hypothetical 10.1 kd protein in gaty-mrp intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2112 b2112 Escherichia coli 562 -11535214 111575 yehe (de:hypothetical 10.1 kd protein in gaty-mrp intergenic region precursor) (db:swissprot) YEHE_ECOLI P33344 ESCHERICHIA COLI 562 -11535214 7000687629 yehe hypothetical 10.1 kd protein in mrp 5 region precursor (db:pir2.dat) G64978 G64978 Escherichia coli 562 -11535214 7500923023 yehe (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:5283) (re:5564) (di:complement) ECOHU47 U00007 g405841 Escherichia coli 562 -11535214 234721 yehe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 190 of 400 of the completegenome.) (nt:f93; 100 pct identical to yehe_ecoli sw: p33344) (le:5206) (re:5487) (di:complement) AE000300 AE000300 g1788430 Escherichia coli 562 -11535214 5000692706 (de:(ecoli_2060) (pn:hypothetical 10) (gn:yehe) (gtcfc:13.7:14.1) (ec:) (yehe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2060 ECOLI_2060 Escherichia coli 562 10053303

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854090	11323	33479	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854097	11324	33480	1581	526

Description

6500731357 yehi:b2118 hypothetical 138.1 kd protein in molr-bglx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2118 b2118 Escherichia coli 562 -11535215 111576 yehi (de:hypothetical 138.1 kd protein in molr-bglx intergenic region) (db:swissprot) YEHI_ECOLI P33346 ESCHERICHIA COLI 562 -11535215 7000687630 yehi hypothetical 138.1 kd protein in molr-bglx intergenic region (db:pir2.dat) E64979 E64979 Escherichia coli 562 -11535215 7500923024 yehi putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 190 of 400 of the completegenome.) (nt:o1210; 99 pct identical to yehi_ecoli sw: p33346) (le:12970) (re:16602) (di:direct) AE000300 AE000300 g1788436 Escherichia coli 562 -11535215 5000692707 (de:(ecoli_2066) (pn:hypothetical 138) (gn:yehi) (gtcfc:13.7:14.1) (ec:) (yehi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2066 ECOLI_2066 Escherichia coli 562 10123572

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854098	11325	33481	858	285

Description

GTC ORF with score 208 to: (or:Arabidopsis thaliana) (sr:thale cress)
(db:genpept-pln2) (de:arabidopsis thaliana bac t12h20.) (nt:similar to
schizosaccharomyces pombe isp4 protein) (le:11336:11441:11976:12205)
(re:11366:11839:12130:12302) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854106	11326	33482	1497	498

Description

6500731358 yehl:b2119 hypothetical 42.4 kd protein in molr-bglx intergenic
region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)
b2119 b2119 Escherichia coli 562 -11535216 111578 yehl (de:hypothetical
42.4 kd protein in molr-bglx intergenic region) (db:swissprot) YEHL_ECOLI
P33348 ESCHERICHIA COLI 562 -11535216 7000687631 yehl hypothetical 42.4 kd
protein in molr-bglx intergenic region (db:pir2.dat) F64979 F64979
Escherichia coli 562 -11535216 7500923025 yehl (sr:escherichia coli k12
bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12
bhb2600.) (le:17299) (re:18453) (di:direct) ECOHU47 U00007 g405848
Escherichia coli 562 -11535216 234727 yehl orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
191 of 400 of the completegenome.) (nt:o384; 100 pct identical yehl_ecoli
sw: p33348) (le:340) (re:1494) (di:direct) AE000301 AE000301 g1788438
Escherichia coli 562 -11535216 5000692708 (de:(ecoli_2067) (pn:hypothetical
42) (gn:yehl) (gtcfc:13.7:14.1) (ec:) (yehl_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2067 ECOLI_2067 Escherichia
coli 562 10053306

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854117	11327	33483	939	312

Description

5000692709 yehm:b2120 hypothetical protein in molr-bglx intergenic region:hypothetical 83.4 kd protein in molr-bglx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2120 b2120 Escherichia coli 562 -11535217 111579 yehm (de:hypothetical 83.4 kd protein in molr-bglx intergenic region) (db:swissprot) YEHM_ECOLI P33349 ESCHERICHIA COLI 562 -11535217 7000687632 hypothetical protein in molr-bglx intergenic region (db:pir2.dat) G64979 G64979 Escherichia coli 562 -11535217 7500923026 yehm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 191 of 400 of the completegenome.) (nt:o759; residues 1-283 are 100 pct identical to) (le:1505) (re:3784) (di:direct) AE000301 AE000301 g1788439 Escherichia coli 562 -11535217 6500731359 yehm hypothetical protein in molr-bglx intergenic region:hypothetical 83.4 kd protein in molr-bglx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2120 b2120 Escherichia coli 562 -11535217

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854119	11328	33484	321	106

Description

6500731360 yehp:b2121 hypothetical 42.1 kd protein in molr-bglx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2121 b2121 Escherichia coli 562 -11535218 111582 yehp (de:hypothetical 42.1 kd protein in molr-bglx intergenic region) (db:swissprot) YEHP_ECOLI P33352 ESCHERICHIA COLI 562 -11535218 7000687633 yehp hypothetical 42.1 kd protein in molr-bglx intergenic region (db:pir2.dat) H64979 H64979 Escherichia coli 562 -11535218 7500923027 yehp (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:20736) (re:21872) (di:direct) ECOHU47 U00007 g405852 Escherichia coli 562 -11535218 234731 yehp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 191 of 400 of the completegenome.) (nt:o378; 100 pct identical to yehp_ecoli sw: p33352) (le:3777) (re:4913) (di:direct) AE000301 AE000301 g1788440 Escherichia coli 562 -11535218 5000692710 (de:(ecoli_2069) (pn:hypothetical 42) (gn:yehp) (gtcfc:13.7:14.1) (ec:) (yehp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2069 ECOLI_2069 Escherichia coli 562 10053310

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854138	11329	33485	1158	386

Description

6500731361 yehq:b2122 hypothetical 68.5 kd protein in molr-bglx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2122 b2122 Escherichia coli 562 -11535219 7000687634 yehq hypothetical 68.5 kd protein in molr-bglx intergenic region (db:pir2.dat) A64980 A64980 Escherichia coli 562 -11535219 234732 yehq (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:21845) (re:23713) (di:direct) ECOHU47 U00007 g405853 Escherichia coli 562 -11535219 7500959826 yehq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 191 of 400 of the completegenome.) (nt:o622; 100 pct identical to yehq_ecoli sw: p33353) (le:4886) (re:6754) (di:direct) AE000301 AE000301 g1788441 Escherichia coli 562 -11535219 111583 yehq_ecoli (de:hypothetical 68.5 kd protein in molr-bglx intergenic region.) P33353 P33353 Escherichia coli 562 -11535219 5000692711 (de:(ecoli_2070) (pn:hypothetical 68) (gn:yehq) (gtcfc:13.7:14.1) (ec:) (yehq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2070 ECOLI_2070 Escherichia coli 562 10053311

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854149	11330	33486	270	89

Description

6500731362 yehr:b2123 hypothetical 17.2 kd protein in molr-bglx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2123 b2123 Escherichia coli 562 -11535220 7000687635 yehr hypothetical 17.2 kd protein in molr-bglx intergenic region (db:pir2.dat) B64980 B64980 Escherichia coli 562 -11535220 234733 yehr (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:strong similarity to an orf from listeria.) (le:23982) (re:24455) (di:direct) ECOHU47 U00007 g405854 Escherichia coli 562 -11535220 7500959789 yehr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 191 of 400 of the completegenome.) (nt:o157; 100 pct identical to yehr_ecoli sw: p33354) (le:7023) (re:7496) (di:direct) AE000301 AE000301 g1788442 Escherichia coli 562 -11535220 111584 yehr_ecoli (de:hypothetical 17.2 kd protein in molr-bglx intergenic region.) P33354 P33354 Escherichia coli 562 -11535220 5000692712 (de:(ecoli_2071) (pn:hypothetical 17) (gn:yehr) (gtcfc:13.7:14.1) (ec:) (yehr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2071 ECOLI_2071 Escherichia coli 562 10053312

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854151	11331	33487	567	188

Description

6500731363 yehs:b2124 hypothetical 18.0 kd protein in molr-bglx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2124 b2124 Escherichia coli 562 -11535221 111585 yehs (de:hypothetical 18.0 kd protein in molr-bglx intergenic region) (db:swissprot) YEHS_ECOLI P33355 ESCHERICHIA COLI 562 -11535221 7000687636 yehs hypothetical 18.0 kd protein in molr-bglx intergenic region (db:pir2.dat) C64980 C64980 Escherichia coli 562 -11535221 7500923030 yehs (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:24495) (re:24965) (di:complement) ECOHU47 U00007 g405855 Escherichia coli 562 -11535221 234734 yehs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 191 of 400 of the completegenome.) (nt:f156; 100 pct identical to yehs_ecoli sw: p33355) (le:7536) (re:8006) (di:complement) AE000301 AE000301 g1788443 Escherichia coli 562 -11535221 5000692713 (de:(ecoli_2072) (pn:hypothetical 18) (gn:yehs) (gtcfc:13.7:14.1) (ec:) (yehs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2072 ECOLI_2072 Escherichia coli 562 10053313

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854155	11332	33488	1290	429

Description

6500731364 yehu:b2126 hypothetical 62.1 kd protein in molr-bglx intergenic region:hypothetical 62.1 kd protein in molr-bglx intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2126 b2126 Escherichia coli 562 -11535222 111587 yehu (de:hypothetical 62.1 kd protein in molr-bglx intergenic region precursor) (db:swissprot) YEHU_ECOLI P33357 ESCHERICHIA COLI 562 -11535222 7000687638 yehu hypothetical 62.1 kd protein in molr-bglx intergenic region (cl:hypothetical protein b2380) (db:pir2.dat) E64980 E64980 Escherichia coli 562 -11535222 7500923032 yehu putative 2-component sensor protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 191 of 400 of the completegenome.) (nt:f561; 99 pct identical to yehu_ecoli sw: p33357) (le:8769) (re:10454) (di:complement) AE000301 AE000301 g1788446 Escherichia coli 562 -11535222 5000692716 (de:(ecoli_2075) (pn:hypothetical 62) (gn:yehu) (gtcfc:13.7:14.1) (ec:) (yehu_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2075 ECOLI_2075 Escherichia coli 562 10123576

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854172	11333	33489	207	68

Description

6500731365 yehv:b2127 hypothetical transcriptional regulator in molr-bglx intergenic region:hypothetical transcriptional regulator in metg-dld intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2127 b2127 Escherichia coli 562 -11535223 111588 yehv (de:hypothetical transcriptional regulator in metg-dld intergenic region) (db:swissprot) YEHV_ECOLI P33358 ESCHERICHIA COLI 562 -11535223 7000687639 yehv hypothetical transcription regulator molr-bglx intergenic region (cl:hypothetical protein b1162) (db:pir2.dat) F64980 F64980 Escherichia coli 562 -11535223 7500923033 yehv (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:similar to merr (hg resistance) proteins.) (le:27635) (re:28366) (di:direct) ECOHU47 U00007 g405858 Escherichia coli 562 -11535223 234737 yehv putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 192 of 400 of the completegenome.) (nt:o243; 100 pct identical to yehv_ecoli sw: p33358) (le:141) (re:872) (di:direct) AE000302 AE000302 g1788448 Escherichia coli 562 -11535223 5000692717 (de:(ecoli_2076) (pn:hypothetical transcriptional regulator in metg-dld intergenic region) (gn:yehv) (gtcfc:13.7:14.1) (ec:) (yehv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2076 ECOLI_2076 Escherichia coli 562 10053316

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854176	11334	33490	450	149

Description

GTC ORF with score 193 to: (de:(yer081w) (pn:putative d-3-phosphoglycerate dehydrogenase yer081w:pgdh:strong similarity to phosphoglycerate dehydrogenases) (gtcfc:5.3) (ec:1.1.1.95) (serx_yeast) (keggfc:5.3) (sgdfc:1.1.1) (db:gtc-saccharomyces cerevisiae)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854177	11335	33491	405	134

Description

6500731366 yehw:b2128 hypothetical 25.5 kd protein in molr-bglx intergenic region:hypothetical abc transporter permease protein yehw (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2128 b2128 Escherichia coli 562 -11535224 111589 yehw (de:hypothetical abc transporter permease protein yehw) (db:swissprot) YEHW_ECOLI P33359 ESCHERICHIA COLI 562 -11535224 7000687640 yehw hypothetical 25.5 kd protein in molr-bglx intergenic region (cl:glycine betaine/carnitine/choline abc transporter) (db:pir2.dat) G64980 G64980 Escherichia coli 562 -11535224 7500923034 yehw (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:probable membrane component of transport complex.) (le:28514) (re:29245) (di:complement) ECOHU47 U00007 g405859 Escherichia coli 562 -11535224 234738 yehw putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 192 of 400 of the completegenome.) (nt:f243; 100 pct identical to yehw_ecoli sw: p33359) (le:1020) (re:1751) (di:complement) AE000302 AE000302 gl788449 Escherichia coli 562 -11535224 5000692718 (de:(ecoli_2077) (pn:hypothetical 25) (gn:yehw) (gtcfc:13.7:14.1) (ec:) (yehw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2077 ECOLI_2077 Escherichia coli 562 10053317

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854178	11336	33492	246	81

Description

GTC ORF with score 296 to: (de:(yer081w) (pn:putative d-3-phosphoglycerate dehydrogenase yer081w:pgdh:strong similarity to phosphoglycerate dehydrogenases) (gtcfc:5.3) (ec:1.1.1.95) (serx_yeast) (keggfc:5.3) (sgdgc:1.1.1) (db:gtc-saccharomyces cerevisiae)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854197	11337	33493	957	318

Description

6500731367 yehx:b2129 hypothetical abc transporter in molr-bglx intergenic region:hypothetical abc transporter atp-binding protein in metg-dld intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2129 b2129 Escherichia coli 562 -11535225 111590 yehx (de:hypothetical abc transporter atp-binding protein yehx) (db:swissprot) YEHX_ECOLI P33360 ESCHERICHIA COLI 562 -11535225 7000687641 yehx hypothetical abc transporter in molr-bglx intergenic region (cl:atp-binding cassette homology) (db:pir2.dat) H64980 H64980 Escherichia coli 562 -11535225 7500923035 yehx (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:abc-type atp-dependent protein protein.) (le:29250) (re:30176) (di:complement) ECOHU47 U00007 g405860 Escherichia coli 562 -11535225 234739 yehx putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 192 of 400 of the completegenome.) (nt:f308; 100 pct identical to yehx_ecoli sw: p33360) (le:1756) (re:2682) (di:complement) AE000302 AE000302 g1788450 Escherichia coli 562 -11535225 5000692719 (de:(ecoli_2078) (pn:hypothetical abc transporter atp-binding protein in metg-dld intergenic region) (gn:yehx) (gtcfc:13.7:14.1) (ec:) (yehx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2078 ECOLI_2078 Escherichia coli 562 10053318

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854205	11338	33494	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854211	11339	33495	486	161

Description

6500731368 yehz:b2131 hypothetical 32.6 kd protein in molr-bglx intergenic region:hypothetical 32.6 kd protein in molr-bglx intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2131 b2131 Escherichia coli 562 -11535226 111592 yehz (de:hypothetical 32.6 kd protein in molr-bglx intergenic region precursor) (db:swissprot) YEHZ_ECOLI P33362 ESCHERICHIA COLI 562 -11535226 7000687643 yehz hypothetical 32.6 kd protein in molr-bglx intergenic region (db:pir2.dat) B64981 B64981 Escherichia coli 562 -11535226 7500923037 yehz (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:31334) (re:32251) (di:complement) ECOHU47 U00007 g405862 Escherichia coli 562 -11535226 234741 yehz putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 192 of 400 of the completgenome.) (nt:f305; 100 pct identical to yehz_ecoli sw: p33362) (le:3839) (re:4756) (di:complement) AE000302 AE000302 g1788452 Escherichia coli 562 -11535226 5000692721 (de:(ecoli_2080) (pn:hypothetical 32) (gn:yehz) (gtcfc:13.7:14.1) (ec:) (yehz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2080 ECOLI_2080 Escherichia coli 562 10053320

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854212	11340	33496	468	155

Description

6500731369 yohc:b2135 hypothetical 22.4 kd protein in pbpg-cdd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2135 b2135 Escherichia coli 562 -11535227 115241 yohc (de:hypothetical 22.4 kd protein in pbpg-cdd intergenic region) (db:swissprot) YOHC_ECOLI P33365 ESCHERICHIA COLI 562 -11535227 7000688175 yohc hypothetical 22.4 kd protein in pbpg-cdd intergenic region (db:pir2.dat) F64981 F64981 Escherichia coli 562 -11535227 7500952098 yohc (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:37814) (re:38425) (di:complement) ECOHU47 U00007 g405865 Escherichia coli 562 -11535227 234745 yohc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completgenome.) (nt:f203; 100 pct identical to yohc_ecoli sw: p33365) (le:113) (re:724) (di:complement) AE000303 AE000303 g1788457 Escherichia coli 562 -11535227 5000692723 (de:(ecoli_2084) (pn:hypothetical 22) (gn:yohc) (gtcfc:13.7:14.1) (ec:) (yohc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2084 ECOLI_2084 Escherichia coli 562 10056966

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854218	11341	33497	315	104

Description

6500731370 yohd:b2136 hypothetical 21.4 kd protein in pbpg-cdd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2136 b2136 Escherichia coli 562 -11535228 7000690924 yohd hypothetical 21.4 kd protein in pbpg-cdd intergenic region (db:pir2.dat) G64981 G64981 Escherichia coli 562 -11535228 7500959794 yohd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:o204; 100 pct identical to yohd_ecoli sw: p33366) (le:834) (re:1448) (di:direct) AE000303 AE000303 g1788458 Escherichia coli 562 -11535228 5000692724 (de:(ecoli_2085) (pn:hypothetical 21) (gn:yohd) (gtcfc:13.7:14.1) (ec:) (yohd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2085 ECOLI_2085 Escherichia coli 562 10123578

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854221	11342	33498	600	199

Description

6500731371 yohg:b2138 hypothetical 43.3 kd protein in pbpg-cdd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2138 b2138 Escherichia coli 562 -11535229 115245 yohg (de:hypothetical 43.3 kd protein in pbpg-cdd intergenic region) (db:swissprot) YOHG_ECOLI P33369 ESCHERICHIA COLI 562 -11535229 7000688177 yohg hypothetical 43.3 kd protein in pbpg-cdd intergenic region (db:pir2.dat) A64982 A64982 Escherichia coli 562 -11535229 7500952100 yohg (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:similar to nodulation protein t and a fusaric acid) (le:40092) (re:41288) (di:complement) ECOHU47 U00007 g405964 Escherichia coli 562 -11535229 234749 yohg putative channel/filament proteins (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:f398; 100 pct identical yohg_ecoli sw: p33369) (le:2392) (re:3588) (di:complement) AE000303 AE000303 g1788460 Escherichia coli 562 -11535229 5000692726 (de:(ecoli_2087) (pn:hypothetical 43) (gn:yohg) (gtcfc:13.7:14.1) (ec:) (yohg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2087 ECOLI_2087 Escherichia coli 562 10056970

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854222	11343	33499	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854225	11344	33500	204	67

Description

6500731372 yohh:b2139 hypothetical 10.4 kd protein in pbpg-cdd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2139 b2139 Escherichia coli 562 -11535230 115246 yohh (de:hypothetical 10.4 kd protein in pbpg-cdd intergenic region) (db:swissprot) YOHH_ECOLI P33370 ESCHERICHIA COLI 562 -11535230 7000688178 yohh hypothetical 10.4 kd protein in pbpg-cdd intergenic region (db:pir2.dat) B64982 B64982 Escherichia coli 562 -11535230 7500952101 yohh (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:41318) (re:41608) (di:complement) ECOHU47 U00007 g405870 Escherichia coli 562 -11535230 234750 yohh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:f96; 100 pct identical to yohh_ecoli sw: p33370) (le:3618) (re:3908) (di:complement) AE000303 AE000303 g1788461 Escherichia coli 562 -11535230 5000692727 (de:(ecoli_2088) (pn:hypothetical 10) (gn:yohh) (gtcfc:13.7:14.1) (ec:) (yohh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2088 ECOLI_2088 Escherichia coli 562 10056971

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854227	11345	33501	414	137

Description

6500731373 yohi:b2140 hypothetical 35.2 kd protein in pbpg-cdd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2140 b2140 Escherichia coli 562 -11535231 115247 yohi (de:hypothetical 35.2 kd protein in pbpg-cdd intergenic region) (db:swissprot) YOHI_ECOLI P33371 ESCHERICHIA COLI 562 -11535231 7000688179 yohi hypothetical 35.2 kd protein in pbpg-cdd intergenic region (db:pir2.dat) C64982 C64982 Escherichia coli 562 -11535231 7500952102 yohi (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:similar to yhdg and an orf from rhodobacter.) (le:42208) (re:43155) (di:complement) ECOHU47 U00007 g405871 Escherichia coli 562 -11535231 234751 yohi putative regulator protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:f315; 100 pct identical to yohi_ecoli sw: p33371) (le:4507) (re:5454) (di:complement) AE000303 AE000303 g1788462 Escherichia coli 562 -11535231 5000692728 (de:(ecoli_2089) (pn:hypothetical 35) (gn:yohi) (gtcfc:13.7:14.1) (ec:) (yohi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2089 ECOLI_2089 Escherichia coli 562 10056972

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854228	11346	33502	1149	382

Description

5000692732 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2145 b2145 Escherichia coli 562 -11535232
7000691564 hypothetical protein b2145 (db:pir2.dat) H64982 H64982
Escherichia coli 562 -11535232 7500960120 b2145 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:o79; this 79 aa orf is 50 pct identical (1 gap)) (le:8669) (re:8908) (di:direct) AE000303 AE000303
g1788467 Escherichia coli 562 -11535232 6500731374 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2145 b2145 Escherichia coli 562 -11535232

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854229	11347	33503	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854244	11348	33504	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854254	11349	33505	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854260	11350	33506	1239	413

Description

5000692733 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2146 b2146 Escherichia coli 562 -11535233
7000691565 hypothetical protein b2146 (db:pir2.dat) A64983 A64983
Escherichia coli 562 -11535233 7500960121 b2146 putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:o412; residues 22-87 are 51 pct identical to) (le:9102) (re:10340) (di:direct) AE000303 AE000303
g1788468 Escherichia coli 562 -11535233 6500731375 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2146 b2146 Escherichia coli 562 -11535233

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854266	11351	33507	519	172

Description

6500731376 yeib:b2152 hypothetical 43.4 kd protein in gals-fole intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2152 b2152 Escherichia coli 562 -11535234 111601 yeib (de:hypothetical 43.4 kd protein in gals-fole intergenic region) (db:swissprot) YEIB_ECOLI P25747 ESCHERICHIA COLI 562 -11535234 7000687645 yeib hypothetical 43.4 kd protein in gals-fole intergenic region (db:pir2.dat) G64983 G64983 Escherichia coli 562 -11535234 7500923043 yeib (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:similar to membrane protein from bacillus.) (le:49555) (re:50712) (di:complement) ECOHU47 U00007 g405874 Escherichia coli 562 -11535234 234759 yeib orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 194 of 400 of the completegenome.) (nt:f385; 100 pct identical to yeib_ecoli sw: p25747) (le:5219) (re:6376) (di:complement) AE000304 AE000304 g1788475 Escherichia coli 562 -11535234 5000692735 (de:(ecoli_2101) (pn:hypothetical 43) (gn:yeib) (gtcfc:13.7:14.1) (ec:) (yeib_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2101 ECOLI_2101 Escherichia coli 562 10053329

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854283	11352	33508	330	109

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854284	11353	33509	705	234

Description

6500731377 yeig:b2154 hypothetical 31.3 kd protein in fole-cira intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2154 b2154 Escherichia coli 562 -11535235 111604 yeig (de:hypothetical 31.3 kd protein in fole-cira intergenic region) (db:swissprot) YEIG_ECOLI P33018 ESCHERICHIA COLI 562 -11535235 7000687648 yeig hypothetical 31.3 kd protein in fole-cira intergenic region (cl:conserved hypothetical protein yjl068c) (db:pir2.dat) A64984 A64984 Escherichia coli 562 -11535235 7500923046 yeig (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:probable esterase (strong match to human esterase) (le:51655) (re:52491) (di:direct) ECOHU47 U00007 g405878 Escherichia coli 562 -11535235 234761 yeig putative esterase ec 3.1.1.-. (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 194 of 400 of the completegenome.) (nt:o278; 100 pct identical to yeig_ecoli sw: p33018) (le:7319) (re:8155) (di:direct) AE000304 AE000304 g1788477 Escherichia coli 562 -11535235 5000692736 (de:(ecoli_2103) (pn:hypothetical 31) (gn:yeig) (gtcfc:13.7:14.1) (ec:) (yeig_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2103 ECOLI_2103 Escherichia coli 562 10053332

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854285	11354	33510	528	175

Description

6500731378 yeie:b2157 hypothetical transcriptional regulator in lysp-nfo
intergenic region:hypothetical transcriptional regulator in lysp-nfo
intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2157 b2157 Escherichia coli 562 -11535236 111603
yeie (de:hypothetical transcriptional regulator in lysp-nfo intergenic
region) (db:swissprot) YEIE_ECOLI P32484 ESCHERICHIA COLI 562 -11535236
7000687647 yeie hypothetical transcription regulator lysp-nfo intergenic
region (cl:transcription activator lysr-type) (db:pir2.dat) D64984 D64984
Escherichia coli 562 -11535236 235031 yeie (sr:escherichia coli k12
bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12
bhb2600.) (nt:member of lysr family.) (le:56482) (re:57363) (di:complement)
ECOHU47 U00007 g405876 Escherichia coli 562 -11535236 7500923045
(sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli lysine
specific permease (lysp) gene, completecds.) (nt:orf 1 function unknown;
lysr homolog) (le:431) (re:1312) (di:direct) ECOLYSP M89774 g466777
Escherichia coli 562 -11535236 234764 yeie putative transcriptional
regulator lysr-type (fn:putative regulator; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 195 of 400 of the
completegenome.) (nt:f293; 100 pct identical to yeie_ecoli sw: p32484)
(le:1851) (re:2732) (di:complement) AE000305 AE000305 g1788481 Escherichia
coli 562 -11535236 5000692737 (de:(ecoli_2106) (pn:hypothetical
transcriptional regulator in lysp-nfo intergenic region) (gn:yeie)
(gtcfc:13.7:14.1) (ec:) (yeie_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2106 ECOLI_2106 Escherichia coli 562
10053331

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854307	11355	33511	402	134

Description

6500731379 yeih:b2158 hypothetical 36.9 kd protein in lysp-nfo intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2158 b2158 Escherichia coli 562 -11535237 111605 yeih (de:hypothetical 36.9 kd protein in lysp-nfo intergenic region) (db:swissprot) YEIH_ECOLI P33019 ESCHERICHIA COLI 562 -11535237 7000687649 yeih hypothetical 36.9 kd protein in lysp-nfo intergenic region (db:pir2.dat) E64984 E64984 Escherichia coli 562 -11535237 7500923047 yeih (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:57462) (re:58511) (di:direct) ECOHU47 U00007 g405879 Escherichia coli 562 -11535237 234765 yeih orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 195 of 400 of the completegenome.) (nt:o349; 100 pct identical to yeih_ecoli sw: p33019) (le:2831) (re:3880) (di:direct) AE000305 AE000305 g1788482 Escherichia coli 562 -11535237 5000692738 (de:(ecoli_2107) (pn:hypothetical 36) (gn:yeih) (gtcfc:13.7:14.1) (ec:) (yeih_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2107 ECOLI_2107 Escherichia coli 562 10053333

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854308	11356	33512	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854311	11357	33513	861	286

Description

6500731380 yeij:b2161 hypothetical 43.4 kd protein in nfo-frua intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2161 b2161 Escherichia coli 562 -11535238 111608 yeij (de:hypothetical 43.4 kd protein in nfo-frua intergenic region) (db:swissprot) YEIJ_ECOLI P33021 ESCHERICHIA COLI 562 -11535238 7000687651 yeij hypothetical 43.4 kd protein in nfo-frua intergenic region (cl:pyrimidine nucleoside transport protein nupc) (db:pir2.dat) H64984 H64984 Escherichia coli 562 -11535238 7500923050 yeij (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:strong match to yeio; weaker match to ecnupc_1.) (le:60639) (re:61889) (di:complement) ECOHU47 U00007 g405881 Escherichia coli 562 -11535238 234768 yeij putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 195 of 400 of the completegenome.) (nt:f416; 100 pct identical to yeij_ecoli sw: p33021) (le:6009) (re:7259) (di:complement) AE000305 AE000305 g1788485 Escherichia coli 562 -11535238 5000692740 (de:(ecoli_2110) (pn:hypothetical 43) (gn:yeij) (gtcfc:13.7:14.1) (ec:) (yeij_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2110 ECOLI_2110 Escherichia coli 562 10053336

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854312	11358	33514	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854313	11359	33515	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854325	11360	33516	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854373	11361	33517	1374	457

Description

6500731381 yeik:b2162 hypothetical 33.7 kd protein in nfo-frua intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2162 b2162 Escherichia coli 562 -11535239 111609 yeik (de:hypothetical 33.7 kd protein in nfo-frua intergenic region) (db:swissprot) YEIK_ECOLI P33022 ESCHERICHIA COLI 562 -11535239 7000687652 yeik hypothetical 33.7 kd protein in nfo-frua intergenic region (cl:yaaf protein) (db:pir2.dat) A64985 A64985 Escherichia coli 562 -11535239 7500923051 yeik (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:strong match to yaaf and a urf from) (le:61989) (re:62930) (di:complement) ECOHU47 U00007 g405882 Escherichia coli 562 -11535239 234769 yeik orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 195 of 400 of the completegenome.) (nt:f313; 100 pct identical to yeik_ecoli sw: p33022) (le:7359) (re:8300) (di:complement) AE000305 AE000305 g1788486 Escherichia coli 562 -11535239 5000692741 (de:(ecoli_2111) (pn:hypothetical 33) (gn:yeik) (gtcfc:13.7:14.1) (ec:) (yeik_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2111 ECOLI_2111 Escherichia coli 562 10053337

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854378	11362	33518	378	125

Description

6500731382 yeil:b2163 hypothetical 25.3 kd protein in nfo-frua intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2163 b2163 Escherichia coli 562 -11535240 111610 yeil (de:hypothetical 25.3 kd protein in nfo-frua intergenic region) (db:swissprot) YEIL_ECOLI P33023 ESCHERICHIA COLI 562 -11535240 7000687653 yeil hypothetical 25.3 kd protein in nfo-frua intergenic region (db:pir2.dat) B64985 B64985 Escherichia coli 562 -11535240 7500923052 yeil (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:63099) (re:63758) (di:direct) ECOHU47 U00007 g405883 Escherichia coli 562 -11535240 234770 yeil putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 195 of 400 of the completegenome.) (nt:o219; 100 pct identical to yeil_ecoli sw: p33023) (le:8469) (re:9128) (di:direct) AE000305 AE000305 g1788487 Escherichia coli 562 -11535240 5000692742 (de:(ecoli_2112) (pn:hypothetical 25) (gn:yeil) (gtcfc:13.7:14.1) (ec:) (yeil_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2112 ECOLI_2112 Escherichia coli 562 10053338

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854379	11363	33519	1638	546

Description

6500731383 yeim:b2164 hypothetical 43.4 kd protein in nfo-frua intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2164 b2164 Escherichia coli 562 -11535241 111611 yeim (de:hypothetical 43.4 kd protein in nfo-frua intergenic region) (db:swissprot) YEIM_ECOLI P33024 ESCHERICHIA COLI 562 -11535241 7000687654 yeim hypothetical 43.4 kd protein in nfo-frua intergenic region (cl:pyrimidine nucleoside transport protein nupc) (db:pir2.dat) C64985 C64985 Escherichia coli 562 -11535241 7500923053 yeim (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:strong match to yeij; weaker match to ecnupc_1.) (le:63829) (re:65079) (di:complement) ECOHU47 U00007 g405886 Escherichia coli 562 -11535241 234771 yeim putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 195 of 400 of the completegenome.) (nt:f416; 100 pct identical to yeim_ecoli sw: p33024) (le:9199) (re:10449) (di:complement) AE000305 AE000305 g1788488 Escherichia coli 562 -11535241 5000692743 (de:(ecoli_2113) (pn:hypothetical 43) (gn:yeim) (gtcfc:13.7:14.1) (ec:) (yeim_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2113 ECOLI_2113 Escherichia coli 562 10053339

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854384	11364	33520	423	140

Description

6500731384 yein:b2165 hypothetical 32.9 kd protein in nfo-frua intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2165 b2165 Escherichia coli 562 -11535242 111613 yein (de:hypothetical 32.9 kd protein in nfo-frua intergenic region) (db:swissprot) YEIN_ECOLI P33025 ESCHERICHIA COLI 562 -11535242 7000687655 yein hypothetical 32.9 kd protein in nfo-frua intergenic region (db:pir2.dat) D64985 D64985 Escherichia coli 562 -11535242 7500923055 yein (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:65173) (re:66111) (di:complement) ECOHU47 U00007 g405885 Escherichia coli 562 -11535242 234772 yein orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 196 of 400 of the completegenome.) (nt:f312; 100 pct identical to yein_ecoli sw: p33025) (le:77) (re:1015) (di:complement) AE000306 AE000306 g1788490 Escherichia coli 562 -11535242 5000692744 (de:(ecoli_2114) (pn:hypothetical 32) (gn:yein) (gtcfc:13.7:14.1) (ec:) (yein_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2114 ECOLI_2114 Escherichia coli 562 10053341

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854386	11365	33521	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854411	11366	33522	303	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854424	11367	33523	417	138

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854425	11368	33524	1047	348

Description

6500731385 yeic:b2166 hypothetical 33.6 kd protein in nfo-frua intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2166 b2166 Escherichia coli 562 -11535243 111602 yeic (de:hypothetical sugar kinase in nfo-frua intergenic region) (db:swissprot) YEIC_ECOLI P30235 ESCHERICHIA COLI 562 -11535243 7000687646 yeic hypothetical 33.6k protein nfo-frua intergenic region (cl:yeii protein) (db:pir2.dat) E64985 E64985 Escherichia coli 562 -11535243 7500923044 yeic (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:similar to pfkb-fruk-gsk carbohydrate kinase family) (le:66099) (re:67040) (di:complement) ECOHU47 U00007 g405875 Escherichia coli 562 -11535243 234773 yeic putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 196 of 400 of the completegenome.) (nt:f313; 100 pct identical to yeic_ecoli sw: p30235) (le:1003) (re:1944) (di:complement) AE000306 AE000306 g1788491 Escherichia coli 562 -11535243 5000692745 (de:(ecoli_2115) (pn:hypothetical 33) (gn:yeic) (gtcfc:13.7:14.1) (ec:) (yeic_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2115 ECOLI_2115 Escherichia coli 562 10053330

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854434	11369	33525	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854461	11370	33526	216	71

Description

6500731386 yeio:b2170 hypothetical 42.7 kd protein in frub
5region:hypothetical 42.7 kd protein in frub-rtn intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2170
b2170 Escherichia coli 562 -11535244 111614 yeio (de:hypothetical 42.7 kd
protein in frub-spr intergenic region) (db:swissprot) YEIO_ECOLI P33026
ESCHERICHIA COLI 562 -11535244 7000687656 yeio probable membrane protein
yeio (db:pir2.dat) A64986 A64986 Escherichia coli 562 -11535244 224663 yeio
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #369(48.6-49.0
min.)) (nt:orf_id:o369#1; similar to (swissprot accession) (le:3548)
(re:4729) (di:direct) D90849 D90849 g1736836 Escherichia coli 562 -11535244
301303 yeio (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to
48 centisome region of e.coli k12 bhb2600.) (le:71607) (re:72788)
(di:direct) ECOHU47 U00007 g405884 Escherichia coli 562 -11535244 234777
yeio putative transport (fn:orf; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 196 of 400 of the completegenome.)
(nt:o393; 100 pct identical to yeio_ecoli sw: p33026) (le:6511) (re:7692)
(di:direct) AE000306 AE000306 g1788495 Escherichia coli 562 -11535244
5000692746 (de:(ecoli_2119) (pn:hypothetical 42) (gn:yeio)
(gtcfc:13.7:14.1) (ec:) (yeio_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2119 ECOLI_2119 Escherichia coli 562
10053342

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854462	11371	33527	882	293

Description

6500731387 yeip:b2171 hypothetical 30.9 kd protein in frub
5region:hypothetical 30.9 kd protein in frub-rtn intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2171
b2171 Escherichia coli 562 -11535245 111616 yeip (de:hypothetical 30.9 kd
protein in frub-spr intergenic region) (db:swissprot) YEIP_ECOLI P33028
ESCHERICHIA COLI 562 -11535245 7000687657 yeip hypothetical 30.9 kd protein
in frub 5region (db:pir2.dat) B64986 B64986 Escherichia coli 562 -11535245
224664 yeip elongation factor p ef-p . (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #369(48.6-49.0 min.)) (nt:orf_id:o369#3; similar to
(swissprot accession) (le:4880) (re:5707) (di:direct) D90849 D90849 g1736837
Escherichia coli 562 -11535245 301304 yeip (sr:escherichia coli k12
bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12
bhb2600.) (nt:homolog of elongation factor p.) (le:72939) (re:73766)
(di:direct) ECOHU47 U00007 g405887 Escherichia coli 562 -11535245 234778
yeip putative elongation factor (fn:putative factor; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 196 of 400 of the
completegenome.) (nt:o275; 100 pct identical to yeip_ecoli sw: p33028)
(le:7843) (re:8670) (di:direct) AE000306 AE000306 g1788496 Escherichia coli
562 -11535245 5000692747 (de:(ecoli_2120) (pn:hypothetical 30) (gn:yeip)
(gtcfc:13.7:14.1) (ec:) (yeip_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2120 ECOLI_2120 Escherichia coli 562
10053344

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854468	11372	33528	330	109

Description

6500731388 yeiq:b2172 hypothetical 54.0 kd protein in fruk
5region:hypothetical 54.0 kd protein in fruk-bcr intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2172
b2172 Escherichia coli 562 -11535246 111617 yeiq (de:hypothetical 54.0 kd
protein in frub-rtn intergenic region) (db:swissprot) YEIQ_ECOLI P33029
ESCHERICHIA COLI 562 -11535246 7000687658 yeiq hypothetical 54.0 kd protein
in fruk 5region (cl:conserved hypothetical protein yel070w) (db:pir2.dat)
C64986 C64986 Escherichia coli 562 -11535246 7500923056 yeiq
(sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome
region of e.coli k12 bhb2600.) (nt:strong match to mannitol dehydrogenase
(mtld).) (le:73989) (re:75455) (di:direct) ECOHU47 U00007 g405888
Escherichia coli 562 -11535246 234779 yeiq putative oxidoreductase
(fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli
k-12 mg1655 section 196 of 400 of the completgenome.) (nt:o488; 100 pct
identical to yeiq_ecoli sw: p33029) (le:8893) (re:10359) (di:direct)
AE000306 AE000306 g1788497 Escherichia coli 562 -11535246 5000692748
(de:(ecoli_2121) (pn:hypothetical 54) (gn:yeiq) (gtcfc:13.7:14.1) (ec:)
(yeiq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_2121 ECOLI_2121 Escherichia coli 562 10053345

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854480	11373	33529	222	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854496	11374	33530	897	298

Description

5000692750 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2174 b2174 Escherichia coli 562 -11535247
7000691566 hypothetical protein b2174 (db:pir2.dat) E64986 E64986
Escherichia coli 562 -11535247 7500960122 b2174 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
197 of 400 of the completgenome.) (nt:o249; this 249 aa orf is 25 pct
identical (22 gaps)) (le:1078) (re:1827) (di:direct) AE000307 AE000307
g1788500 Escherichia coli 562 -11535247 6500731389 hypothetical protein
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2174
b2174 Escherichia coli 562 -11535247

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854501	11375	33531	561	186

Description

6500731390 spr:b2175 hypothetical protein:lipoprotein precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2175 b2175 Escherichia coli 562 -11535248 4000708794 spr (de:lipoprotein spr precursor) (db:swissprot) SPR_ECOLI P77685 ESCHERICHIA COLI 562 -11535248 7000686660 hypothetical protein b2175 (cl:conserved hypothetical protein hi1314) (db:pir2.dat) F64986 F64986 Escherichia coli 562 -11535248 222979 spr spr (sr:escherichia coli (strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli dna for spr, complete cds.) (nt:similar to new lipoprotein c (nlpc,swiss prot) (le:379) (re:945) (di:direct) D86610 D86610 g1498150 Escherichia coli 562 -11535248 224667 probable lipoprotein nlpc homolog precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #369(48.6-49.0 min.)) (nt:orf_id:o369#8; similar to (swissprot accession) (le:9663) (re:10229) (di:direct) D90849 D90849 g1736840 Escherichia coli 562 -11535248 301307 spr putative lipoprotein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 197 of 400 of the completegenome.) (nt:o188; this 188 aa orf is 57 pct identical (3 gaps)) (le:2239) (re:2805) (di:direct) AE000307 AE000307 g1788501 Escherichia coli 562 -11535248 5000692751 (de:(ecoli_2124) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2124 ECOLI_2124 Escherichia coli 562 10119264

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854510	11376	33532	228	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854523	11377	33533	840	279

Description

6500731391 rtn:b2176 hypothetical protein:protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2176 b2176 Escherichia coli 562 -11535249 1500687032 rtn (de:rtn protein) (db:swissprot) RTN_ECOLI P76446 ESCHERICHIA COLI 562 -11535249 7000686529 hypothetical protein b2176 (db:pir2.dat) G64986 G64986 Escherichia coli 562 -11535249 224668 yjcc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #369(48.6-49.0 min.)) (nt:orf_id:o369#9; similar to (swissprot accession) (le:10410) (re:11966) (di:direct) D90849 D90849 g1736841 Escherichia coli 562 -11535249 301308 rtn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 197 of 400 of the completegenome.) (nt:o518; this 518 aa orf is 27 pct identical (26 gaps)) (le:2986) (re:4542) (di:direct) AE000307 AE000307 g1788502 Escherichia coli 562 -11535249 5000692752 (de:(ecoli_2125) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2125 ECOLI_2125 Escherichia coli 562 10063416

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854524	11378	33534	753	250

Description

6500731392 yeja:b2177 hypothetical protein in bcr 5 region:hypothetical 69.9 kd protein in rtn-bcr intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2177 b2177 Escherichia coli 562 -11535250 7000687660 yeja hypothetical protein in bcr 5 region (cl:periplasmic oligopeptide-binding protein) (db:pir2.dat) H64986 H64986 Escherichia coli 562 -11535250 7500923061 yeja orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 197 of 400 of the completegenome.) (nt:o606; 99 pct identical to 412 aa fragment) (le:4618) (re:6438) (di:direct) AE000307 AE000307 g1788503 Escherichia coli 562 -11535250 111623 yeja (de:hypothetical 69.9 kd protein in rtn-bcr intergenic region precursor) (db:swissprot) YEJA_ECOLI P33913 ESCHERICHIA COLI 562 -11535250 5000692753 (de:(ecoli_2126) (pn:hypothetical protein in bcr 5"region:fragment) (gn:yeja) (gtcfc:13.7:14.1) (ec:)) (yeja_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2126 ECOLI_2126 Escherichia coli 562 10123593

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854529	11379	33535	525	174

Description

6500731393 yejb:b2178 hypothetical 40.4 kd protein in bcr 5 region:hypothetical abc transporter permease protein yejb (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2178 b2178 Escherichia coli 562 -11535251 111624 yejb (de:hypothetical abc transporter permease protein yejb) (db:swissprot) YEJB_ECOLI P33914 ESCHERICHIA COLI 562 -11535251 7000687661 yejb hypothetical 40.4 kd protein in bcr 5 region (db:pir2.dat) A64987 A64987 Escherichia coli 562 -11535251 224670 yejb oligopeptide transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #369(48.6-49.0 min.)) (nt:orf_id:o369#13; similar to (swissprot accession) (le:13862) (re:14956) (di:direct) D90849 D90849 g1736843 Escherichia coli 562 -11535251 301310 yejb putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 197 of 400 of the completegenome.) (nt:o364; 99 pct identical to yejb_ecoli sw: p33914) (le:6439) (re:7533) (di:direct) AE000307 AE000307 g1788504 Escherichia coli 562 -11535251 5000692754 (de:(ecoli_2127) (pn:hypothetical 40) (gn:yejb) (gtcfc:13.7:14.1) (ec:) (yejb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2127 ECOLI_2127 Escherichia coli 562 10120021

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854549	11380	33536	438	145

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854553	11381	33537	213	70

Description

GTC ORF with score 201 to: (sr:baker's yeast) (db:genpept-pln2) (de:saccharomyces cerevisiae import protein tim9p (tim9) gene, nucleargene encoding mitochondrial protein, complete cds.) (nt:mitochondrial intermembrane space protein;) (le:1) (re:264) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854564	11382	33538	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854574	11383	33539	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854578	11384	33540	336	111

Description

6500731394 yeje:b2179 hypothetical 38.1 kd protein in bcr 5 region:hypothetical abc transporter permease protein yeje (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2179 b2179 Escherichia coli 562 -11535252 111627 yeje (de:hypothetical abc transporter permease protein yeje) (db:swissprot) YEJE_ECOLI P33915 ESCHERICHIA COLI 562 -11535252 7000687663 yeje hypothetical 38.1 kd protein in bcr 5 region (db:pir2.dat) B64987 B64987 Escherichia coli 562 -11535252 224671 yeje dciac protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #369(48.6-49.0 min.)) (nt:orf_id:o369#14; similar to (pir accession number) (le:14956) (re:15981) (di:direct) D90849 D90849 g1736844 Escherichia coli 562 -11535252 301311 probable tran...:yeja-yejb/c-y...:operon yeje (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:probable membrane-bound component of transport) (le:2326) (re:3351) (di:direct) ECOHU49 U00008 g405908 Escherichia coli 562 -11535252 234783 yeje putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 197 of 400 of the completegenome.) (nt:o341; 100 pct identical to yeje_ecoli sw: p33915) (le:7533) (re:8558) (di:direct) AE000307 AE000307 g1788505 Escherichia coli 562 -11535252 5000692755 (de:(ecoli_2128) (pn:hypothetical 38) (gn:yeje) (gtcfc:13.7:14.1) (ec:) (yeje_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2128 ECOLI_2128 Escherichia coli 562 10053355

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854580	11385	33541	840	279

Description

6500731395 yejf:b2180 hypothetical abc transporter in bcr
5region:hypothetical abc transporter atp-binding protein in frub-bcr
intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2180 b2180 Escherichia coli 562 -11535253 111628
yejf (de:hypothetical abc transporter atp-binding protein yejf)
(db:swissprot) YEJF_ECOLI P33916 ESCHERICHIA COLI 562 -11535253 7000687664
yejf probable oligopeptide transport protein yejf (cl:unassigned atp-binding
cassette proteins:atp-binding cassette homology) (db:pir2.dat) C64987 C64987
Escherichia coli 562 -11535253 7500923062 probable
tran...:yeja-yejb/c-y...:operon yejf (sr:escherichia coli k12 bhb2600)
(db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.)
(nt:abc-type atp-dependent transport protein, perhaps) (le:3353) (re:4942)
(di:direct) ECOHU49 U00008 g405909 Escherichia coli 562 -11535253 234784
yejf putative atp-binding component of a transport (fn:putative transport;
not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
197 of 400 of the completegenome.) (nt:o529; 100 pct identical to yejf_ecoli
sw: p33916) (le:8560) (re:10149) (di:direct) AE000307 AE000307 g1788506
Escherichia coli 562 -11535253 5000692756 (de:(ecoli_2129) (pn:hypothetical
abc transporter atp-binding protein in bcr 5"region) (gn:yejf)
(gtcfc:13.7:14.1) (ec:) (yejf_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2129 ECOLI_2129 Escherichia coli 562
10053356

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854583	11386	33542	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854584	11387	33543	837	278

Description

GTC ORF with score 156 to: (sr:mus musculus (strain:c57/bl6) adult male
liver cdna to mrna) (db:genpept-rod) (de:mouse mrna for protein tyrosine
phosphatase, partial cds.) (nt:nt1-60: transmembrane region, nt250-984:
ptpase) (le:<1) (re:1086) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854591	11388	33544	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854610	11389	33545	504	167

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854611	11390	33546	396	131

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854615	11391	33547	204	67

Description

6500731396 yejg:b2181 hypothetical 12.5 kd protein in bcr
5region:hypothetical 12.5 kd protein in rtn-bcr intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2181
b2181 Escherichia coli 562 -11535254 111629 yejg (de:hypothetical 12.5 kd
protein in rtn-bcr intergenic region) (db:swissprot) YEJG_ECOLI P33917
ESCHERICHIA COLI 562 -11535254 7000687665 yejg hypothetical 12.5 kd protein
in bcr 5region (db:pir2.dat) D64987 D64987 Escherichia coli 562 -11535254
7500923063 yejg (sr:escherichia coli k12 bhb2600) (db:genpept-bct1)
(de:centisome 49 region of e.coli k12 bhb2600.) (nt:gtg start codon.)
(le:4946) (re:5290) (di:complement) ECOHU49 U00008 g405910 Escherichia coli
562 -11535254 234785 yejg orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 197 of 400 of the
completegenome.) (nt:f114; 100 pct identical to yejg_ecoli sw: p33917)
(le:10153) (re:10497) (di:complement) AE000307 AE000307 g1788507 Escherichia
coli 562 -11535254 5000692757 (de:(ecoli_2130) (pn:hypothetical 12)
(gn:yejg) (gtcfc:13.7:14.1) (ec:) (yejg_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) ECOLI_2130 ECOLI_2130 Escherichia coli 562
10053357

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854618	11392	33548	1248	415

Description

6500731397 yejd:b2183 hypothetical 25.9 kd protein in bcr-rply intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2183 b2183 Escherichia coli 562 -11535255 111625 rsua (ec:4.2.1.70) (de:hydrolyase)) (db:swissprot) RSUA_ECOLI P33918 ESCHERICHIA COLI 562 -11535255 7000687662 yejd hypothetical 25.9 kd protein in bcr-rply intergenic region (cl:conserved hypothetical protein hi1243) (db:pir2.dat) F64987 F64987 Escherichia coli 562 -11535255 7500891163 yejd (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:match to orf from b.subtilis; weaker match to orf) (le:6841) (re:7536) (di:complement) ECOHU49 U00008 g405907 Escherichia coli 562 -11535255 234787 rsua 16s pseudouridylate 516 synthase (fn:enzyme; rna synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 198 of 400 of the completegenome.) (nt:f231; formerly designated yejd) (le:1415) (re:2110) (di:complement) AE000308 AE000308 g1788510 Escherichia coli 562 -11535255 5000692758 (de:(ecoli_2132) (pn:hypothetical 25) (gn:yejd) (gtcfc:13.7:14.1) (ec:) (yejd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2132 ECOLI_2132 Escherichia coli 562 10053353

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854620	11393	33549	261	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854634	11394	33550	228	75

Description

6500731398 yejk:b2186 hypothetical 37.8 kd protein in rply-prol intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2186 b2186 Escherichia coli 562 -11535256 111633 yejk (de:hypothetical 37.8 kd protein in rply-prol intergenic region) (db:swissprot) YEJK_ECOLI P33920 ESCHERICHIA COLI 562 -11535256 7000687667 yejk hypothetical 37.8 kd protein in rply-prol intergenic region (db:pir2.dat) A64988 A64988 Escherichia coli 562 -11535256 7500923065 yejk (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (le:9993) (re:11000) (di:complement) ECOHU49 U00008 g405914 Escherichia coli 562 -11535256 234791 yejk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 198 of 400 of the completegenome.) (nt:f335; 100 pct identical to yejk_ecoli sw: p33920) (le:4567) (re:5574) (di:complement) AE000308 AE000308 g1788513 Escherichia coli 562 -11535256 5000692760 (de:(ecoli_2135) (pn:hypothetical 37) (gn:yejk) (gtcfc:13.7:14.1) (ec:) (yejk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2135 ECOLI_2135 Escherichia coli 562 10053361

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854639	11395	33551	543	180

Description

6500731399 yejl:b2187 hypothetical 8.3 kd protein in rply-prol intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2187 b2187 Escherichia coli 562 -11535257 111635 yejl (de:hypothetical 8.3 kd protein in rply-prol intergenic region) (db:swissprot) YEJL_ECOLI P33921 ESCHERICHIA COLI 562 -11535257 7000687668 yejl hypothetical 8.3 kd protein in rply-prol intergenic region (cl:hypothetical protein hi0840) (db:pir2.dat) B64988 B64988 Escherichia coli 562 -11535257 7500923067 yejl (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (le:11182) (re:11409) (di:direct) ECOHU49 U00008 g405915 Escherichia coli 562 -11535257 234792 yejl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 198 of 400 of the completegenome.) (nt:o75; 100 pct identical to yejl_ecoli sw: p33921) (le:5756) (re:5983) (di:direct) AE000308 AE000308 g1788514 Escherichia coli 562 -11535257 5000692761 (de:(ecoli_2136) (pn:hypothetical 8) (gn:yejl) (gtcfc:13.7:14.1) (ec:) (yejl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2136 ECOLI_2136 Escherichia coli 562 10053363

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854643	11396	33552	186	61

Description

6500731400 yejm:b2188 hypothetical 67.3 kd protein in rply-prol intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2188 b2188 Escherichia coli 562 -11535258 111637 yejm (de:hypothetical 67.3 kd protein in rply-prol intergenic region) (db:swissprot) YEJM_ECOLI P33922 ESCHERICHIA COLI 562 -11535258 7000687669 yejm hypothetical 67.3 kd protein in rply-prol intergenic region (cl:hypothetical protein hi0841) (db:pir2.dat) C64988 C64988 Escherichia coli 562 -11535258 7500923069 yejm (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (le:11429) (re:13189) (di:direct) ECOHU49 U00008 g453987 Escherichia coli 562 -11535258 234793 yejm putative sulfatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 198 of 400 of the completengenome.) (nt:o586; 100 pct identical to yejm_ecoli sw: p33922) (le:6003) (re:7763) (di:direct) AE000308 AE000308 g1788515 Escherichia coli 562 -11535258 5000692762 (de:(ecoli_2137) (pn:hypothetical 67) (gn:yejm) (gtcfc:13.7:14.1) (ec:)) (yejm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2137 ECOLI_2137 Escherichia coli 562 10053365

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854645	11397	33553	624	207

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854647	11398	33554	603	200

Description

5000692764 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2191 b2191 Escherichia coli 562 -11535259 7000691567 hypothetical protein b2191 (db:pir2.dat) E64988 E64988 Escherichia coli 562 -11535259 7500960123 b2191 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 198 of 400 of the completengenome.) (nt:o40; this 40 aa orf is 38 pct identical (1 gap)) (le:10532) (re:10654) (di:direct) AE000308 AE000308 g1788517 Escherichia coli 562 -11535259 6500731401 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2191 b2191 Escherichia coli 562 -11535259

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854657	11399	33555	219	72

Description

6500731402 yojf:napd:b2207 hypothetical 9.5 kd protein in napa-napf
intergenic region:napd protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2207 b2207 Escherichia coli 562 -11535260 115261
napd (de:napd protein) (db:swissprot) NAPD_ECOLI P33938 ESCHERICHIA COLI 562
-11535260 7000685917 yojf hypothetical 9.5 kd protein in napa-napf
intergenic region (cl:hypothetical protein hi0343) (db:pir2.dat) E64990
E64990 Escherichia coli 562 -11535260 224674 yojf (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #373(49.5-49.9 min.))
(nt:orf_id:o372#2; similar to (swissprot accession) (le:2269) (re:2532)
(di:complement) D90850 D90850 g1736848 Escherichia coli 562 -11535260
301314 yojf (sr:escherichia coli k12 bhb2600) (db:genpept-bct1)
(de:centisome 49 region of e.coli k12 bhb2600.) (nt:may be part of aeg-46.5
operon.) (le:29801) (re:30064) (di:complement) ECOHU49 U00008 g405935
Escherichia coli 562 -11535260 234810 napd orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
199 of 400 of the completegenome.) (nt:f87; formerly designated yojf)
(le:12474) (re:12737) (di:complement) AE000309 AE000309 g1788535 Escherichia
coli 562 -11535260 5000692778 (de:(ecoli_2156) (pn:hypothetical 9)
(gn:yojf) (gtcfc:13.7:14.1) (ec:) (yojf_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2156 ECOLI_2156 Escherichia coli 562
10056986

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854659	11400	33556	1212	404

Description

6500731403 yoji:b2211 hypothetical abc transporter in eco-alkb intergenic region:hypothetical abc transporter atp-binding protein in eco-alkb intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2211 b2211 Escherichia coli 562 -11535261 115264 yoji (de:hypothetical abc transporter atp-binding protein yoji) (db:swissprot) YOJI_ECOLI P33941 ESCHERICHIA COLI 562 -11535261 7000688184 yoji hypothetical abc transporter in eco-alkb intergenic region (cl:atp-binding cassette homology) (db:pir2.dat) A64991 A64991 Escherichia coli 562 -11535261 224678 yoji atp-binding protein syrd. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #373(49.5-49.9 min..)) (nt:orf_id:o372#6; similar to (swissprot accession) (le:6490) (re:8133) (di:complement) D90850 D90850 g1736852 Escherichia coli 562 -11535261 301318 yoji (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:abc-type atp-dependent transport protein. match to) (le:34023) (re:35666) (di:complement) ECOHU49 U00008 g453991 Escherichia coli 562 -11535261 234814 yoji putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 200 of 400 of the completgenome.) (nt:f547; 100 pct identical to yoji_ecoli sw: p33941) (le:3292) (re:4935) (di:complement) AE000310 AE000310 g1788540 Escherichia coli 562 -11535261 5000692781 (de:(ecoli_2160) (pn:hypothetical abc transporter atp-binding protein in eco-alkb intergenic region) (gn:yoji) (gtcfc:13.7:14.1) (ec:) (yoji_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2160 ECOLI_2160 Escherichia coli 562 10056989

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854661	11401	33557	1344	448

Description

5000692789 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2225 b2225 Escherichia coli 562 -11535262 7000691568 hypothetical protein b2225 (db:pir2.dat) G64992 G64992 Escherichia coli 562 -11535262 7500960124 b2225 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 202 of 400 of the completgenome.) (nt:f258; this 258 aa orf is 27 pct identical (1 gap)) (le:67) (re:843) (di:complement) AE000312 AE000312 g1788556 Escherichia coli 562 -11535262 6500731404 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2225 b2225 Escherichia coli 562 -11535262

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854664	11402	33558	429	143

Description

5000692790 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2226 b2226 Escherichia coli 562 -11535263
7000691569 hypothetical protein b2226 (db:pir2.dat) H64992 H64992
Escherichia coli 562 -11535263 7500960125 b2226 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 202 of 400 of the completegenome.) (nt:f549; this 549 aa orf is 25 pct identical (5 gaps)) (le:848) (re:2497) (di:complement) AE000312 AE000312 g1788557 Escherichia coli 562 -11535263 6500731405 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2226 b2226 Escherichia coli 562 -11535263

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854670	11403	33559	1221	406

Description

5000692791 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2227 b2227 Escherichia coli 562 -11535264
7000691570 hypothetical protein b2227 (db:pir2.dat) A64993 A64993
Escherichia coli 562 -11535264 7500960126 b2227 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 202 of 400 of the completegenome.) (nt:f161) (le:2498) (re:2983) (di:complement) AE000312 AE000312 g1788558 Escherichia coli 562 -11535264 6500731406 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2227 b2227 Escherichia coli 562 -11535264

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854683	11404	33560	1584	527

Description

5000692792 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2228 b2228 Escherichia coli 562 -11535265
7000691571 hypothetical protein b2228 (db:pir2.dat) B64993 B64993
Escherichia coli 562 -11535265 7500960127 b2228 putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 202 of 400 of the completegenome.) (nt:f1337; 28 pct identical (10 gaps) to 149 residues) (le:2999) (re:7012) (di:complement) AE000312 AE000312 g1788559 Escherichia coli 562 -11535265 6500731407 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2228 b2228 Escherichia coli 562 -11535265

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854695	11405	33561	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854704	11406	33562	648	215

Description

5000692793 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2229 b2229 Escherichia coli 562 -11535266
7000691572 hypothetical protein b2229 (db:pir2.dat) C64993 C64993
Escherichia coli 562 -11535266 7500960128 b2229 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 202 of 400 of the completegenome.) (nt:f216; this 216 aa orf is 26 pct identical (7 gaps)) (le:7036) (re:7686) (di:complement) AE000312 AE000312 g1788560 Escherichia coli 562 -11535266 6500731408 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2229 b2229 Escherichia coli 562 -11535266

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854707	11407	33563	186	62

Description

6500731409 yfae:b2236 hypothetical 9.3 kd protein in nrdb
5region:hypothetical 9.3 kd protein in nrdb-inaa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2236 b2236 Escherichia coli 562 -11535267 111799 yfae (de:hypothetical 9.3 kd protein in nrdb-inaa intergenic region) (db:swissprot) YFAE_ECOLI P37910 ESCHERICHIA COLI 562 -11535267 7000687674 yfae hypothetical 9.3 kd protein in nrdb 5region (db:pir2.dat) B64994 B64994 Escherichia coli 562 -11535267 224742 yfae (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #377(50.5-50.9 min.)) (nt:similar to (swissprot accession number p37910)) (le:8798) (re:9052) (di:direct) D90855 D90855 g1799583 Escherichia coli 562 -11535267 7500923316 yfae orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 203 of 400 of the completegenome.) (nt:o84; 98 pct identical to yfae_ecoli sw: p37910) (le:9051) (re:9305) (di:direct) AE000313 AE000313 g1788568 Escherichia coli 562 -11535267 5000692796 (de:(ecoli_2185) (pn:hypothetical 9) (gn:yfae) (gtcfc:13.7:14.1) (ec:) (yfae_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2185 ECOLI_2185 Escherichia coli 562 10120043

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854710	11408	33564	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854714	11409	33565	297	98

Description

6500731410 yfah:b2238 hypothetical 7.5 kd protein in inaa-glpq intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2238 b2238 Escherichia coli 562 -11535268 111802 yfah (de:hypothetical 7.5 kd protein in inaa-glpq intergenic region) (db:swissprot) YFAH_ECOLI P45505 ESCHERICHIA COLI 562 -11535268 7000687675 yfah hypothetical 7.5 kd protein in inaa-glpq intergenic region (db:pir2.dat) D64994 D64994 Escherichia coli 562 -11535268 224744 yfah (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #377(50.5-50.9 min.)) (nt:similar to (swissprot accession number p45505)) (le:9971) (re:10177) (di:direct) D90855 D90855 g1799585 Escherichia coli 562 -11535268 7500923318 yfah orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 204 of 400 of the completegenome.) (nt:o68; 100 pct identical to yfah_ecoli sw: p45505) (le:138) (re:344) (di:direct) AE000314 AE000314 g1788571 Escherichia coli 562 -11535268 5000692798 (de:(ecoli_2187) (pn:hypothetical 7) (gn:yfah) (gtcfc:13.7:14.1) (ec:) (yfah_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2187 ECOLI_2187 Escherichia coli 562 10053530

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854716	11410	33566	423	140

Description

6500731411 yfad:b2244 hypothetical protein:hypothetical 34.9 kd protein in glpc-ais intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2244 b2244 Escherichia coli 562 -11535269 111798 yfad (de:hypothetical 34.9 kd protein in glpc-ais intergenic region) (db:swissprot) YFAD_ECOLI P37014 ESCHERICHIA COLI 562 -11535269 7000687673 hypothetical protein b2244 (db:pir2.dat) B64995 B64995 Escherichia coli 562 -11535269 224750 yhga (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #377(50.5-50.9 min.)) (nt:similar to (swissprot accession number p31667)) (le:17188) (re:18087) (di:direct) D90855 D90855 g1799591 Escherichia coli 562 -11535269 224754 yhga (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #379(50.8-51.2 min.)) (nt:similar to (swissprot accession number p31667)) (le:298) (re:1197) (di:direct) D90856 D90856 g1799596 Escherichia coli 562 -11535269 7500923315 yfad orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 204 of 400 of the completegenome.) (nt:o299; this 299 aa orf is 59 pct identical (3 gaps)) (le:7355) (re:8254) (di:direct) AE000314 AE000314 g1788577 Escherichia coli 562 -11535269 5000692799 (de:(ecoli_2193) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2193 ECOLI_2193 Escherichia coli 562 10120046

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854717	11411	33567	189	62

Description

5000692800 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2245 b2245 Escherichia coli 562 -11535270 7000691573 hypothetical protein b2245 (cl:2,4-dihydroxyhept-2-ene-1,7) (db:pir2.dat) C64995 C64995 Escherichia coli 562 -11535270 7500960129 b2245 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 204 of 400 of the completegenome.) (nt:f267; 45 pct identical (5 gaps) to yhaf_ecoli) (le:8493) (re:9296) (di:complement) AE000314 AE000314 g1788578 Escherichia coli 562 -11535270 6500731412 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2245 b2245 Escherichia coli 562 -11535270

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854739	11412	33568	441	146

Description

5000692801 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2246 b2246 Escherichia coli 562 -11535271
7000691574 hypothetical protein b2246 (db:pir2.dat) D64995 D64995
Escherichia coli 562 -11535271 7500960130 b2246 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 204 of 400 of the completegenome.) (nt:f442; 31 pct identical (9 gaps) to 425 residues) (le:9314) (re:10642) (di:complement) AE000314 AE000314 g1788579 Escherichia coli 562 -11535271 6500731413 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2246 b2246 Escherichia coli 562 -11535271

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854747	11413	33569	612	203

Description

5000692802 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2247 b2247 Escherichia coli 562 -11535272
7000691575 hypothetical protein b2247 (db:pir2.dat) E64995 E64995
Escherichia coli 562 -11535272 224758 yidu (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #379(50.8-51.2 min.)) (nt:similar to (swissprot accession number p31458)) (le:3602) (re:4819) (di:complement) D90856 D90856 g1799600 Escherichia coli 562 -11535272 7500960131 b2247 putative racemase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 204 of 400 of the completegenome.) (nt:f405; this 405 aa orf is 30 pct identical (25 gaps)) (le:10660) (re:11877) (di:complement) AE000314 AE000314 g1788580 Escherichia coli 562 -11535272 6500731414 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2247 b2247 Escherichia coli 562 -11535272

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854754	11414	33570	600	199

Description

5000692803 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2248 b2248 Escherichia coli 562 -11535273
7500923321 yfax (de:hypothetical transcriptional regulator in glpc-ais interegenic region) (db:swissprot) YFAX_ECOLI P77732 ESCHERICHIA COLI 562 -11535273 7000691576 hypothetical protein b2248 (db:pir2.dat) F64995 F64995 Escherichia coli 562 -11535273 224759 yjhi (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #379(50.8-51.2 min.)) (nt:similar to (swissprot accession number p39360)) (le:4822) (re:5604) (di:complement) D90856 D90856 g1799601 Escherichia coli 562 -11535273 7500923324 b2248 putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 204 of 400 of the completgenome.) (nt:f260; residues 71-246 are 30 pct identical to) (le:11880) (re:12662) (di:complement) AE000314 AE000314 g1788581 Escherichia coli 562 -11535273 6500731415 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2248 b2248 Escherichia coli 562 -11535273

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854765	11415	33571	243	80

Description

5000692804 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2249 b2249 Escherichia coli 562 -11535274
7000691577 hypothetical protein b2249 (db:pir2.dat) G64995 G64995 Escherichia coli 562 -11535274 224760 cina putative competence-damage protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #379(50.8-51.2 min.)) (nt:similar to (swissprot accession number p46323)) (le:5824) (re:7026) (di:complement) D90856 D90856 g1799602 Escherichia coli 562 -11535274 7500960132 b2249 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completgenome.) (nt:f400; this 400 aa orf is 37 pct identical (0 gaps)) (le:140) (re:1342) (di:complement) AE000315 AE000315 g1788583 Escherichia coli 562 -11535274 6500731416 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2249 b2249 Escherichia coli 562 -11535274

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854767	11416	33572	1158	385

Description

5000692805 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2250 b2250 Escherichia coli 562 -11535275
7000691578 hypothetical protein b2250 (db:pir2.dat) H64995 H64995
Escherichia coli 562 -11535275 7500960133 b2250 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completegenome.) (nt:f187; this 187 aa orf is 27 pct identical (12 gaps)) (le:1442) (re:2005) (di:complement) AE000315 AE000315 g1788584 Escherichia coli 562 -11535275 6500731417 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2250 b2250 Escherichia coli 562 -11535275

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854770	11417	33573	492	163

Description

6500731418 yfao:b2251 hypothetical protein:hypothetical 16.4 kd protein in glpc-ais intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2251 b2251 Escherichia coli 562 -11535276 111806 yfao (de:hypothetical 16.4 kd protein in glpc-ais intergenic region) (db:swissprot) YFAO_ECOLI P52006 ESCHERICHIA COLI 562 -11535276 7000687677 hypothetical protein b2251 (cl:mutt domain homology) (db:pir2.dat) A64996 A64996 Escherichia coli 562 -11535276 224761 yfao (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #379(50.8-51.2 min.)) (nt:similar to (swissprot accession number p52006)) (le:7946) (re:8371) (di:direct) D90856 D90856 g1799603 Escherichia coli 562 -11535276 7500923320 yfao orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completegenome.) (nt:o141; this 141 aa orf is 30 pct identical (8 gaps)) (le:2263) (re:2688) (di:direct) AE000315 AE000315 g1788585 Escherichia coli 562 -11535276 5000692806 (de:(ecoli_2200) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2200 ECOLI_2200 Escherichia coli 562 10120056

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854775	11418	33574	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854800	11419	33575	339	112
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854806	11420	33576	375	124
<u>Description</u>				

GTC ORF with score 103 to: (db:genpept-bct2) (de:salmonella typhimurium strain lt2 nadp+-linked malic enzyme (maeb),partial cds; insertion element is200 transposase, complete cds; eutoperon, complete sequence; and unknown genes.) (le:2386) (re:3075) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854808	11421	33577	549	182
<u>Description</u>				

5000692808 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2253 b2253 Escherichia coli 562 -11535277
7500923338 yfbe (de:hypothetical 42.9 kd protein in ais-pmrd intergenic region) (db:swissprot) YFBE_ECOLI P77690 ESCHERICHIA COLI 562 -11535277
7000689058 hypothetical protein b2253 (cl:erythromycin resistance protein) (db:pir2.dat) C64996 C64996 Escherichia coli 562 -11535277 224763 ipa-65d spore coat polysaccharide biosynthesis protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #379(50.8-51.2 min.)) (nt:similar to (swissprot accession number p39623)) (le:9287) (re:10459) (di:direct) D90856 D90856 g1799605 Escherichia coli 562 -11535277 7500923341 b2253 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completegenome.) (nt:o390; this 390 aa orf is 45 pct identical (4 gaps)) (le:3604) (re:4776) (di:direct) AE000315 AE000315 g1788587 Escherichia coli 562 -11535277
6500731419 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2253 b2253 Escherichia coli 562 -11535277

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854811	11422	33578	2163	720

Description

5000692809 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2254 b2254 Escherichia coli 562 -11535278
7500923342 ybf (de:hypothetical 36.3 kd protein in ais-pmrd intergenic region) (db:swissprot) YBF_ECOWI P77757 ESCHERICHIA COLI 562 -11535278
7000691579 hypothetical protein b2254 (cl:stress response protein csbb) (db:pir2.dat) D64996 D64996 Escherichia coli 562 -11535278 224764 dpm1 dolichol-phosphate mannosyltransferase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #379(50.8-51.2 min.)) (nt:similar to (swissprot accession number p14020)) (le:10463) (re:11431) (di:direct) D90856 D90856 g1799606 Escherichia coli 562 -11535278 7500923345 b2254 putative sugar transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completegenome.) (nt:o322; this 322 aa orf is 26 pct identical (16 gaps)) (le:4780) (re:5748) (di:direct) AE000315 AE000315 g1788588 Escherichia coli 562 -11535278 6500731420 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2254 b2254 Escherichia coli 562 -11535278

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854820	11423	33579	1023	341

Description

5000692810 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2255 b2255 Escherichia coli 562 -11535279
7000691580 hypothetical protein b2255 (db:pir2.dat) E64996 E64996 Escherichia coli 562 -11535279 224765 fmt methionyl-trna formyltransferase ec 2.1.2.9 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #379(50.8-51.2 min.)) (nt:similar to (swissprot accession number p23882)) (le:11431) (re:13413) (di:direct) D90856 D90856 g1799607 Escherichia coli 562 -11535279 224769 fmt methionyl-trna formyltransferase ec 2.1.2.9 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #380(51.1-51.4 min.)) (nt:similar to (swissprot accession number p23882)) (le:666) (re:2648) (di:direct) D90857 D90857 g1799612 Escherichia coli 562 -11535279 7500960134 b2255 putative transformylase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completegenome.) (nt:o660; this 660 aa orf is 30 pct identical (9 gaps)) (le:5748) (re:7730) (di:direct) AE000315 AE000315 g1788589 Escherichia coli 562 -11535279 6500731421 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2255 b2255 Escherichia coli 562 -11535279

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854847	11424	33580	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854857	11425	33581	318	105

Description

5000692811 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2256 b2256 Escherichia coli 562 -11535280
7000691581 hypothetical protein b2256 (db:pir2.dat) F64996 F64996
Escherichia coli 562 -11535280 7500960135 b2256 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completegenome.) (nt:o296; this 296 aa orf is 24 pct identical (2 gaps)) (le:7727) (re:8617) (di:direct) AE000315 AE000315
g1788590 Escherichia coli 562 -11535280 6500731422 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2256 b2256 Escherichia coli 562 -11535280

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854861	11426	33582	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854862	11427	33583	1236	411

Description

5000692812 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2257 b2257 Escherichia coli 562 -11535281
7000691582 hypothetical protein b2257 (db:pir2.dat) G64996 G64996
Escherichia coli 562 -11535281 7500960136 b2257 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completegenome.) (nt:o550; this 550 aa orf is 24 pct identical (23 gaps)) (le:8617) (re:10269) (di:direct) AE000315 AE000315
g1788591 Escherichia coli 562 -11535281 6500731423 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2257 b2257 Escherichia coli 562 -11535281

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854864	11428	33584	453	150

Description

5000692813 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2258 b2258 Escherichia coli 562 -11535282
7000691583 hypothetical protein b2258 (db:pir2.dat) H64996 H64996
Escherichia coli 562 -11535282 7500960137 b2258 putative transport/receptor protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completegenome.) (nt:o222; this 222 aa orf is 25 pct identical (9 gaps)) (le:10319) (re:10987) (di:direct) AE000315 AE000315 g1788592 Escherichia coli 562 -11535282 6500731424 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2258 b2258 Escherichia coli 562 -11535282

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854873	11429	33585	1293	430

Description

6500731425 elab:b2266 hypothetical protein:elab protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2266 b2266 Escherichia coli 562 -11535283 111816 elab (de:elab protein) (db:swissprot) ELAB_ECOLI P52084 ESCHERICHIA COLI 562 -11535283 7000685148 hypothetical protein b2266 (cl:conserved hypothetical protein b2672) (db:pir2.dat) H64997 H64997 Escherichia coli 562 -11535283 224780 yfbd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #380(51.1-51.4 min.)) (nt:similar to (swissprot accession number p52084)) (le:13349) (re:13654) (di:complement) D90857 D90857 g1799623 Escherichia coli 562 -11535283 224787 yfbd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #401(51.3-51.6 min.)) (nt:similar to (swissprot accession number p52084)) (le:2808) (re:3113) (di:complement) D90858 D90858 g1799631 Escherichia coli 562 -11535283 7500880985 elab (sr:escherichia coli strain=k12) (db:genpept-bct1) (de:escherichia coli ela locus, menf gene, partial cds, elab, elaa,elac and elad genes, complete cds.) (nt:putative 10 kd protein) (le:728) (re:1033) (di:complement) ECU58768 U58768 g1381659 Escherichia coli 562 -11535283 239739 elab orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 206 of 400 of the completegenome.) (nt:f101; 41 pct identical amino acid sequence and) (le:7144) (re:7449) (di:complement) AE000316 AE000316 g1788601 Escherichia coli 562 -11535283 5000692816 (de:(ecoli_2215) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2215 ECOLI_2215 Escherichia coli 562 10120072

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854890	11430	33586	534	177

Description

6500731426 elaa:b2267 hypothetical protein:elaa protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2267 b2267
Escherichia coli 562 -11535284 111815 elaa (de:elaa protein) (db:swissprot)
ELAA_ECOLI P52077 ESCHERICHIA COLI 562 -11535284 7000685147 hypothetical
protein b2267 (cl:hypothetical protein b2267) (db:pir2.dat) A64998 A64998
Escherichia coli 562 -11535284 224781 yfbc (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #380(51.1-51.4 min.)) (nt:similar to
(swissprot accession number p52077)) (le:13709) (re:14170) (di:complement)
D90857 D90857 g1799624 Escherichia coli 562 -11535284 224788 yfbc
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #401(51.3-51.6
min.)) (nt:similar to (swissprot accession number p52077)) (le:3168)
(re:3629) (di:complement) D90858 D90858 g1799632 Escherichia coli 562
-11535284 7500880984 elaa (sr:escherichia coli strain=k12)
(db:genpept-bct1) (de:escherichia coli ela locus, menf gene, partial cds,
elab, elaa,elac and elad genes, complete cds.) (nt:putative 17 kd protein)
(le:1088) (re:1549) (di:complement) ECU58768 U58768 g1381660 Escherichia
coli 562 -11535284 239740 elaa orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 206 of 400 of the
completegenome.) (nt:f153; this 153 aa orf is 38 pct identical (4 gaps))
(le:7504) (re:7965) (di:complement) AE000316 AE000316 g1788602 Escherichia
coli 562 -11535284 5000692817 (de:(ecoli_2216) (pn:function not assigned)
(gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia
coli)) ECOLI_2216 ECOLI_2216 Escherichia coli 562 10120073

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854898	11431	33587	750	249

Description

6500731427 elac:b2268 hypothetical protein:elac protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2268 b2268 Escherichia coli 562 -11535285 1500687382 elac (de:elac protein) (db:swissprot) ELAC_ECOLI Q47012 ESCHERICHIA COLI 562 -11535285 7000685149 hypothetical protein b2268 (cl:conserved hypothetical protein mj1502) (db:pir2.dat) B64998 B64998 Escherichia coli 562 -11535285 224782 yqjk (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #380(51.1-51.4 min.)) (nt:similar to (swissprot accession number p54548)) (le:14217) (re:15152) (di:direct) D90857 D90857 g1799625 Escherichia coli 562 -11535285 224789 yqjk (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #401(51.3-51.6 min.)) (nt:similar to (swissprot accession number p54548)) (le:3676) (re:4611) (di:direct) D90858 D90858 g1799633 Escherichia coli 562 -11535285 7500880986 elac orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 206 of 400 of the completegenome.) (nt:o311; this 311 aa orf is 35 pct identical (9 gaps)) (le:8012) (re:8947) (di:direct) AE000316 AE000316 g1788603 Escherichia coli 562 -11535285 5000692818 (de:(ecoli_2217) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2217 ECOLI_2217 Escherichia coli 562 10064854

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854906	11432	33588	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854913	11433	33589	1128	375

Description

6500731428 elad:b2269 hypothetical protein:elad protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2269 b2269 Escherichia coli 562 -11535286 7000691584 hypothetical protein b2269 (db:pir2.dat) C64998 C64998 Escherichia coli 562 -11535286 7500960138 elad putative sulfatase / phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 206 of 400 of the completegenome.) (nt:o403; this 403 aa orf is 18 pct identical (19 gaps)) (le:9135) (re:10346) (di:direct) AE000316 AE000316 g1788604 Escherichia coli 562 -11535286 5000692819 (de:(ecoli_2218) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2218 ECOLI_2218 Escherichia coli 562 10123622

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854925	11434	33590	324	107

Description

6500731429 yfbk:b2270 hypothetical protein:hypothetical 63.6 kd protein in elad-nuon intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2270 b2270 Escherichia coli 562 -11535287
 1500686263 yfbk (de:hypothetical 63.6 kd protein in elad-nuon intergenic region) (db:swissprot) YFBK_ECOLI P76481 ESCHERICHIA COLI 562 -11535287
 7000687678 hypothetical protein b2270 (db:pir2.dat) D64998 D64998 Escherichia coli 562 -11535287 7500923346 yfbk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f575; this 575 aa orf is 25 pct identical (24 gaps)) (le:66) (re:1793) (di:complement) AE000317 AE000317 g1788606 Escherichia coli 562 -11535287 5000692820 (de:(ecoli_2219) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2219 ECOLI_2219 Escherichia coli 562 10061016

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854927	11435	33591	414	137

Description

6500731430 yfbl:b2271 hypothetical protein:hypothetical 36.2 kd protein in elad-nuon intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2271 b2271 Escherichia coli 562 -11535288
 7000687679 hypothetical protein b2271 (db:pir2.dat) E64998 E64998 Escherichia coli 562 -11535288 7500960140 yfbl putative aminopeptidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:o325; this 325 aa orf is 28 pct identical (17 gaps)) (le:1925) (re:2902) (di:direct) AE000317 AE000317 g1788607 Escherichia coli 562 -11535288 1500686264 yfbl_ecoli (de:hypothetical 36.2 kd protein in elad-nuon intergenic region,) P76482 P76482 Escherichia coli 562 -11535288 5000692821 (de:(ecoli_2220) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2220 ECOLI_2220 Escherichia coli 562 10061017

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854938	11436	33592	1002	333

Description

6500731431 yfbm:b2272 hypothetical protein:hypothetical 19.0 kd protein in elad-nuon intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2272 b2272 Escherichia coli 562 -11535289
 1500686265 yfbm (de:hypothetical 19.0 kd protein in elad-nuon intergenic region) (db:swissprot) YFBM_ECOLI P76483 ESCHERICHIA COLI 562 -11535289
 7000687680 hypothetical protein b2272 (db:pir2.dat) F64998 F64998 Escherichia coli 562 -11535289 7500923348 yfbm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:o167) (le:3005) (re:3508) (di:direct) AE000317 AE000317 g1788608 Escherichia coli 562 -11535289 5000692822 (de:(ecoli_2221) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2221 ECOLI_2221 Escherichia coli 562 10061018

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854965	11437	33593	1563	520

Description

6500731432 yfbn:b2273 hypothetical protein:hypothetical 28.0 kd protein in elad-nuon intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2273 b2273 Escherichia coli 562 -11535290
 1500686266 yfbn (de:hypothetical 28.0 kd protein in elad-nuon intergenic region) (db:swissprot) YFBN_ECOLI P76484 ESCHERICHIA COLI 562 -11535290
 7000687681 hypothetical protein b2273 (db:pir2.dat) G64998 G64998 Escherichia coli 562 -11535290 7500923349 yfbn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:f238; this 238 aa orf is 20 pct identical (8 gaps)) (le:3781) (re:4497) (di:complement) AE000317 AE000317 g1788609 Escherichia coli 562 -11535290 5000692823 (de:(ecoli_2222) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2222 ECOLI_2222 Escherichia coli 562 10061019

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854966	11438	33594	819	272

Description

5000692824 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2274 b2274 Escherichia coli 562 -11535291
7000691585 hypothetical protein b2274 (db:pir2.dat) H64998 H64998
Escherichia coli 562 -11535291 7500960141 b2274 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:ol58) (le:4652) (re:5128) (di:direct) AE000317 AE000317 gl788610 Escherichia coli 562 -11535291 6500731433
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2274 b2274 Escherichia coli 562 -11535291

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854978	11439	33595	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854979	11440	33596	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854981	11441	33597	468	155

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501854982	11442	33598	489	162

Description

GTC ORF with score 179 to: (or:Anolis pulchellus) (fn:precursor of yolk proteins, serum transport) (db:genpept-vrt) (de:anolis pulchellus vitellogenin mrna, partial cds.) (nt:apvtg5; similar to chicken and xenopus phosvitin) (le:<1) (re:546) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854993	11443	33599	690	229

Description

5000692825 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2275 b2275 Escherichia coli 562 -11535292
 7000691586 hypothetical protein b2275 (db:pir2.dat) A64999 A64999
 Escherichia coli 562 -11535292 7500960142 b2275 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 207 of 400 of the completegenome.) (nt:o283; this 283 aa orf is 20 pct identical (5 gaps)) (le:5184) (re:6035) (di:direct) AE000317 AE000317 g1788611 Escherichia coli 562 -11535292 6500731434 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2275 b2275 Escherichia coli 562 -11535292

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501854997	11444	33600	1116	371

Description

5000692827 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2290 b2290 Escherichia coli 562 -11535293
 7000691587 hypothetical protein b2290 (db:pir2.dat) H65000 H65000
 Escherichia coli 562 -11535293 224814 aspartate aminotransferase ec 2.6.1.1 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #404(51.7-52.1 min.)) (nt:similar to (swissprot accession number p23034)) (le:10880) (re:12097) (di:direct) D90860 D90860 g1799660 Escherichia coli 562 -11535293 7500960143 b2290 putative aminotransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 208 of 400 of the completegenome.) (nt:o405; residues 6-400 are 76 pct identical to) (le:3687) (re:4904) (di:direct) AE000318 AE000318 g1788627 Escherichia coli 562 -11535293 6500731435 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2290 b2290 Escherichia coli 562 -11535293

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855010	11445	33601	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855013	11446	33602	582	193

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855017	11447	33603	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855034	11448	33604	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855071	11449	33605	384	127

Description

5000692828 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2291 b2291 Escherichia coli 562 -11535294
7000691588 hypothetical protein b2291 (db:pir2.dat) A65001 A65001 Escherichia coli 562 -11535294 7500960144 b2291 putative alpha helix protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 208 of 400 of the completegenome.) (nt:o199) (le:4988) (re:5587) (di:direct) AE000318 AE000318 g1788628 Escherichia coli 562 -11535294 6500731436 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2291 b2291 Escherichia coli 562 -11535294

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855073	11450	33606	297	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855076	11451	33607	588	195

Description

6500731437 yfbs:b2292 hypothetical protein:hypothetical 65.9 kd protein in lrha-acka intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2292 b2292 Escherichia coli 562 -11535295
4000709406 yfbs (de:hypothetical 65.9 kd protein in lrha-acka intergenic region) (db:swissprot) YFBS_ECOLI P77741 ESCHERICHIA COLI 562 -11535295
7000687682 hypothetical protein b2292 (db:pir2.dat) B65001 B65001 Escherichia coli 562 -11535295 224815 ag45 46 kd membrane protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #404(51.7-52.1 min.)) (nt:similar to (swissprot accession number p46838)) (le:12839) (re:14671) (di:complement) D90860 D90860 g1799661 Escherichia coli 562 -11535295 7500923350 yfbs putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 208 of 400 of the completegenome.) (nt:f610; this 610 aa orf is 26 pct identical (8 gaps)) (le:5646) (re:7478) (di:complement) AE000318 AE000318 g1788629 Escherichia coli 562 -11535295 5000692829 (de:(ecoli_2241) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2241 ECOLI_2241 Escherichia coli 562 10120093

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501855078	11452	33608	501	166

Description

5000692830 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2293 b2293 Escherichia coli 562 -11535296
7500923351 yfbt (de:hypothetical 23.7 kd protein in lrha-acka intergenic
region) (db:swissprot) YFBT_ECOLI P77625 ESCHERICHIA COLI 562 -11535296
7000691589 hypothetical protein b2293 (cl:hypothetical protein b2690)
(db:pir2.dat) C65001 C65001 Escherichia coli 562 -11535296 224816 dogl
2-deoxyglucose-6-phosphate phosphatase 1 ec (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #404(51.7-52.1 min.)) (nt:similar to
(swissprot accession number p38774)) (le:14758) (re:15426) (di:complement)
D90860 D90860 g1799662 Escherichia coli 562 -11535296 7500923353 dogl
2-deoxyglucose-6-phosphate phosphatase 1 ec (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #405(52.0-52.3 min.)) (nt:similar to
(swissprot accession number p38774)) (le:1428) (re:2096) (di:complement)
D90861 D90861 g1799667 Escherichia coli 562 -11535296 7500923354 yfbt
putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 208 of 400 of the completengenome.)
(nt:f222; this 222 aa orf is 35 pct identical (15 gaps)) (le:7565) (re:8233)
(di:complement) AE000318 AE000318 g1788630 Escherichia coli 562 -11535296
224820 dogl 2-deoxyglucose-6-phosphate phosphatase 1 ec (sr:escherichia
coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #404(51.7-52.1 min.)) (nt:similar to
(swissprot accession number p38774)) (le:14758) (re:15426) (di:complement)
D90860 D90860 g1799662 Escherichia coli 562 -11535296 6500731438
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2293 b2293 Escherichia coli 562 -11535296

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501855079	11453	33609	363	120

Description

5000692831 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2294 b2294 Escherichia coli 562 -11535297
7000691590 hypothetical protein b2294 (cl:hypothetical protein mjecs11)
(db:pir2.dat) D65001 D65001 Escherichia coli 562 -11535297 7500960145 b2294
orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 208 of 400 of the completengenome.) (nt:f170; this
170 aa orf is 38 pct identical (7 gaps)) (le:8226) (re:8738) (di:complement)
AE000318 AE000318 g1788631 Escherichia coli 562 -11535297 6500731439
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2294 b2294 Escherichia coli 562 -11535297

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855091	11454	33610	1332	443

Description

5000692832 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2295 b2295 Escherichia coli 562 -11535298
7000689503 hypothetical protein b2295 (cl:hypothetical protein hil205) (db:pir2.dat) E65001 E65001 Escherichia coli 562 -11535298 224817 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #404(51.7-52.1 min.)) (nt:similar to (swissprot accession number p44127)) (le:15996) (re:16451) (di:complement) D90860 D90860 g1799663 Escherichia coli 562 -11535298 224821 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #405(52.0-52.3 min.)) (nt:similar to (swissprot accession number p44127)) (le:2666) (re:3121) (di:complement) D90861 D90861 g1799668 Escherichia coli 562 -11535298 7500955805 b2295 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 208 of 400 of the completegenome.) (nt:f151; residues 75-137 are 50 pct identical to) (le:8803) (re:9258) (di:complement) AE000318 AE000318 g1788632 Escherichia coli 562 -11535298 6500731440 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2295 b2295 Escherichia coli 562 -11535298

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855108	11455	33611	648	215

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855109	11456	33612	702	233

Description

5000692833 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2298 b2298 Escherichia coli 562 -11535299
7000691591 hypothetical protein b2298 (db:pir2.dat) H65001 H65001 Escherichia coli 562 -11535299 7500960146 yfcc putative s-transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 209 of 400 of the completegenome.) (nt:o513; this 513 aa orf is 31 pct identical (30 gaps)) (le:2381) (re:3922) (di:direct) AE000319 AE000319 g1788636 Escherichia coli 562 -11535299 6500731441 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2298 b2298 Escherichia coli 562 -11535299

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855114	11457	33613	588	195

Description

5000692834 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2299 b2299 Escherichia coli 562 -11535300
7000691592 hypothetical protein b2299 (db:pir2.dat) A65002 A65002
Escherichia coli 562 -11535300 7500960147 b2299 putative regulator
(fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 209 of 400 of the completegenome.) (nt:f180; this
180 aa orf is 32 pct identical (2 gaps)) (le:3955) (re:4497) (di:complement)
AE000319 AE000319 g1788637 Escherichia coli 562 -11535300 6500731442
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2299 b2299 Escherichia coli 562 -11535300

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855121	11458	33614	525	174

Description

6500731443 yfce:b2300 hypothetical protein:hypothetical 20.1 kd protein in
pta-folx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2300 b2300 Escherichia coli 562 -11535301
1500686267 yfce (de:hypothetical 20.1 kd protein in pta-folx intergenic
region) (db:swissprot) YFCE_ECOLI P76495 ESCHERICHIA COLI 562 -11535301
7000687684 hypothetical protein b2300 (db:pir2.dat) B65002 B65002
Escherichia coli 562 -11535301 7500923368 yfce orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
209 of 400 of the completegenome.) (nt:f184; this 184 aa orf is 29 pct
identical (12 gaps)) (le:4555) (re:5109) (di:complement) AE000319 AE000319
g1788638 Escherichia coli 562 -11535301 5000692835 (de:(ecoli_2249)
(pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) ECOLI_2249 ECOLI_2249 Escherichia
coli 562 10061020

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855141	11459	33615	918	305

Description

6500731444 yfcf:b2301 hypothetical protein:hypothetical 24.3 kd protein in pta-folx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2301 b2301 Escherichia coli 562 -11535302 1500686162 yfcf (de:hypothetical 24.3 kd protein in pta-folx intergenic region) (db:swissprot) YFCF_ECOLI P77544 ESCHERICHIA COLI 562 -11535302 7000687685 hypothetical protein b2301 (db:pir2.dat) C65002 C65002 Escherichia coli 562 -11535302 224825 carsr8 glutathione s-transferase 1 ec 2.5.1.18 sr8 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #405(52.0-52.3 min.)) (nt:similar to (swissprot accession number p28342)) (le:9830) (re:10474) (di:complement) D90861 D90861 g1799672 Escherichia coli 562 -11535302 224834 carsr8 glutathione s-transferase 1 ec 2.5.1.18 sr8 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (swissprot accession number p28342)) (le:3418) (re:4062) (di:complement) D90862 D90862 g1799682 Escherichia coli 562 -11535302 7500923369 yfcf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 209 of 400 of the completegenome.) (nt:f214; this 214 aa orf is 30 pct identical (3 gaps)) (le:5162) (re:5806) (di:complement) AE000319 AE000319 g1788639 Escherichia coli 562 -11535302 5000692836 (de:(ecoli_2250) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2250 ECOLI_2250 Escherichia coli 562 10060719

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855144	11460	33616	207	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855155	11461	33617	285	94

Description

6500731445 yfcg:b2302 hypothetical protein:hypothetical 24.5 kd protein in pta-folx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2302 b2302 Escherichia coli 562 -11535303
1500686163 yfcg (de:hypothetical 24.5 kd protein in pta-folx intergenic region) (db:swissprot) YFCG_ECOLI P77526 ESCHERICHIA COLI 562 -11535303
7000687686 hypothetical protein b2302 (cl:hypothetical protein b2302) (db:pir2.dat) D65002 D65002 Escherichia coli 562 -11535303 224826 n1165 ure2 protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #405(52.0-52.3 min.)) (nt:similar to (swissprot accession number p23202)) (le:10610) (re:11257) (di:direct) D90861 D90861 g1799673 Escherichia coli 562 -11535303 224835 n1165 ure2 protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (swissprot accession number p23202)) (le:4198) (re:4845) (di:direct) D90862 D90862 g1799683 Escherichia coli 562 -11535303 7500923370 yfcg putative s-transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 209 of 400 of the completegenome.) (nt:o215; residues 70-169 are 49 pct identical (2 gaps)) (le:5942) (re:6589) (di:direct) AE000319 AE000319 g1788640 Escherichia coli 562 -11535303 5000692837 (de:(ecoli_2251) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2251 ECOLI_2251 Escherichia coli 562 10060720

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855156	11462	33618	447	148

Description

6500731446 folx:b2303 hypothetical protein:d-erythro-7:8-dihydroneopterin triphosphate epimerase:dihydroneopterin triphosphate 2-epimerase (gtcfc:14.1) (ec:5.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2303 b2303 Escherichia coli 562 -11535304 7000691593 hypothetical protein b2303 (db:pir2.dat) E65002 E65002 Escherichia coli 562 -11535304 224827 ygig (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #405(52.0-52.3 min.)) (nt:similar to (swissprot accession number p31055)) (le:11314) (re:11676) (di:direct) D90861 D90861 g1799674 Escherichia coli 562 -11535304 224836 ygig (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (swissprot accession number p31055)) (le:4902) (re:5264) (di:direct) D90862 D90862 g1799684 Escherichia coli 562 -11535304 7500960148 folx 7:8 dihydroneopterintriphosphate epimerase (db:genpept-bct1) (de:e.coli folx gene.) (le:160) (re:522) (di:direct) ECFOLXG X96709 g1770237 Escherichia coli 562 -11535304 232909 folx d-erythro-7:8-dihydroneopterin tri p epimerase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 209 of 400 of the completegenome.) (nt:o120) (le:6646) (re:7008) (di:direct) AE000319 AE000319 g1788641 Escherichia coli 562 -11535304 5000692838 (de:(ecoli_2252) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2252 ECOLI_2252 Escherichia coli 562 10120100

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855160	11463	33619	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855176	11464	33620	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855181	11465	33621	627	208

Description

GTC ORF with score 168 to: (or:Homo sapiens) (sr:human) (db:genpept-pri2)
 (de:homo sapiens chromosome 19, cosmid r32516, complete sequence.)
 (nt:hypothetical partial protein; most similar to) (le:<2487:2694:3741)
 (re:2603:2856:3886) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855182	11466	33622	594	198

Description

5000692839 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli) b2304 b2304 Escherichia coli 562 -11535305
 7000691594 hypothetical protein b2304 (cl:cell division inhibitor yfhf)
 (db:pir2.dat) F65002 F65002 Escherichia coli 562 -11535305 224828
 mtcyl90.27 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
 minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
 #405(52.0-52.3 min.)) (nt:similar to (swissprot accession number q10403))
 (le:11697) (re:12590) (di:direct) D90861 D90861 g1799675 Escherichia coli
 562 -11535305 224837 mtcyl90.27 (sr:escherichia coli (strain:k12) dna,
 clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
 kohara clone #406(52.2-52.5 min.)) (nt:similar to (swissprot accession
 number q10403)) (le:5285) (re:6178) (di:direct) D90862 D90862 g1799685
 Escherichia coli 562 -11535305 7500960149 b2304 putative sugar nucleotide
 epimerase (fn:putative enzyme; not classified) (db:genpept-bct2)
 (de:escherichia coli k-12 mg1655 section 209 of 400 of the completegenome.)
 (nt:o297; this 297 aa orf is 41 pct identical (6 gaps)) (le:7029) (re:7922)
 (di:direct) AE000319 AE000319 g1788642 Escherichia coli 562 -11535305
 6500731447 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli) b2304 b2304 Escherichia coli 562 -11535305

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855189	11467	33623	1383	460

Description

6500731448 yfci:b2305 hypothetical protein:hypothetical 34.2 kd protein in folx-hisp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2305 b2305 Escherichia coli 562 -11535306 1500686268 yfci (de:hypothetical 34.2 kd protein in folx-hisp intergenic region) (db:swissprot) YFCI_ECOLI P77768 ESCHERICHIA COLI 562 -11535306 7000687687 hypothetical protein b2305 (db:pir2.dat) G65002 G65002 Escherichia coli 562 -11535306 224829 yhga (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #405(52.0-52.3 min.)) (nt:similar to (swissprot accession number p31667)) (le:12638) (re:13528) (di:complement) D90861 D90861 g1799676 Escherichia coli 562 -11535306 224838 yhga (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (swissprot accession number p31667)) (le:6226) (re:7116) (di:complement) D90862 D90862 g1799686 Escherichia coli 562 -11535306 7500923371 yfci orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 209 of 400 of the completegenome.) (nt:f296; this 296 aa orf is 66 pct identical (4 gaps)) (le:7970) (re:8860) (di:complement) AE000319 AE000319 g1788643 Escherichia coli 562 -11535306 5000692840 (de:(ecoli_2254) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2254 ECOLI_2254 Escherichia coli 562 10061021

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855232	11468	33624	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855241	11469	33625	228	75

Description

5000692847 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2322 b2322 Escherichia coli 562 -11535307
7000689516 hypothetical protein b2322 (cl:hypothetical protein b2322) (db:pir2.dat) H65004 H65004 Escherichia coli 562 -11535307 224866 yhhs (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to (swissprot accession number p37621)) (le:9584) (re:10762) (di:complement) D90863 D90863 g1799715 Escherichia coli 562 -11535307 7500955824 unknown (db:genpept-bct1) (de:escherichia coli beta-ketoacyl-acp synthase i (fabb) gene, partialcds, div (div) and 4-phosphoerythronate dehydrogenase (pdx) genes,complete cds.) (nt:orf1) (le:286) (re:1464) (di:direct) ECU76961 U76961 g1684786 Escherichia coli 562 -11535307 240029 b2322 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 211 of 400 of the completegenome.) (nt:f392; this 392 aa orf is 41 pct identical (2 gaps)) (le:2290) (re:3468) (di:complement) AE000321 AE000321 g1788662 Escherichia coli 562 -11535307 6500731449 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2322 b2322 Escherichia coli 562 -11535307

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855261	11470	33626	1587	528

Description

5000692848 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2324 b2324 Escherichia coli 562 -11535308
7000691595 hypothetical protein b2324 (db:pir2.dat) B65005 B65005 Escherichia coli 562 -11535308 224868 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to (swissprot accession number p44246)) (le:12346) (re:14412) (di:direct) D90863 D90863 g1799717 Escherichia coli 562 -11535308 7500960150 b2324 putative peptidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 211 of 400 of the completegenome.) (nt:o688; this 688 aa orf is 44 pct identical (5 gaps)) (le:5052) (re:7118) (di:direct) AE000321 AE000321 g1788664 Escherichia coli 562 -11535308 6500731450 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2324 b2324 Escherichia coli 562 -11535308

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855262	11471	33627	867	288

Description

5000692849 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2325 b2325 Escherichia coli 562 -11535309
7000691596 hypothetical protein b2325 (db:pir2.dat) C65005 C65005
Escherichia coli 562 -11535309 7500960151 b2325 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 211 of 400 of the completengenome.) (nt:f92; this 92 aa orf is 31 pct identical (4 gaps)) (le:7239) (re:7517) (di:complement) AE000321 AE000321 g1788665 Escherichia coli 562 -11535309 6500731451 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2325 b2325 Escherichia coli 562 -11535309

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855264	11472	33628	726	241

Description

5000692850 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2326 b2326 Escherichia coli 562 -11535310
7000691597 hypothetical protein b2326 (db:pir2.dat) D65005 D65005
Escherichia coli 562 -11535310 7500960152 b2326 putative transporting atpase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 211 of 400 of the completengenome.) (nt:f182; 54 pct identical (1 gap) to 165 residues) (le:7551) (re:8099) (di:complement) AE000321 AE000321 g1788666 Escherichia coli 562 -11535310 6500731452 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2326 b2326 Escherichia coli 562 -11535310

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855268	11473	33629	930	309

Description

6500731453 yfca:b2327 hypothetical 28.6 kd protein in mepa
5region:hypothetical 28.6 kd protein in fabb-mepa intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2327
b2327 Escherichia coli 562 -11535311 7500923363 yfca (de:hypothetical 28.6
kd protein in fabb-mepa intergenic region) (db:swissprot) YFCA_ECOLI P14008
ESCHERICHIA COLI 562 -11535311 163330 yfca hypothetical 28.6 k protein mepa
3 region (db:pir2.dat) S08346 S08346 Escherichia coli 562 -11535311 224870
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8
min.)) (nt:similar to (pir accession number s08346)) (le:15393) (re:16202)
(di:complement) D90863 D90863 g1799719 Escherichia coli 562 -11535311
5000692851 (db:genpept-bct1) (de:e. coli mepa gene for
penicillin-insensitive murein endopeptidase.) (nt:unidentified orf (269 aa))
(le:941) (re:1750) (di:direct) ECMEPAMR X16909 g41996 Escherichia coli 562
-11535311 233371 yfca putative structural protein (fn:putative structure;
not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
211 of 400 of the completegenome.) (nt:f269; 100 pct identical to yfca_ecoli
sw: p14008) (le:8099) (re:8908) (di:complement) AE000321 AE000321 g1788667
Escherichia coli 562 -11535311 111824 yfca (de:hypothetical 28.6 kd protein
in fabb-mepa intergenic region) (db:swissprot) YFCA_ECOLI P14008 ESCHERICHIA
COLI 562 -11535311

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855269	11474	33630	210	69

Description

6500731454 yfcb:b2330 hypothetical adenine-specific methylase in aroc 3region:hypothetical adenine-specific methylase in aroc-fadl intergenic region (gtcfc:14.1) (ec:2.1.1.72) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2330 b2330 Escherichia coli 562 -11535312 111826 yfcb (ec:2.1.1.72) (de:(ec 2.1.1.72)) (db:swissprot) YFCB_ECOLI P39199 ESCHERICHIA COLI 562 -11535312 7000687683 yfcb site-specific dna-methyltransferase adenine-specific::hypothetical:aroc 3region (ec:2.1.1.72) (db:pir2.dat) H65005 H65005 Escherichia coli 562 -11535312 224875 yfcb (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #409(52.8-53.1 min.)) (nt:similar to (swissprot accession number p39199)) (le:1110) (re:2375) (di:complement) D90864 D90864 g1799725 Escherichia coli 562 -11535312 7500923365 yfcb putative adenine-specific methylase (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:2.1.1.72) (de:escherichia coli k-12 mg1655 section 211 of 400 of the completegenome.) (nt:f421; 100 pct identical to fragment yfcb_ecoli) (le:10856) (re:12121) (di:complement) AE000321 AE000321 g1788670 Escherichia coli 562 -11535312 5000692852 (de:(ecoli_2279) (pn:hypothetical adenine-specific methylase in aroc:3"region:fragment) (gn:yfcb) (gtcfc:13.7:14.1) (ec:2.1.1.72) (yfcb_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2279 ECOLI_2279 Escherichia coli 562 10120123

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855302	11475	33631	675	224

Description

5000692853 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2331 b2331 Escherichia coli 562 -11535313 7000691598 hypothetical protein b2331 (db:pir2.dat) A65006 A65006 Escherichia coli 562 -11535313 224876 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #409(52.8-53.1 min.)) (nt:similar to (swissprot accession number p44126)) (le:2208) (re:2759) (di:direct) D90864 D90864 g1799726 Escherichia coli 562 -11535313 7500960153 b2331 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 211 of 400 of the completegenome.) (nt:o183; this 183 aa orf is 53 pct identical (2 gaps)) (le:11954) (re:12505) (di:direct) AE000321 AE000321 g1788671 Escherichia coli 562 -11535313 6500731455 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2331 b2331 Escherichia coli 562 -11535313

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855303	11476	33632	894	297

Description

5000692854 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2332 b2332 Escherichia coli 562 -11535314
 7000691599 hypothetical protein b2332 (db:pir2.dat) B65006 B65006 Escherichia coli 562 -11535314 7500960154 b2332 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f278; this 278 aa orf is 35 pct identical (5 gaps)) (le:66) (re:902) (di:complement) AE000322 AE000322 g1788673 Escherichia coli 562 -11535314 6500731456 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2332 b2332 Escherichia coli 562 -11535314

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855307	11477	33633	243	80

Description

5000692855 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2333 b2333 Escherichia coli 562 -11535315
 7000691600 hypothetical protein b2333 (db:pir2.dat) C65006 C65006 Escherichia coli 562 -11535315 7500960155 b2333 putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f179; this 179 aa orf is 33 pct identical (7 gaps)) (le:889) (re:1428) (di:complement) AE000322 AE000322 g1788674 Escherichia coli 562 -11535315 6500731457 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2333 b2333 Escherichia coli 562 -11535315

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855316	11478	33634	489	162

Description

5000692856 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2334 b2334 Escherichia coli 562 -11535316
 7000691601 hypothetical protein b2334 (cl:fimbrial protein smfe) (db:pir2.dat) D65006 D65006 Escherichia coli 562 -11535316 7500960156 b2334 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f162) (le:1425) (re:1913) (di:complement) AE000322 AE000322 g1788675 Escherichia coli 562 -11535316 6500731458 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2334 b2334 Escherichia coli 562 -11535316

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855325	11479	33635	306	101

Description

5000692857 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2335 b2335 Escherichia coli 562 -11535317
7000691602 hypothetical protein b2335 (cl:fimbrial protein smfe) (db:pir2.dat) E65006 E65006 Escherichia coli 562 -11535317 7500960157 b2335 putative fimbrial protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f170; this 170 aa orf is 27 pct identical (12 gaps)) (le:1910) (re:2422) (di:complement) AE000322 AE000322 g1788676 Escherichia coli 562 -11535317 6500731459 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2335 b2335 Escherichia coli 562 -11535317

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855338	11480	33636	192	63

Description

5000692858 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2336 b2336 Escherichia coli 562 -11535318
7000687688 yfcs (de:precursor) (db:swissprot) YFCS_ECOLI P77599 ESCHERICHIA COLI 562 -11535318 7000687689 hypothetical protein b2336 (cl:chaperone protein papd) (db:pir2.dat) F65006 F65006 Escherichia coli 562 -11535318 224877 pmfd chaperone protein pmfd precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #409(52.8-53.1 min.)) (nt:similar to (swissprot accession number p53520)) (le:5186) (re:5938) (di:complement) D90864 D90864 g1799727 Escherichia coli 562 -11535318 7500923372 yfcs putative chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f250; this 250 aa orf is 43 pct identical (2 gaps)) (le:2422) (re:3174) (di:complement) AE000322 AE000322 g1788677 Escherichia coli 562 -11535318 6500731460 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2336 b2336 Escherichia coli 562 -11535318

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855347	11481	33637	249	82

Description

5000692859 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2337 b2337 Escherichia coli 562 -11535319
7000691603 hypothetical protein b2337 (db:pir2.dat) G65006 G65006
Escherichia coli 562 -11535319 224878 papc outer membrane usher protein papc precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #409(52.8-53.1 min.)) (nt:similar to (swissprot accession number p07110)) (le:5958) (re:6854) (di:complement) D90864 D90864 g1799728 Escherichia coli 562 -11535319 7500960158 b2337 putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f298; this 298 aa orf is 45 pct identical (11 gaps)) (le:3194) (re:4090) (di:complement) AE000322 AE000322 g1788678 Escherichia coli 562 -11535319 6500731461 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2337 b2337 Escherichia coli 562 -11535319

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855353	11482	33638	435	144

Description

5000692860 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2338 b2338 Escherichia coli 562 -11535320
7000687691 hypothetical protein b2338 (db:pir2.dat) H65006 H65006
Escherichia coli 562 -11535320 224879 papc outer membrane usher protein papc precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #409(52.8-53.1 min.)) (nt:similar to (swissprot accession number p07110)) (le:6867) (re:8603) (di:complement) D90864 D90864 g1799729 Escherichia coli 562 -11535320 7500923373 yfcu putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f578; this 578 aa orf is 46 pct identical (21 gaps)) (le:4103) (re:5839) (di:complement) AE000322 AE000322 g1788679 Escherichia coli 562 -11535320 7000687690 yfcu (de:region precursor) (db:swissprot) YFCU_ECOLI P77196 ESCHERICHIA COLI 562 -11535320 6500731462 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2338 b2338 Escherichia coli 562 -11535320

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855354	11483	33639	195	64

Description

5000692861 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2339 b2339 Escherichia coli 562 -11535321
7000691604 hypothetical protein b2339 (db:pir2.dat) A65007 A65007
Escherichia coli 562 -11535321 224880 smfa fimbria a protein precursor.
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #409(52.8-53.1 min.)) (nt:similar to (swissprot accession number p13421)) (le:8685)
(re:9248) (di:complement) D90864 D90864 g1799730 Escherichia coli 562 -11535321 7500960159 b2339 putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f187; this 187 aa orf is 34 pct identical (16 gaps)) (le:5921) (re:6484) (di:complement) AE000322 AE000322 g1788680 Escherichia coli 562 -11535321 6500731463 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2339 b2339 Escherichia coli 562 -11535321

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855365	11484	33640	192	63

Description

5000692862 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2340 b2340 Escherichia coli 562 -11535322
7500891663 sixa (ec:3.1.3.-) (de:phosphohistidine phosphatase sixa, (rx6)) (db:swissprot) SIXA_ECOLI P76502 ESCHERICHIA COLI 562 -11535322 7000691605
hypothetical protein b2340 (cl:hypothetical protein hi1338) (db:pir2.dat) B65007 B65007 Escherichia coli 562 -11535322 7000691606 rx6 (sr:escherichia coli (sub_species:k-12, strain:mc4100) dna) (db:genpept-bct1)
(de:escherichia coli gene for rx6, complete cds.) (le:48) (re:533)
(di:direct) D86298 D86298 g2897694 Escherichia coli 562 -11535322
7500891666 b2340 orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f161; residues 80-152 are 43 pct identical to)
(le:7165) (re:7650) (di:complement) AE000322 AE000322 g1788681 Escherichia coli 562 -11535322 6500731464 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2340 b2340
Escherichia coli 562 -11535322

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855366	11485	33641	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855367	11486	33642	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855369	11487	33643	234	77

Description

5000692863 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2341 b2341 Escherichia coli 562 -11535323
7500923374 yfcx (ec:4.2.1.17:1.1.1.35:5.1.2.3) (de:(ec 1.1.1.35); 3-hydroxybutyryl-coa epimerase,)) (db:swissprot) YFCX_ECOLI P77399
ESCHERICHIA COLI 562 -11535323 7000691607 hypothetical protein b2341 (cl:enoyl-coa hydratase/3-hydroxyacyl-coa dehydrogenase:3-hydroxyacyl-coa dehydrogenase homology:enoyl-coa hydratase homology) (db:pir2.dat) C65007 C65007 Escherichia coli 562 -11535323 224882 hadh mitochondrial trifunctional enzyme alpha subunit (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #409(52.8-53.1 min.)) (nt:similar to (swissprot accession number p40939)) (le:10617) (re:12761) (di:complement) D90864 D90864 g1799732 Escherichia coli 562 -11535323 7500923376 hadh mitochondrial trifunctional enzyme alpha subunit (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #410(53.0-53.4 min.)) (nt:similar to (swissprot accession number p40939)) (le:1517) (re:3661) (di:complement) D90865 D90865 g1799739 Escherichia coli 562 -11535323 7500923377 b2341 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f714; this 714 aa orf is 42 pct identical (28 gaps)) (le:7853) (re:9997) (di:complement) AE000322 AE000322 g1788682 Escherichia coli 562 -11535323 224888 hadh mitochondrial trifunctional enzyme alpha subunit (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #409(52.8-53.1 min.)) (nt:similar to (swissprot accession number p40939)) (le:10617) (re:12761) (di:complement) D90864 D90864 g1799732 Escherichia coli 562 -11535323 6500731465 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2341 b2341 Escherichia coli 562 -11535323

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855375	11488	33644	453	150

Description

5000692864 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2342 b2342 Escherichia coli 562 -11535324
7000691608 hypothetical protein b2342 (cl:long-chain-fatty-acid beta-oxidation multienzyme complex beta chain) (db:pir2.dat) D65007 D65007 Escherichia coli 562 -11535324 7500960160 b2342 putative acyltransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 212 of 400 of the completegenome.) (nt:f436; this 436 aa orf is 38 pct identical (3 gaps)) (le:9997) (re:11307) (di:complement) AE000322 AE000322 g1788683 Escherichia coli 562 -11535324 6500731466 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2342 b2342 Escherichia coli 562 -11535324

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855382	11489	33645	672	223

Description

5000692865 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2343 b2343 Escherichia coli 562 -11535325
7500923378 yfcz (de:hypothetical 11.3 kd protein in sixa-fadI intergenic region) (db:swissprot) YFCZ_ECOLI P76504 ESCHERICHIA COLI 562 -11535325
7000689504 c4-dicarboxylate transport protein homolog b2343 (cl:c4-dicarboxylate carrier protein) (db:pir2.dat) E65007 E65007 Escherichia coli 562 -11535325 7500923380 b2343 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 213 of 400 of the completegenome.) (nt:f102; this 102 aa orf is 44 pct identical (0 gaps)) (le:121) (re:429) (di:complement) AE000323 AE000323 g1788685 Escherichia coli 562 -11535325 6500731467 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2343 b2343 Escherichia coli 562 -11535325

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855402	11490	33646	474	157

Description

5000692866 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2345 b2345 Escherichia coli 562 -11535326
7000691609 hypothetical protein b2345 (db:pir2.dat) G65007 G65007 Escherichia coli 562 -11535326 7500960161 b2345 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 213 of 400 of the completegenome.) (nt:o352; this 352 aa orf is 25 pct identical (14 gaps)) (le:2483) (re:3541) (di:direct) AE000323 AE000323 g1788687 Escherichia coli 562 -11535326 6500731468 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2345 b2345 Escherichia coli 562 -11535326

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855405	11491	33647	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855416	11492	33648	1200	400

Description

6500731469 yfdc:b2347 hypothetical 34.5 kd protein in argw
5region:hypothetical 34.5 kd protein in vacj-argw intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2347
b2347 Escherichia coli 562 -11535327 111837 yfdc (de:hypothetical 34.5 kd
protein in vacj-argw intergenic region) (db:swissprot) YFDC_ECOLI P37327
ESCHERICHIA COLI 562 -11535327 7000687692 yfdc hypothetical 34.5 kd protein
in argw 5region (db:pir2.dat) A65008 A65008 Escherichia coli 562 -11535327
224894 yfdc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#410(53.0-53.4 min.)) (nt:similar to (swissprot accession number p37327))
(le:9800) (re:10732) (di:direct) D90865 D90865 g1799745 Escherichia coli 562
-11535327 7500923386 yfdc putative transport (fn:putative transport; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 213
of 400 of the completegenome.) (nt:o310; 100 pct identical to yfdc_ecoli sw:
p37327) (le:4772) (re:5704) (di:direct) AE000323 AE000323 g1788689
Escherichia coli 562 -11535327 5000692868 (de:(ecoli_2296) (pn:hypothetical
34) (gn:yfdc) (gtcfc:13.7:14.1) (ec:) (yfdc_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2296 ECOLI_2296 Escherichia
coli 562 10053565

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855417	11493	33649	408	135

Description

5000692870 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2350 b2350 Escherichia coli 562 -11535328
7000691610 hypothetical protein b2350 (cl:hypothetical protein b2350) (db:pir2.dat) C65008 C65008 Escherichia coli 562 -11535328 224896 rfbi rfbi protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #410(53.0-53.4 min.)) (nt:similar to (swissprot accession number p37785)) (le:12354) (re:12716) (di:direct) D90865 D90865 g1799747 Escherichia coli 562 -11535328 224903 rfbi rfbi protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #411(53.2-53.6 min.)) (nt:similar to (swissprot accession number p37785)) (le:864) (re:1226) (di:direct) D90866 D90866 g1799755 Escherichia coli 562 -11535328 7500960162 b2350 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 213 of 400 of the completegenome.) (nt:ol20; this 120 aa orf is 45 pct identical (0 gaps)) (le:7326) (re:7688) (di:direct) AE000323 AE000323 g1788691 Escherichia coli 562 -11535328 6500731470 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2350 b2350 Escherichia coli 562 -11535328

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501855425	11494	33650	720	239

Description

5000692871 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2351 b2351 Escherichia coli 562 -11535329
7500923388 yfdh (de:hypothetical 34.6 kd protein in intc-dsdc intergenic region) (db:swissprot) YFDH_ECOLI P77293 ESCHERICHIA COLI 562 -11535329
7000691611 hypothetical protein b2351 (cl:stress response protein csbb) (db:pir2.dat) D65008 D65008 Escherichia coli 562 -11535329 224897 dpml dolichol-phosphate mannosyltransferase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #410(53.0-53.4 min.)) (nt:similar to (swissprot accession number p14020)) (le:12713) (re:13633) (di:direct) D90865 D90865 g1799748 Escherichia coli 562 -11535329 7500923390 dpml dolichol-phosphate mannosyltransferase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #411(53.2-53.6 min.)) (nt:similar to (swissprot accession number p14020)) (le:1223) (re:2143) (di:direct) D90866 D90866 g1799756 Escherichia coli 562 -11535329 7500923391 b2351 putative glycan biosynthesis enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 213 of 400 of the completegenome.) (nt:o306; this 306 aa orf is 28 pct identical (1 gap)) (le:7685) (re:8605) (di:direct) AE000323 AE000323 g1788692 Escherichia coli 562 -11535329 224904 dpml dolichol-phosphate mannosyltransferase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #410(53.0-53.4 min.)) (nt:similar to (swissprot accession number p14020)) (le:12713) (re:13633) (di:direct) D90865 D90865 g1799748 Escherichia coli 562 -11535329 6500731471 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2351 b2351 Escherichia coli 562 -11535329

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501855426	11495	33651	186	61

Description

5000692872 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2352 b2352 Escherichia coli 562 -11535330
7000691612 hypothetical protein b2352 (db:pir2.dat) E65008 E65008 Escherichia coli 562 -11535330 7500960163 b2352 putative ligase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 213 of 400 of the completegenome.) (nt:o443; this 443 aa orf is 25 pct identical (7 gaps)) (le:8602) (re:9933) (di:direct) AE000323 AE000323 g1788693 Escherichia coli 562 -11535330 6500731472 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2352 b2352 Escherichia coli 562 -11535330

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855455	11496	33652	1413	470

Description

5000692873 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2353 b2353 Escherichia coli 562 -11535331
7000691613 hypothetical protein b2353 (db:pir2.dat) F65008 F65008
Escherichia coli 562 -11535331 224898 ycfa (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #410(53.0-53.4 min.)) (nt:similar to (swissprot accession number p09153)) (le:15260) (re:15604) (di:direct)
D90865 D90865 g1799749 Escherichia coli 562 -11535331 224905 ycfa (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #411(53.2-53.6 min.)) (nt:similar to (swissprot accession number p09153)) (le:3770) (re:4114) (di:direct) D90866 D90866 g1799757 Escherichia coli 562 -11535331
7500960164 b2353 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:ol14; this 114 aa orf is 83 pct identical (0 gaps)) (le:180) (re:524) (di:direct) AE000324 AE000324 g1788695 Escherichia coli 562 -11535331 6500731473 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2353 b2353 Escherichia coli 562 -11535331

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855462	11497	33653	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855482	11498	33654	489	162

Description

5000692874 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2354 b2354 Escherichia coli 562 -11535332
 7502852263 yfdk (de:hypothetical 16.4 kd protein in intc-dsdc intergenic region) (db:swissprot) YFDK_ECOLI P77656 ESCHERICHIA COLI 562 -11535332
 7000691614 hypothetical protein b2354 (db:pir2.dat) G65008 G65008 Escherichia coli 562 -11535332 224901 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #410(53.0-53.4 min.)) (nt:similar to (swissprot accession number p09154)) (le:15576) (re:16016) (di:complement) D90865 D90865 g1799752 Escherichia coli 562 -11535332 224908 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #411(53.2-53.6 min.)) (nt:similar to (swissprot accession number p09154)) (le:4086) (re:4526) (di:complement) D90866 D90866 g1799760 Escherichia coli 562 -11535332 7500960165 b2354 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:f146; this 146 aa orf is 69 pct identical (0 gaps)) (le:496) (re:936) (di:complement) AE000324 AE000324 g1788696 Escherichia coli 562 -11535332 6500731474 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2354 b2354 Escherichia coli 562 -11535332

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855495	11499	33655	264	87

Description

6500731475 yfdl:b2355 hypothetical protein:hypothetical 18.3 kd protein in intc-dsdc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2355 b2355 Escherichia coli 562 -11535333
 4000708206 yfdl (de:hypothetical 18.3 kd protein in intc-dsdc intergenic region) (db:swissprot) YFDL_ECOLI P76508 ESCHERICHIA COLI 562 -11535333
 7000687694 hypothetical protein b2355 (db:pir2.dat) H65008 H65008 Escherichia coli 562 -11535333 7500923392 yfdl putative rna polymerase beta (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:f172; 33 pct identical (10 gaps) to 93 residues) (le:963) (re:1481) (di:complement) AE000324 AE000324 g1788697 Escherichia coli 562 -11535333 5000692875 (de:(ecoli_2303) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2303 ECOLI_2303 Escherichia coli 562 10123649

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855497	11500	33656	3003	1000

Description

5000692876 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2356 b2356 Escherichia coli 562 -11535334
7000691615 hypothetical protein b2356 (db:pir2.dat) A65009 A65009
Escherichia coli 562 -11535334 7500960166 yfdm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:f102; 34 pct identical to 43 residues from) (le:1531) (re:1839) (di:complement) AE000324 AE000324 g1788698
Escherichia coli 562 -11535334 6500731476 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2356 b2356
Escherichia coli 562 -11535334

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855501	11501	33657	1803	600

Description

6500731477 yfdn:b2357 hypothetical protein:hypothetical 18.8 kd protein in intc-dsdc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2357 b2357 Escherichia coli 562 -11535335
1500686270 yfdn (de:hypothetical 18.8 kd protein in intc-dsdc intergenic region) (db:swissprot) YFDN_ECOLI P76510 ESCHERICHIA COLI 562 -11535335
7000687695 hypothetical protein b2357 (db:pir2.dat) B65009 B65009
Escherichia coli 562 -11535335 7500923393 yfdn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:f164) (le:1806) (re:2300) (di:complement) AE000324 AE000324 g1788699 Escherichia coli 562 -11535335
5000692877 (de:(ecoli_2305) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2305
ECOLI_2305 Escherichia coli 562 10061024

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855502	11502	33658	426	141

Description

6500731478 yfdo:b2358 hypothetical protein:hypothetical 14.4 kd protein in intc-dsdc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2358 b2358 Escherichia coli 562 -11535336
 1500686271 yfdo (de:hypothetical 14.4 kd protein in intc-dsdc intergenic region) (db:swissprot) YFDO_ECOLI P76511 ESCHERICHIA COLI 562 -11535336
 7000687696 hypothetical protein b2358 (db:pir2.dat) C65009 C65009 Escherichia coli 562 -11535336 7500923394 yfdo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:f122; this 122 aa orf is 48 pct identical (0 gaps)) (le:2297) (re:2665) (di:complement) AE000324 AE000324 g1788700 Escherichia coli 562 -11535336 5000692878 (de:(ecoli_2306) (pn:function not assigned) (gn:fro) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2306 ECOLI_2306 Escherichia coli 562 10061025

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855511	11503	33659	522	173

Description

5000692879 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2359 b2359 Escherichia coli 562 -11535337
 7000691616 hypothetical protein b2359 (db:pir2.dat) D65009 D65009 Escherichia coli 562 -11535337 7500960167 b2359 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:o148; this 148 aa orf is 26 pct identical (7 gaps)) (le:2939) (re:3385) (di:direct) AE000324 AE000324 g1788701 Escherichia coli 562 -11535337 6500731479 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2359 b2359 Escherichia coli 562 -11535337

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855533	11504	33660	534	177

Description

5000692880 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2360 b2360 Escherichia coli 562 -11535338
 7000691617 hypothetical protein b2360 (db:pir2.dat) E65009 E65009 Escherichia coli 562 -11535338 7500960168 b2360 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:o274; this 274 aa orf is 30 pct identical (12 gaps)) (le:3451) (re:4275) (di:direct) AE000324 AE000324 g1788702 Escherichia coli 562 -11535338 6500731480 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2360 b2360 Escherichia coli 562 -11535338

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855538	11505	33661	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855547	11506	33662	921	307

Description

5000692881 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2361 b2361 Escherichia coli 562 -11535339
7000691618 hypothetical protein b2361 (db:pir2.dat) F65009 F65009
Escherichia coli 562 -11535339 7500960169 b2361 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:ol87; this 187 aa orf is 31 pct identical (10 gaps)) (le:4376) (re:4939) (di:direct) AE000324 AE000324
g1788703 Escherichia coli 562 -11535339 6500731481 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2361 b2361 Escherichia coli 562 -11535339

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855548	11507	33663	360	119

Description

5000692882 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2362 b2362 Escherichia coli 562 -11535340
7000691619 hypothetical protein b2362 (db:pir2.dat) G65009 G65009
Escherichia coli 562 -11535340 7500960170 b2362 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:ol20; this 120 aa orf is 28 pct identical (5 gaps)) (le:4930) (re:5292) (di:direct) AE000324 AE000324
g1788704 Escherichia coli 562 -11535340 6500731482 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2362 b2362 Escherichia coli 562 -11535340

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855549	11508	33664	534	177

Description

GTC ORF with score 120 to: (sr:caenorhabditis elegans strain-bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c33c12.) (nt:strong similarity to glycosyl hydrolases) (le:21872:22613:22824) (re:22103:22776:22904) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855554	11509	33665	468	155

Description

5000692883 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2363 b2363 Escherichia coli 562 -11535341
 7000691620 hypothetical protein b2363 (db:pir2.dat) H65009 H65009 Escherichia coli 562 -11535341 7500960171 b2363 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:o101; this 101 aa orf is 35 pct identical (0 gaps)) (le:5292) (re:5597) (di:direct) AE000324 AE000324 g1788705 Escherichia coli 562 -11535341 6500731483 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2363 b2363 Escherichia coli 562 -11535341

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855556	11510	33666	207	68

Description

6500731484 yfde:b2371 hypothetical protein:hypothetical 43.3 kd protein in evgs-gluk intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2371 b2371 Escherichia coli 562 -11535342
 500684972 yfde (de:hypothetical 43.3 kd protein in evgs-gluk intergenic region) (db:swissprot) YFDE_ECOLI P76518 ESCHERICHIA COLI 562 -11535342
 7000687693 hypothetical protein b2371 (db:pir2.dat) H65010 H65010 Escherichia coli 562 -11535342 7500923387 yfde putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 215 of 400 of the completegenome.) (nt:f394; this 394 aa orf is 25 pct identical (18 gaps)) (le:7469) (re:8653) (di:complement) AE000325 AE000325 g1788714 Escherichia coli 562 -11535342 5000692887 (de:(ecoli_2319) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2319 ECOLI_2319 Escherichia coli 562 10061022

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855558	11511	33667	849	283

Description

GTC ORF with score 125 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid zc449.) (nt:coded for by c. elegans cDNA yk61e11.3; coded for) (le:30120:30310:30457) (re:30261:30413:31468) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855586	11512	33668	606	201

Description

GTC ORF with score 160 to: (fn:inactive trans-sialidase) (sr:trypanosoma cruzi (strain y) trypomastigote dna, clone 121) (db:genpept-inv) (de:trypanosoma cruzi tcts-121 gene for trans-sialidase, complete cds.) (le:1) (re:2895) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855610	11513	33669	192	63

Description

5000692888 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2372 b2372 Escherichia coli 562 -11535343
7000691621 hypothetical protein b2372 (db:pir2.dat) A65011 A65011
Escherichia coli 562 -11535343 7500960172 b2372 putative receptor protein (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 215 of 400 of the completegenome.) (nt:f314; this 314 aa orf is 26 pct identical (11 gaps)) (le:8688) (re:9632) (di:complement)
AE000325 AE000325 g1788715 Escherichia coli 562 -11535343 6500731485
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2372 b2372 Escherichia coli 562 -11535343

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855611	11514	33670	468	155

Description

5000692889 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2373 b2373 Escherichia coli 562 -11535344
7500887437 yfdu (ec:4.1.1.8) (de:probable oxalyl-coa decarboxylase,) (db:swissprot) OXC_ECOLI P78093 ESCHERICHIA COLI 562 -11535344 7000691622
hypothetical protein b2373 (cl:oxalyl-coa decarboxylase:thiamine pyrophosphate-binding domain homology) (db:pir2.dat) B65011 B65011
Escherichia coli 562 -11535344 7500887439 b2373 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 215 of 400 of the completegenome.) (nt:f564; this 564 aa orf is 55 pct identical (7 gaps)) (le:9702) (re:11396) (di:complement)
AE000325 AE000325 g1788716 Escherichia coli 562 -11535344 6500731486
hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2373 b2373 Escherichia coli 562 -11535344

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855613	11515	33671	318	105

Description

5000692890 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2374 b2374 Escherichia coli 562 -11535345
 7000691623 hypothetical protein b2374 (db:pir2.dat) C65011 C65011 Escherichia coli 562 -11535345 224934 baif bile acid-inducible operon protein f. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #414(53.8-54.2 min.)) (nt:similar to (swissprot accession number p19413)) (le:481) (re:1731) (di:complement) D90868 D90868 g1799788 Escherichia coli 562 -11535345 7500960173 b2374 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 215 of 400 of the completegenome.) (nt:f416) (le:11450) (re:12700) (di:complement) AE000325 AE000325 g1788717 Escherichia coli 562 -11535345 6500731487 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2374 b2374 Escherichia coli 562 -11535345

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855632	11516	33672	597	199

Description

5000692891 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2375 b2375 Escherichia coli 562 -11535346
 7000691624 hypothetical protein b2375 (db:pir2.dat) D65011 D65011 Escherichia coli 562 -11535346 7500960174 b2375 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:f211; this 211 aa orf is 28 pct identical (4 gaps)) (le:287) (re:922) (di:complement) AE000326 AE000326 g1788719 Escherichia coli 562 -11535346 6500731488 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2375 b2375 Escherichia coli 562 -11535346

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855633	11517	33673	666	221

Description

6500731489 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2376 b2376 Escherichia coli 562 -11535347
 7502852264 ypdI (de:hypothetical 10.2 kd lipoprotein in evgs-ddg region precursor) (db:swissprot) YPDI_ECOLI O32528 ESCHERICHIA COLI 562 -11535347
 7000691625 hypothetical protein b2376 (db:pir2.dat) E65011 E65011 Escherichia coli 562 -11535347 7500960175 b2376 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:o91; residues 33-89 are 28 pct identical to) (le:1218) (re:1493) (di:direct) AE000326 AE000326 g2367134 Escherichia coli 562 -11535347

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855635	11518	33674	414	137

Description

5000692892 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2377 b2377 Escherichia coli 562 -11535348
 7000691626 hypothetical protein b2377 (db:pir2.dat) F65011 F65011
 Escherichia coli 562 -11535348 7500960176 b2377 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:f80; this 80 aa orf is 30 pct identical (9 gaps)) (le:1570) (re:1812) (di:complement) AE000326 AE000326 g1788720 Escherichia coli 562 -11535348 6500731490 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2377 b2377 Escherichia coli 562 -11535348

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855645	11519	33675	279	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855649	11520	33676	228	75

Description

5000692893 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2378 b2378 Escherichia coli 562 -11535349
 7000691627 probable lauroyl acyltransferase b2378:probable lipid a biosynthesis protein b2378 (db:pir2.dat) G65011 G65011 Escherichia coli 562 -11535349 7500960177 ddg putative heat shock protein (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:o328; this 328 aa orf is 55 pct identical (1 gap)) (le:2099) (re:3085) (di:direct) AE000326 AE000326 g1788721 Escherichia coli 562 -11535349 6500731491 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2378 b2378 Escherichia coli 562 -11535349

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501855656	11521	33677	666	221

Description

5000692894 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2379 b2379 Escherichia coli 562 -11535350
7502852265 yfdz (ec:2.6.1.-) (de:hypothetical aminotransferase yfdz,) (db:swissprot) YFDZ_ECOLI P77434 ESCHERICHIA COLI 562 -11535350 7000691628 hypothetical protein b2379 (cl:aspartate transaminase) (db:pir2.dat) H65011 H65011 Escherichia coli 562 -11535350 224936 ipa-85d probable aspartate aminotransferase ec 2.6.1.1 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #414(53.8-54.2 min.)) (nt:similar to (swissprot accession number p39643)) (le:5534) (re:6772) (di:complement) D90868 D90868 g1799790 Escherichia coli 562 -11535350 7500960178 b2379 putative aminotransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:f412; this 412 aa orf is 35 pct identical (4 gaps)) (le:3577) (re:4815) (di:complement) AE000326 AE000326 g1788722 Escherichia coli 562 -11535350 6500731492 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2379 b2379 Escherichia coli 562 -11535350

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501855657	11522	33678	531	176

Description

5000692895 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2380 b2380 Escherichia coli 562 -11535351
7000691629 hypothetical protein b2380 (cl:hypothetical protein b2380) (db:pir2.dat) A65012 A65012 Escherichia coli 562 -11535351 7500955825 b2380 putative sensor protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:o565; this 565 aa orf is 30 pct identical (26 gaps)) (le:5191) (re:6888) (di:direct) AE000326 AE000326 g1788723 Escherichia coli 562 -11535351 6500731493 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2380 b2380 Escherichia coli 562 -11535351

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501855662	11523	33679	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855665	11524	33680	183	60

Description

5000692896 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2381 b2381 Escherichia coli 562 -11535352
7000691630 hypothetical protein b2381 (cl:yeht protein:response regulator homology) (db:pir2.dat) B65012 B65012 Escherichia coli 562 -11535352 224938 mrke mrke protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #414(53.8-54.2 min.)) (nt:similar to (swissprot accession number p21649)) (le:8860) (re:9594) (di:direct) D90868 D90868 g1799792 Escherichia coli 562 -11535352 7500960179 b2381 putative 2-component transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:o244; this 244 aa orf is 87 pct identical (1 gap)) (le:6903) (re:7637) (di:direct) AE000326 AE000326 g1788724 Escherichia coli 562 -11535352 6500731494 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2381 b2381 Escherichia coli 562 -11535352

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855675	11525	33681	441	146

Description

5000692897 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2382 b2382 Escherichia coli 562 -11535353
7502852266 ypdC (de:hypothetical transcriptional regulator in ddg-glK intergenic region) (db:swissprot) YPDC_ECOLI P77396 ESCHERICHIA COLI 562 -11535353 7000691631 hypothetical protein b2382 (cl:hypothetical protein b2382) (db:pir2.dat) C65012 C65012 Escherichia coli 562 -11535353 224939 yijO (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #414(53.8-54.2 min.)) (nt:similar to (swissprot accession number p32677)) (le:9607) (re:10464) (di:direct) D90868 D90868 g1799793 Escherichia coli 562 -11535353
7500960180 b2382 putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:o285; this 285 aa orf is 34 pct identical (4 gaps)) (le:7650) (re:8507) (di:direct) AE000326 AE000326 g1788725 Escherichia coli 562 -11535353 6500731495 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2382 b2382 Escherichia coli 562 -11535353

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501855681	11526	33682	1119	372

Description

5000692898 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2383 b2383 Escherichia coli 562 -11535354

7000691632 hypothetical protein b2383 (cl:phosphotransferase system enzyme i homology) (db:pir2.dat) D65012 D65012 Escherichia coli 562 -11535354

224940 ptsa phosphoenolpyruvate-protein phosphotransferase (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #414(53.8-54.2 min.)) (nt:similar to (swissprot accession number p32670)) (le:10467) (re:12962) (di:complement) D90868 D90868 g1799794 Escherichia coli 562 -11535354 7500960181 b2383 putative pts system enzyme iia component:enzyme (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:f831; this 831 aa orf is 46 pct identical (11 gaps)) (le:8510) (re:11005) (di:complement) AE000326 AE000326 g1788726 Escherichia coli 562 -11535354 6500731496 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2383 b2383 Escherichia coli 562 -11535354

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501855687	11527	33683	246	81

Description

5000692899 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2384 b2384 Escherichia coli 562 -11535355

7000691633 hypothetical protein b2384 (cl:thermophilic aminopeptidase i alpha chain) (db:pir2.dat) E65012 E65012 Escherichia coli 562 -11535355

224941 frvx putative frv operon protein frvx. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #414(53.8-54.2 min.)) (nt:similar to (swissprot accession number p32153)) (le:12987) (re:14024) (di:complement) D90868 D90868 g1799795 Escherichia coli 562 -11535355 7500960182 b2384 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:f345; this 345 aa orf is 35 pct identical (14 gaps)) (le:11030) (re:12067) (di:complement) AE000326 AE000326 g1788727 Escherichia coli 562 -11535355 6500731497 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2384 b2384 Escherichia coli 562 -11535355

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855689	11528	33684	1995	665

Description

5000692900 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2385 b2385 Escherichia coli 562 -11535356
7000691634 hypothetical protein b2385 (cl:x-pro aminopeptidase) (db:pir2.dat) F65012 F65012 Escherichia coli 562 -11535356 7500960183 b2385 putative peptidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:f361; this 361 aa orf is 35 pct identical (9 gaps)) (le:12067) (re:13152) (di:complement) AE000326 AE000326 g1788728 Escherichia coli 562 -11535356 6500731498 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2385 b2385 Escherichia coli 562 -11535356

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855690	11529	33685	192	63

Description

5000692901 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2386 b2386 Escherichia coli 562 -11535357
7000691635 hypothetical protein b2386 (db:pir2.dat) G65012 G65012 Escherichia coli 562 -11535357 224943 frua pts system:fructose-specific iibc component (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #414(53.8-54.2 min.)) (nt:similar to (swissprot accession number p44714)) (le:15123) (re:16370) (di:complement) D90868 D90868 g1799797 Escherichia coli 562 -11535357 7500960184 b2386 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:f415; this 415 aa orf is 30 pct identical (11 gaps)) (le:13167) (re:14414) (di:complement) AE000326 AE000326 g1788729 Escherichia coli 562 -11535357 6500731499 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2386 b2386 Escherichia coli 562 -11535357

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855692	11530	33686	1344	447

Description

5000692902 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2387 b2387 Escherichia coli 562 -11535358
 7000691636 hypothetical protein b2387 (cl:phosphotransferase system, fructose-like component iib) (db:pir2.dat) H65012 H65012 Escherichia coli 562 -11535358 7500960185 b2387 putative pts system enzyme iib component (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 216 of 400 of the completegenome.) (nt:f108; this 108 aa orf is 45 pct identical (0 gaps)) (le:14436) (re:14762) (di:complement) AE000326 AE000326 g1788730 Escherichia coli 562 -11535358
 6500731500 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2387 b2387 Escherichia coli 562 -11535358

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855706	11531	33687	843	280

Description

5000692903 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2389 b2389 Escherichia coli 562 -11535359
 7000691637 hypothetical protein b2389 (db:pir2.dat) B65013 B65013 Escherichia coli 562 -11535359 7500960186 b2389 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 217 of 400 of the completegenome.) (nt:o418 was o397; this 397 aa orf is 26 pct identical) (le:1309) (re:2565) (di:direct) AE000327 AE000327 g1788733 Escherichia coli 562 -11535359 6500731501 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2389 b2389 Escherichia coli 562 -11535359

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855708	11532	33688	522	173

Description

5000692904 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2390 b2390 Escherichia coli 562 -11535360
 7000691638 hypothetical protein b2390 (db:pir2.dat) C65013 C65013 Escherichia coli 562 -11535360 7500960187 b2390 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 217 of 400 of the completegenome.) (nt:o108; o108; odd ... overlapping orf with frame) (le:2680) (re:3006) (di:direct) AE000327 AE000327 g1788734 Escherichia coli 562 -11535360 6500731502 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2390 b2390 Escherichia coli 562 -11535360

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855712	11533	33689	528	175

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855727	11534	33690	507	168

Description

5000692905 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2391 b2391 Escherichia coli 562 -11535361
7000691639 hypothetical protein b2391 (db:pir2.dat) D65013 D65013
Escherichia coli 562 -11535361 7500960188 b2391 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
217 of 400 of the completegenome.) (nt:o114; o114; odd ... overlapping orf
with frame) (le:2744) (re:3088) (di:direct) AE000327 AE000327 g1788735
Escherichia coli 562 -11535361 6500731503 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2391 b2391
Escherichia coli 562 -11535361

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855750	11535	33691	1233	410

Description

GTC ORF with score 115 to: (db:genpept-inv) (de:caenorhabditis elegans
cosmid t18d3, complete sequence.) (nt:cdna est embl:z14951 comes from this
gene; cdna est) (le:16866:17104:18030:18390) (re:17055:17375:18334:18489)
(di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855755	11536	33692	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855762	11537	33693	432	143

Description

5000692906 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2392 b2392 Escherichia coli 562 -11535362
7500923414 yfep (de:hypothetical 44.2 kd protein in glk-nupc intergenic region) (db:swissprot) YFEP_ECOLI P77145 ESCHERICHIA COLI 562 -11535362
7000691640 hypothetical protein b2392 (db:pir2.dat) E65013 E65013 Escherichia coli 562 -11535362 224949 spac27f1.08 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #416(54.1-54.5 min.)) (nt:similar to (swissprot accession number q10177)) (le:4312) (re:5550) (di:complement) D90869 D90869 g1799804 Escherichia coli 562 -11535362 7500923417 b2392 putative transport system permease (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 217 of 400 of the completegenome.) (nt:f412; this 412 aa orf is 36 pct identical (40 gaps)) (le:3147) (re:4385) (di:complement) AE000327 AE000327 g1788736 Escherichia coli 562 -11535362 6500731504 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2392 b2392 Escherichia coli 562 -11535362

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855772	11538	33694	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855773	11539	33695	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855783	11540	33696	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855797	11541	33697	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855798	11542	33698	1053	350
<u>Description</u>				
5000692907 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2394 b2394 Escherichia coli 562 -11535363				
7000689461 yi81_1 probable transposase t31:protein b2394 (cl:is186 probable transposase t31) (db:pir1.dat) QQEC47 G65013 Escherichia coli 562 -11535363				
7500953708 yi44 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:48690) (re:49808) (di:direct) ECU82598 U82598 g1778498 Escherichia coli 562 -11535363 240094 yi81_3 is186 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 217 of 400 of the completegenome.) (nt:o372; phage stats) (le:6004) (re:7122) (di:direct) AE000327 AE000327 g1788738 Escherichia coli 562 -11535363				
6500731505 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2394 b2394 Escherichia coli 562 -11535363				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855800	11543	33699	540	180
<u>Description</u>				
6500731506 yfed:b2399 hypothetical 14.9 kd protein in glty-alaw intergenic region:hypothetical 14.9 kd protein in alaw-gltx intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2399 b2399 Escherichia coli 562 -11535364 237625 yfed (de:hypothetical 14.9 kd protein in alaw-gltx intergenic region) (db:swissprot) YFED_ECOLI P27238 ESCHERICHIA COLI 562 -11535364 163439 yfed hypothetical 14.9k protein glty-alaw intergenic region (cl:yfec protein) (db:pir2.dat) S11409 S11409 Escherichia coli 562 -11535364 224958 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #416(54.1-54.5 min.)) (nt:similar to (pir accession number s11409)) (le:11657) (re:12049) (di:direct) D90869 D90869 g1799813 Escherichia coli 562 -11535364 7500923407 orf130 (db:genpept-bct1) (de:escherichia coli k12 valu, gltx and alaw region.) (le:3344) (re:3736) (di:complement) ECGLTXVA X63976 g41597 Escherichia coli 562 -11535364 5000692910 (sr:escherichia coli (sub_strain n99, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli alaw (transfer rna-ala), valu (transfer rna-valand transfer rna-lys) operons and glutamyl-trna synthetase (gltx)gene, complete cds.) (nt:orf130) (le:3344) (r... ECOUXW M13687 g148257 Escherichia coli 562 -11535364 233020 yfed orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 218 of 400 of the completegenome.) (nt:o130; 100 pct identical to yfed_ecoli sw: p27238) (le:502) (re:894) (di:direct) AE000328 AE000328 g1788742 Escherichia coli 562 -11535364 111852 yfed (de:hypothetical 14.9 kd protein in alaw-gltx intergenic region) (db:swissprot) YFED_ECOLI P27238 ESCHERICHIA COLI 562 -11535364				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855807	11544	33700	858	285

Description

6500731507 yfen:b2408 hypothetical 29.2 kd protein in xapa-lig intergenic region:orf254 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2408 b2408 Escherichia coli 562 -11535365 7500923413 yfen (de:hypothetical 29.2 kd protein in xapa-lig intergenic region (orf254)) (db:swissprot) YFEN_ECOLI P45564 ESCHERICHIA COLI 562 -11535365 7000687700 yfen hypothetical 29.2 kd protein in xapa-lig intergenic region (db:pir2.dat) G65014 G65014 Escherichia coli 562 -11535365 224966 yfen (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #417(54.4-54.6 min.)) (nt:similar to (swissprot accession number p45564)) (le:4453) (re:5217) (di:direct) D90870 D90870 g1799822 Escherichia coli 562 -11535365 5000692912 (db:genpept-bct1) (de:e.coli xapa, xapb and xapr genes.) (nt:orf254) (le:2746) (re:3510) (di:direct) ECXAPAA X73828 g929585 Escherichia coli 562 -11535365 240382 yfen putative sugar hydrolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 218 of 400 of the completegenome.) (nt:o254; 100 pct identical to yxap_ecoli sw: p45564) (le:6816) (re:7580) (di:direct) AE000328 AE000328 g1788747 Escherichia coli 562 -11535365 111863 yfen (de:hypothetical 29.2 kd protein in xapa-lig intergenic region (orf254)) (db:swissprot) YFEN_ECOLI P45564 ESCHERICHIA COLI 562 -11535365

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855823	11545	33701	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855834	11546	33702	579	192

Description

5000692913 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2409 b2409 Escherichia coli 562 -11535366
7500923418 yfer (de:hypothetical transcriptional regulator in xapa-lig intergenic region) (db:swissprot) YFER_ECOLI P77500 ESCHERICHIA COLI 562 -11535366 7000691641 hypothetical protein b2409 (cl:hypothetical protein b2409) (db:pir2.dat) H65014 H65014 Escherichia coli 562 -11535366 224967 yybe (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #417(54.4-54.6 min.)) (nt:similar to (swissprot accession number p37499)) (le:5256) (re:6182) (di:complement) D90870 D90870 g1799823 Escherichia coli 562 -11535366 7500923421 yfer putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 218 of 400 of the completegenome.) (nt:f308) (le:7619) (re:8545) (di:complement) AE000328 AE000328 g1788748 Escherichia coli 562 -11535366 6500731508 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2409 b2409 Escherichia coli 562 -11535366

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855837	11547	33703	405	135

Description

6500731509 zipa:b2412 hypothetical protein:cell division protein zipa (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2412 b2412 Escherichia coli 562 -11535367 7000691642 hypothetical protein b2412 (db:pir2.dat) C65015 C65015 Escherichia coli 562 -11535367 224971 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #417(54.4-54.6 min.)) (nt:similar to (swissprot accession number p44113)) (le:9574) (re:10560) (di:complement) D90870 D90870 g1799827 Escherichia coli 562 -11535367 7500960189 zipa cell division protein involved in ftsz ring (fn:membrane; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 219 of 400 of the completegenome.) (nt:f328 was f159 and f169; ??? pct identical (2 gaps)) (le:66) (re:1052) (di:complement) AE000329 AE000329 g1788752 Escherichia coli 562 -11535367 5000692915 (de:(ecoli_2353) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2353 ECOLI_2353 Escherichia coli 562 10120185

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855839	11548	33704	381	126

Description

6500731510 yfek:b2419 hypothetical protein:hypothetical 13.7 kd protein in pdxk-cysm intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2419 b2419 Escherichia coli 562 -11535368 118675 yfek (de:hypothetical 13.7 kd protein in pdxk-cysm intergenic region) (db:swissprot) YFEK_ECOLI Q47702 ESCHERICHIA COLI 562 -11535368 7000687699 hypothetical protein b2419 (db:pir2.dat) B65016 B65016 Escherichia coli 562 -11535368 224981 yfek (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #418(54.6-54.9 min.)) (nt:similar to (swissprot accession number p40195)) (le:5710) (re:6084) (di:direct) D90871 D90871 g1799838 Escherichia coli 562 -11535368 224990 yfek (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #419(54.7-55.1 min.)) (nt:similar to (swissprot accession number p40195)) (le:471) (re:845) (di:direct) D90872 D90872 g1799848 Escherichia coli 562 -11535368 7500923412 yfek orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 219 of 400 of the completgenome.) (nt:o124; residues 1-117 are 83 pct identical to) (le:7161) (re:7535) (di:direct) AE000329 AE000329 g1788759 Escherichia coli 562 -11535368 5000692917 (de:(ecoli_2360) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2360 ECOLI_2360 Escherichia coli 562 10061026

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855843	11549	33705	534	177

Description

6500731511 yfef:ucpa:b2426 hypothetical protein in cysp
5region:oxidoreductase ucpa (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b2426 b2426 Escherichia coli 562
-11535369 111853 ucpa (ec:1.-.-.-) (de:oxidoreductase ucpa,) (db:swissprot)
UCPA_ECOLI P37440 ESCHERICHIA COLI 562 -11535369 7000686853 yfef
hypothetical protein in cysp 5region (cl:ribitol dehydrogenase:short-chain
alcohol dehydrogenase homology) (db:pir2.dat) A65017 A65017 Escherichia coli
562 -11535369 224997 yfef (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #419(54.7-55.1 min.)) (nt:similar to (swissprot accession
number p37440)) (le:6961) (re:7818) (di:complement) D90872 D90872 g1799855
Escherichia coli 562 -11535369 7500893735 ucpa putative oxidoreductase
(fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli
k-12 mg1655 section 220 of 400 of the completgenome.) (nt:f285; formerly
designated yfef) (le:2396) (re:3253) (di:complement) AE000330 AE000330
g1788766 Escherichia coli 562 -11535369 5000692919 (de:(ecoli_2366)
(pn:hypothetical oxidoreductase in cysp 5"region:fragment) (gn:yfef)
(gtcfc:13.7:14.1) (ec:1.-.-.-) (yfef_ecoli) (keggfc:11.1) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2366 ECOLI_2366 Escherichia coli 562
10120195

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855857	11550	33706	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855869	11551	33707	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855870	11552	33708	783	260

Description

6500731512 yfet:b2427 hypothetical protein:hypothetical 31.2 kd protein in cysp-amia intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2427 b2427 Escherichia coli 562 -11535370
1500687308 yfet (de:hypothetical 31.2 kd protein in cysp-amia intergenic region) (db:swissprot) YFET_ECOLI P77245 ESCHERICHIA COLI 562 -11535370
7000687701 hypothetical protein b2427 (cl:hypothetical protein ybbh) (db:pir2.dat) B65017 B65017 Escherichia coli 562 -11535370 224998 yfhh (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #419(54.7-55.1 min.)) (nt:similar to (swissprot accession number p37767)) (le:7881) (re:8738) (di:complement) D90872 D90872 g1799856 Escherichia coli 562 -11535370 7500923422 yfet orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completegenome.) (nt:f285; 35 pct identical (5 gaps) to 282 residues of) (le:3316) (re:4173) (di:complement) AE000330 AE000330 g1788767 Escherichia coli 562 -11535370 5000692920 (de:(ecoli_2367) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2367 ECOLI_2367 Escherichia coli 562 10064594

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855873	11553	33709	240	79

Description

6500731513 yfeu:b2428 hypothetical protein:hypothetical 31.2 kd protein in cysp-amia intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2428 b2428 Escherichia coli 562 -11535371
1500686272 yfeu (de:hypothetical 31.2 kd protein in cysp-amia intergenic region) (db:swissprot) YFEU_ECOLI P76535 ESCHERICHIA COLI 562 -11535371
7000687702 hypothetical protein b2428 (cl:conserved hypothetical protein b2428) (db:pir2.dat) C65017 C65017 Escherichia coli 562 -11535371
7500923423 yfeu putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completegenome.) (nt:o298; this 298 aa orf is 56 pct identical (0 gaps)) (le:4337) (re:5233) (di:direct) AE000330 AE000330 g1788768 Escherichia coli 562 -11535371 5000692921 (de:(ecoli_2368) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2368 ECOLI_2368 Escherichia coli 562 10061027

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855881	11554	33710	522	173
<u>Description</u>				
5000692922 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2429 b2429 Escherichia coli 562 -11535372				
7000691644 hypothetical protein b2429 (cl:phosphotransferase system sucrose-specific enzyme ii, factor ii) (db:pir2.dat) D65017 D65017 Escherichia coli 562 -11535372 225001 ipa-49d pts system:sucrose-specific iibc component (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #419(54.7-55.1 min.)) (nt:similar to (swissprot accession number p05306)) (le:9801) (re:11225) (di:direct) D90872 D90872 g1799859 Escherichia coli 562 -11535372 225004 ipa-49d pts system:sucrose-specific iibc component (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #420(54.9-55.2 min.)) (nt:similar to (swissprot accession number p05306)) (le:611) (re:2035) (di:direct) D90873 D90873 g1799863 Escherichia coli 562 -11535372				
7500960191 b2429 putative pts enzyme ii (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completegenome.) (nt:o474; 33 pct identical (29 gaps) to 436 residues) (le:5237) (re:6661) (di:direct) AE000330 AE000330 g1788769 Escherichia coli 562 -11535372 6500731514 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2429 b2429 Escherichia coli 562 -11535372				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855887	11555	33711	849	283

Description

5000692923 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2430 b2430 Escherichia coli 562 -11535373
7000691645 hypothetical protein b2430 (db:pir2.dat) E65017 E65017
Escherichia coli 562 -11535373 225002 ampc beta-lactamase precursor ec 3.5.2.6 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #419(54.7-55.1 min.)) (nt:similar to (swissprot accession number p24735)) (le:11143) (re:12534) (di:direct) D90872 D90872 g1799860 Escherichia coli 562 -11535373 225005 ampc beta-lactamase precursor ec 3.5.2.6 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #420(54.9-55.2 min.)) (nt:similar to (swissprot accession number p24735)) (le:1953) (re:3344) (di:direct) D90873 D90873 g1799864 Escherichia coli 562 -11535373
7500960192 b2430 putative beta-lactamase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completgenome.) (nt:o463; 24 pct identical (44 gaps) to 338 residues) (le:6579) (re:7970) (di:direct) AE000330 AE000330 g1788770 Escherichia coli 562 -11535373 6500731515 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2430 b2430 Escherichia coli 562 -11535373

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501855900	11556	33712	642	213

Description

5000692924 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2431 b2431 Escherichia coli 562 -11535374
7000691646 hypothetical protein b2431 (db:pir2.dat) F65017 F65017
Escherichia coli 562 -11535374 7500960193 b2431 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completgenome.) (nt:f308; this 308 aa orf is 25 pct identical (21 gaps)) (le:8210) (re:9136) (di:complement) AE000330 AE000330 g1788771 Escherichia coli 562 -11535374 6500731516 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2431 b2431 Escherichia coli 562 -11535374

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855901	11557	33713	570	189

Description

5000692925 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2432 b2432 Escherichia coli 562 -11535375
 7000691647 hypothetical protein b2432 (db:pir2.dat) G65017 G65017
 Escherichia coli 562 -11535375 7500960194 b2432 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completegenome.) (nt:f191; this 191 aa orf is 31 pct identical (12 gaps)) (le:9205) (re:9780) (di:complement) AE000330 AE000330 g1788772 Escherichia coli 562 -11535375 6500731517 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2432 b2432 Escherichia coli 562 -11535375

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855921	11558	33714	369	122

Description

5000692926 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2433 b2433 Escherichia coli 562 -11535376
 7000691648 hypothetical protein b2433 (db:pir2.dat) H65017 H65017
 Escherichia coli 562 -11535376 7500960195 b2433 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completegenome.) (nt:f151; this 151 aa orf is 29 pct identical (9 gaps)) (le:9841) (re:10296) (di:complement) AE000330 AE000330 g1788773 Escherichia coli 562 -11535376 6500731518 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2433 b2433 Escherichia coli 562 -11535376

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855927	11559	33715	534	177

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855928	11560	33716	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855967	11561	33717	507	169
<u>Description</u>				
5000692927 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2434 b2434 Escherichia coli 562 -11535377				
7000691649 hypothetical protein b2434 (db:pir2.dat) A65018 A65018 Escherichia coli 562 -11535377 7500960196 b2434 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 220 of 400 of the completegenome.) (nt:f178; this 178 aa orf is 26 pct identical (11 gaps)) (le:10277) (re:10813) (di:complement) AE000330 AE000330 g1788774 Escherichia coli 562 -11535377 6500731519 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2434 b2434 Escherichia coli 562 -11535377				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855976	11562	33718	360	119
<u>Description</u>				
6500731520 yfeg:b2437 hypothetical transcriptional regulator in hemf 3region:hypothetical transcriptional regulator in hemf-eutc intergenic region:orf3 (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2437 b2437 Escherichia coli 562 -11535378 111855 yfeg (de:(orf3)) (db:swissprot) YFEG_ECOLI P36547 ESCHERICHIA COLI 562 -11535378 7000687697 yfeg hypothetical transcription regulator hemf 3-region (db:pir2.dat) D65018 D65018 Escherichia coli 562 -11535378 225008 yfeg (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #420(54.9-55.2 min.)) (nt:similar to (swissprot accession number p36547)) (le:8068) (re:9120) (di:complement) D90873 D90873 g1799867 Escherichia coli 562 -11535378 225014 yfeg (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #421(55.1-55.5 min.)) (nt:similar to (swissprot accession number p36547)) (le:964) (re:2016) (di:complement) D90874 D90874 g1799874 Escherichia coli 562 -11535378 7500923410 yfeg putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:f350; 99 pct identical to yfeg_ecoli sw: p36547) (le:1860) (re:2912) (di:complement) AE000331 AE000331 g1788778 Escherichia coli 562 -11535378 5000692928 (de:(ecoli_2377) (pn:hypothetical transcriptional regulator in hemf:3"region:orf3) (gn:yfeg) (gtcfc:13.7:14.1) (ec:) (yfeg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2377 ECOLI_2377 Escherichia coli 562 10120201				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855981	11563	33719	519	173

Description

GTC ORF with score 111 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c07g1.) (nt:coded for by c. elegans cDNA yk9h5.5; coded for by) (le:19388:19575:19797) (re:19478:19741:19919) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501855999	11564	33720	1017	338

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856002	11565	33721	753	250

Description

5000692929 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2438 b2438 Escherichia coli 562 -11535379
7000691650 hypothetical protein b2438 (db:pir2.dat) E65018 E65018 Escherichia coli 562 -11535379 7500960197 b2438 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:f168; this 168 aa orf is 48 pct identical (0 gaps)) (le:2958) (re:3464) (di:complement) AE000331 AE000331 g1788779 Escherichia coli 562 -11535379 6500731521 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2438 b2438 Escherichia coli 562 -11535379

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856020	11566	33722	567	188

Description

5000692930 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2439 b2439 Escherichia coli 562 -11535380
7000691651 hypothetical protein b2439 (db:pir2.dat) F65018 F65018 Escherichia coli 562 -11535380 7500960198 b2439 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:f219; this 219 aa orf is 30 pct identical (17 gaps)) (le:3471) (re:4130) (di:complement) AE000331 AE000331 g1788780 Escherichia coli 562 -11535380 6500731522 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2439 b2439 Escherichia coli 562 -11535380

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856025	11567	33723	1200	399

Description

5000692931 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2442 b2442 Escherichia coli 562 -11535381
 7000691652 hypothetical protein b2442 (cl:satellite phage p4 integrase) (db:pir2.dat) A65019 A65019 Escherichia coli 562 -11535381 7500960199 b2442 putative prophage integrase (fn:is, phage, tn; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completengenome.) (nt:o431; this 431 aa orf is 40 pct identical (14 gaps)) (le:6501) (re:7796) (di:direct) AE000331 AE000331 g1788783 Escherichia coli 562 -11535381 6500731523 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2442 b2442 Escherichia coli 562 -11535381

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856029	11568	33724	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856030	11569	33725	1014	337

Description

5000692932 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2443 b2443 Escherichia coli 562 -11535382
 7000691653 hypothetical protein b2443 (db:pir2.dat) B65019 B65019 Escherichia coli 562 -11535382 7500960200 b2443 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completengenome.) (nt:o213; this 213 aa orf is 29 pct identical (13 gaps)) (le:7987) (re:8628) (di:direct) AE000331 AE000331 g1788784 Escherichia coli 562 -11535382 6500731524 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2443 b2443 Escherichia coli 562 -11535382

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856031	11570	33726	423	140

Description

5000692933 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2444 b2444 Escherichia coli 562 -11535383
7000691654 hypothetical protein b2444 (db:pir2.dat) C65019 C65019 Escherichia coli 562 -11535383 7500960201 b2444 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:o81) (le:9098) (re:9343) (di:direct) AE000331 AE000331 g1788785 Escherichia coli 562 -11535383 6500731525 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2444 b2444 Escherichia coli 562 -11535383

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856045	11571	33727	207	69

Description

5000692934 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2445 b2445 Escherichia coli 562 -11535384
7000691655 hypothetical protein b2445 (db:pir2.dat) D65019 D65019 Escherichia coli 562 -11535384 7500960202 b2445 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:o127; this 127 aa orf is 33 pct identical (4 gaps)) (le:9340) (re:9723) (di:direct) AE000331 AE000331 g1788786 Escherichia coli 562 -11535384 6500731526 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2445 b2445 Escherichia coli 562 -11535384

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856059	11572	33728	219	72

Description

5000692935 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2446 b2446 Escherichia coli 562 -11535385
7000691656 hypothetical protein b2446 (db:pir2.dat) E65019 E65019 Escherichia coli 562 -11535385 7500960203 b2446 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:o138; this 138 aa orf is 25 pct identical (7 gaps)) (le:9841) (re:10257) (di:direct) AE000331 AE000331 g1788787 Escherichia coli 562 -11535385 6500731527 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2446 b2446 Escherichia coli 562 -11535385

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856060	11573	33729	480	159

Description

5000692936 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2447 b2447 Escherichia coli 562 -11535386
 7000691657 hypothetical protein b2447 (db:pir2.dat) F65019 F65019
 Escherichia coli 562 -11535386 7500960204 b2447 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 221 of 400 of the completegenome.) (nt:ol97) (le:10254) (re:10847) (di:direct) AE000331 AE000331 g1788788 Escherichia coli 562 -11535386
 6500731528 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2447 b2447 Escherichia coli 562 -11535386

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856061	11574	33730	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856063	11575	33731	420	139

Description

5000692937 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2448 b2448 Escherichia coli 562 -11535387
 7000691658 hypothetical protein b2448 (db:pir2.dat) G65019 G65019
 Escherichia coli 562 -11535387 7500960205 b2448 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:ol30; this 130 aa orf is 29 pct identical (6 gaps)) (le:260) (re:652) (di:direct) AE000332 AE000332 g1788790 Escherichia coli 562 -11535387 6500731529 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2448 b2448
 Escherichia coli 562 -11535387

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856072	11576	33732	2331	777

Description

5000692938 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2449 b2449 Escherichia coli 562 -11535388
 7000691659 hypothetical protein b2449 (db:pir2.dat) H65019 H65019
 Escherichia coli 562 -11535388 7500960206 b2449 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:o130 was o103; 34 pct identical (0 gaps) to) (le:663) (re:1055) (di:direct) AE000332 AE000332 g1788791
 Escherichia coli 562 -11535388 6500731530 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2449 b2449
 Escherichia coli 562 -11535388

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856102	11577	33733	636	211

Description

GTC ORF with score 160 to: (fn:copper transport protein; is only expressed in) (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae copper transporter 3 (ctr3) gene, completecds.) (nt:ctr3p; similar to orf 19931.6 encoded by genbank) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856108	11578	33734	477	158

Description

5000692939 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2450 b2450 Escherichia coli 562 -11535389
 7000691660 hypothetical protein b2450 (db:pir2.dat) A65020 A65020
 Escherichia coli 562 -11535389 7500960207 b2450 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:o279; 30 pct identical (2 gaps) to 53 residues of) (le:1176) (re:2015) (di:direct) AE000332 AE000332 g1788792
 Escherichia coli 562 -11535389 6500731531 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2450 b2450
 Escherichia coli 562 -11535389

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856109	11579	33735	321	106

Description

5000692940 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2451 b2451 Escherichia coli 562 -11535390
 7000691661 hypothetical protein b2451 (db:pir2.dat) B65020 B65020
 Escherichia coli 562 -11535390 7500960208 b2451 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:f467; this 467 aa orf is 31 pct identical (2 gaps)) (le:2164) (re:3567) (di:complement) AE000332 AE000332 g1788793 Escherichia coli 562 -11535390 6500731532 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2451 b2451 Escherichia coli 562 -11535390

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856111	11580	33736	525	174

Description

5000692948 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2459 b2459 Escherichia coli 562 -11535391
 7000691662 hypothetical protein b2459 (db:pir2.dat) B65021 B65021
 Escherichia coli 562 -11535391 7500960209 b2459 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:f267; this 267 aa orf is 30 pct identical (4 gaps)) (le:10185) (re:10988) (di:complement) AE000332 AE000332 g1788801 Escherichia coli 562 -11535391 6500731533 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2459 b2459 Escherichia coli 562 -11535391

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856116	11581	33737	738	245

Description

5000692949 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2460 b2460 Escherichia coli 562 -11535392
 7000691663 hypothetical protein b2460 (db:pir2.dat) C65021 C65021
 Escherichia coli 562 -11535392 7500960210 b2460 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:f233; this 233 aa orf is 23 pct identical (2 gaps)) (le:10985) (re:11686) (di:complement) AE000332 AE000332 g1788802 Escherichia coli 562 -11535392 6500731534 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2460 b2460 Escherichia coli 562 -11535392

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856117	11582	33738	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856132	11583	33739	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856144	11584	33740	393	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856145	11585	33741	249	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856147	11586	33742	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856149	11587	33743	1068	355

Description

5000692950 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli) b2461 b2461 Escherichia coli 562 -11535393
 7000691664 hypothetical protein b2461 (db:pir2.dat) D65021 D65021
 Escherichia coli 562 -11535393 7500960211 b2461 orf:hypothetical protein
 (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
 222 of 400 of the completegenome.) (nt:f159 was f126; this 126 aa orf is 33
 pct identical) (le:11661) (re:12140) (di:complement) AE000332 AE000332
 g1788803 Escherichia coli 562 -11535393 6500731535 hypothetical protein
 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2461
 b2461 Escherichia coli 562 -11535393

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501856161	11588	33744	441	146

Description

5000692951 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2462 b2462 Escherichia coli 562 -11535394
 7000691665 hypothetical protein b2462 (db:pir2.dat) E65021 E65021 Escherichia coli 562 -11535394 7500960212 b2462 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:f135) (le:12153) (re:12560) (di:complement) AE000332 AE000332 g1788804 Escherichia coli 562 -11535394
 6500731536 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2462 b2462 Escherichia coli 562 -11535394

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501856162	11589	33745	750	249

Description

5000692952 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2463 b2463 Escherichia coli 562 -11535395
 7000691666 hypothetical protein b2463 (db:pir2.dat) F65021 F65021 Escherichia coli 562 -11535395 7500960213 b2463 putative multimodular enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 223 of 400 of the completegenome.) (nt:f759; this 759 aa orf is 68 pct identical (1 gap)) (le:141) (re:2420) (di:complement) AE000333 AE000333 g1788806 Escherichia coli 562 -11535395
 6500731537 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2463 b2463 Escherichia coli 562 -11535395

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501856163	11590	33746	315	104

Description

5000692954 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2466 b2466 Escherichia coli 562 -11535396
 7500952193 ypfg (de:hypothetical 38.7 kd protein in tkfb-narq intergenic region precursor) (db:swissprot) YPFG_ECOLI P76559 ESCHERICHIA COLI 562 -11535396 7000691667 hypothetical protein b2466 (db:pir2.dat) A65022 A65022 Escherichia coli 562 -11535396 7500952195 b2466 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 223 of 400 of the completegenome.) (nt:f347; this 347 aa orf is 34 pct identical (4 gaps)) (le:5777) (re:6820) (di:complement) AE000333 AE000333 g1788809 Escherichia coli 562 -11535396 6500731538 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2466 b2466 Escherichia coli 562 -11535396

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856187	11591	33747	1974	658

Description

GTC ORF with score 250 to: (sr:saccharomyces cerevisiae dna)
(db:genpept-pln1) (de:saccharomyces cerevisiae gtpase-activating protein
homologue (bud2)gene, complete cds.) (nt:' similar to gtpase activating
protein for ras) (le:397) (re:3711) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856188	11592	33748	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856201	11593	33749	684	227

Description

6500731539 yffb:b2471 hypothetical 13.6 kd protein in dape
5region: hypothetical 13.6 kd protein in acrd-dape intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2471
b2471 Escherichia coli 562 -11535397 7500923433 yffb (de: hypothetical 13.6
kd protein in acrd-dape intergenic region) (db:swissprot) YFFB_ECOLI P24178
ESCHERICHIA COLI 562 -11535397 162589 yffb 14k hypothetical protein 5 of
dape (cl: hypothetical protein yjbd) (db:pir2.dat) (mp:53 min) B42959 B42959
Escherichia coli 562 -11535397 225033 (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #422(55.5-55.8 min.)) (nt:similar to (pir accession
number b42959)) (le:14340) (re:14696) (di:direct) D90875 D90875 g1799894
Escherichia coli 562 -11535397 225037 (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #423(55.7-56.1 min.)) (nt:similar to (pir accession
number b42959)) (le:2196) (re:2552) (di:direct) D90876 D90876 g1799899
Escherichia coli 562 -11535397 5000692958 (db:genpept-bct1) (de:escherichia
coli dape gene for succinyldiaminopimelatedesuccinylase.) (nt:orf) (le:663)
(re:1019) (di:direct) ECDAPE X57403 g41233 Escherichia coli 562 -11535397
232643 yffb orf: hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 224 of 400 of the completegenome.)
(nt:ol18; 100 pct identical to yffb_ecoli sw: p24178) (le:3764) (re:4120)
(di:direct) AE000334 AE000334 g178815 Escherichia coli 562 -11535397
111873 yffb (de: hypothetical 13.6 kd protein in acrd-dape intergenic
region) (db:swissprot) YFFB_ECOLI P24178 ESCHERICHIA COLI 562 -11535397

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856204	11594	33750	417	138

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856210	11595	33751	537	178

Description

6500731540 ypfh:b2473 hypothetical protein:hypothetical 25.7 kd protein in dape-purc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2473 b2473 Escherichia coli 562 -11535398
 1500686275 ypfh (de:hypothetical 25.7 kd protein in dape-purc intergenic region) (db:swissprot) YPFH_ECOLI P76561 ESCHERICHIA COLI 562 -11535398
 7000688214 hypothetical protein b2473 (db:pir2.dat) H65022 H65022 Escherichia coli 562 -11535398 7500952196 ypfh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 224 of 400 of the completengenome.) (nt:f240) (le:5589) (re:6311) (di:complement) AE000334 AE000334 g1788817 Escherichia coli 562 -11535398
 5000692959 (de:(ecoli_2413) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2413 ECOLI_2413 Escherichia coli 562 10061030

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856211	11596	33752	606	201

Description

6500731541 ypfi:b2474 hypothetical protein:hypothetical 74.9 kd protein in dape-purc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2474 b2474 Escherichia coli 562 -11535399
 1500686276 ypfi (de:hypothetical 74.9 kd protein in dape-purc intergenic region) (db:swissprot) YPFI_ECOLI P76562 ESCHERICHIA COLI 562 -11535399
 7000688215 hypothetical protein b2474 (db:pir2.dat) A65023 A65023 Escherichia coli 562 -11535399 7500952197 ypfi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 224 of 400 of the completengenome.) (nt:f671; this 671 aa orf is 38 pct identical (13 gaps)) (le:6361) (re:8376) (di:complement) AE000334 AE000334 g1788818 Escherichia coli 562 -11535399 5000692960 (de:(ecoli_2414) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2414 ECOLI_2414 Escherichia coli 562 10061031

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501856221	11597	33753	465	154

Description

5000692961 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2475 b2475 Escherichia coli 562 -11535400
 7000691668 hypothetical protein b2475 (db:pir2.dat) B65023 B65023
 Escherichia coli 562 -11535400 7500960214 b2475 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 224 of 400 of the completegenome.) (nt:f287; this 287 aa orf is 28 pct identical (6 gaps)) (le:8391) (re:9254) (di:complement) AE000334 AE000334 g1788819 Escherichia coli 562 -11535400 6500731542 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2475 b2475 Escherichia coli 562 -11535400

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501856228	11598	33754	1221	406

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501856229	11599	33755	258	85

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501856230	11600	33756	276	91

Description

6500731543 yffe:b2481 hypothetical 22.2 kd protein in bcp 3region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2481 b2481 Escherichia coli 562 -11535401 7000690927 yffe hypothetical 22.2k protein bcp 3region (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) H65023 H65023 Escherichia coli 562 -11535401 7500959798 hyfa hydrogenase 4 fe-s subunit (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:o218; formerly designated yffe) (le:3468) (re:4124) (di:direct) AE000335 AE000335 g1788826 Escherichia coli 562 -11535401 5000692964 (de:(ecoli_2421) (pn:hypothetical 22) (gn:yffe) (gtcfc:13.7:14.1) (ec:) (yffe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2421 ECOLI_2421 Escherichia coli 562 10123704

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856231	11601	33757	1248	416

Description

GTC ORF with score 437 to: (sr:norway rat) (db:genpept) (de:rattus norvegicus sh3 domain binding protein (cr16) mrna,alternatively spliced, complete cds.) (nt:sh3 domain binding protein; alternatively spliced) (le:192) (re:1649) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856234	11602	33758	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856242	11603	33759	273	90

Description

6500731544 hyfb:b2482 hypothetical protein:hydrogenase-4 component b (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2482 b2482 Escherichia coli 562 -11535402 111877 hyfb (ec:1.-.-.-) (de:hydrogenase-4 component b,) (db:swissprot) HYFB_ECOLI P23482 ESCHERICHIA COLI 562 -11535402 7000685584 hypothetical protein b2482 bcp 3 region (cl:formate hydrogenlyase chain 3) (db:pir2.dat) A65024 A65024 Escherichia coli 562 -11535402 225048 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #423(55.7-56.1 min.)) (nt:similar to (pir accession number d49749)) (le:12768) (re:14786) (di:direct) D90876 D90876 g1799910 Escherichia coli 562 -11535402 225058 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #424(55.9-56.3 min.)) (nt:similar to (pir accession number d49749)) (le:5508) (re:7526) (di:direct) D90877 D90877 g1805541 Escherichia coli 562 -11535402 7000685585 hyfb hyfb (db:genpept-bct1) (de:escherichia coli pl77 (o177), bacterioferritin comigratory protein(bcp), putative hydrogenase-4 complex (hyfabcdefghijr), andputative formate transporter (focb) gene, complete cds and putativepermease p75 (perm) gene partial cds.)... ECOORF123 M63654 g2668496 Escherichia coli 562 -11535402 235286 hyfb hydrogenase 4 membrane subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:o672; this 672 aa orf is 36 pct identical (31 gaps)) (le:4124) (re:6142) (di:direct) AE000335 AE000335 g1788827 Escherichia coli 562 -11535402 5000692965 (de:(ecoli_2422) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2422 ECOLI_2422 Escherichia coli 562 10120220

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856246	11604	33760	318	105
<u>Description</u>				

5000692966 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2483 b2483 Escherichia coli 562 -11535403
7000691669 hypothetical protein b2483 (db:pir2.dat) B65024 B65024
Escherichia coli 562 -11535403 225049 hevD formate hydrogenlyase subunit 4 fhl subunit 4 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #423(55.7-56.1 min.)) (nt:similar to (swissprot accession number p16430)) (le:14776) (re:15744) (di:direct) D90876 D90876 g1799911 Escherichia coli 562 -11535403 225059 hevD formate hydrogenlyase subunit 4 fhl subunit 4 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #424(55.9-56.3 min.)) (nt:similar to (swissprot accession number p16430)) (le:7516) (re:8484) (di:direct) D90877 D90877 g1805542 Escherichia coli 562 -11535403
7500960215 hyfC hydrogenase 4 membrane subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:o322; this 322 aa orf is 52 pct identical (3 gaps)) (le:6132) (re:7100) (di:direct) AE000335 AE000335 g1788828 Escherichia coli 562 -11535403 6500731545 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2483 b2483 Escherichia coli 562 -11535403

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856250	11605	33761	225	74
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856276	11606	33762	756	252
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856282	11607	33763	459	152
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856300	11608	33764	183	60

Description

6500731546 hyfd:b2484 hypothetical protein:hydrogenase-4 component d (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2484 b2484 Escherichia coli 562 -11535404 1500687110 hyfd (ec:1.-.-.-) (de:hydrogenase-4 component d,) (db:swissprot) HYFD_ECOLI P77416 ESCHERICHIA COLI 562 -11535404 7000685586 hypothetical protein b2484 (db:pir2.dat) C65024 C65024 Escherichia coli 562 -11535404 225060 ndh5 nadh dehydrogenase ubiquinone ec 1.6.5.3 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #424(55.9-56.3 min.)) (nt:similar to (pir accession number a00454)) (le:8501) (re:9940) (di:direct) D90877 D90877 g1805543 Escherichia coli 562 -11535404 7500883714 hyfd hyf d (db:genpept-bct1) (de:escherichia coli p177 (o177), bacterioferritin comigratory protein(bcp), putative hydrogenase-4 complex (hyfabcdefghijr), andputative formate transporter (focb) gene, complete cds and putativepermease p75 (perm) gene partial cds.)... ECOORF123 M63654 g1616953 Escherichia coli 562 -11535404 235288 hyfd hydrogenase 4 membrane subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:o479; this 479 aa orf is 35 pct identical (39 gaps)) (le:7117) (re:8556) (di:direct) AE000335 AE000335 g1788829 Escherichia coli 562 -11535404 5000692967 (de:(ecoli_2424) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2424 ECOLI_2424 Escherichia coli 562 10063732

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856305	11609	33765	222	74

Description

6500731547 hyfe:b2485 hypothetical protein:hydrogenase-4 component e (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2485 b2485 Escherichia coli 562 -11535405 1500686957 hyfe (ec:1.-.-.-) (de:hydrogenase-4 component e,) (db:swissprot) HYFE_ECOLI P77524 ESCHERICHIA COLI 562 -11535405 7000685587 hypothetical protein b2485 (db:pir2.dat) D65024 D65024 Escherichia coli 562 -11535405 225061 mtcy251.03 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #424(55.9-56.3 min.)) (nt:similar to (swissprot accession number q10882)) (le:9952) (re:10602) (di:direct) D90877 D90877 g1805544 Escherichia coli 562 -11535405 7000685588 hyfe hyf e (db:genpept-bct1) (de:escherichia coli p177 (ol77), bacterioferritin comigratory protein(bcp), putative hydrogenase-4 complex (hyfabcdefghijr), andputative formate transporter (focb) gene, complete cds and putativepermease p75 (perm) gene partial cds.)... ECOORF123 M63654 g2668497 Escherichia coli 562 -11535405 235289 hyfe hydrogenase 4 membrane subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:o216; this 216 aa orf is 26 pct identical (3 gaps)) (le:8568) (re:9218) (di:direct) AE000335 AE000335 g1788830 Escherichia coli 562 -11535405 5000692968 (de:(ecoli_2425) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2425 ECOLI_2425 Escherichia coli 562 10063153

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856307	11610	33766	303	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856319	11611	33767	669	222

Description

GTC ORF with score 113 to: (de:(ydr264c) (pn:ankyrin repeat-containing protein akr1:ankyrin repeat-containing protein) (gn:d9954:akr1) (gtcfc:12.9) (ec:) (akr1_yeast) (keggfc:11.2) (sgdfc:3.3.0:10.1.6) (db:gtc-saccharomyces cerevisiae))

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856334	11612	33768	972	323

Description

6500731548 hyff:b2486 hypothetical protein:hydrogenase-4 component f (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2486 b2486 Escherichia coli 562 -11535406 1500687111 hyff (ec:1.-.-.-) (de:hydrogenase-4 component f,) (db:swissprot) HYFF_ECOLI P77437 ESCHERICHIA COLI 562 -11535406 7000685589 hypothetical protein b2486 (db:pir2.dat) E65024 E65024 Escherichia coli 562 -11535406 225062 hevco formate hydrogenlyase subunit 3 fhl subunit 3 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #424(55.9-56.3 min.)) (nt:similar to (swissprot accession number p16429)) (le:10607) (re:12187) (di:direct) D90877 D90877 g1805545 Escherichia coli 562 -11535406 7500883715 hyff hyf f (db:genpept-bct1) (de:escherichia coli p177 (o177), bacterioferritin comigratory protein(bcp), putative hydrogenase-4 complex (hyfabcdefghijr), andputative formate transporter (focb) gene, complete cds and putativepermease p75 (perm) gene partial cds.)... ECOORF123 M63654 g1616955 Escherichia coli 562 -11535406 235290 hyff hydrogenase 4 membrane subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completgenome.) (nt:o526; this 526 aa orf is 27 pct identical (27 gaps)) (le:9223) (re:10803) (di:direct) AE000335 AE000335 g1788831 Escherichia coli 562 -11535406 5000692969 (de:(ecoli_2426) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2426 ECOLI_2426 Escherichia coli 562 10063733

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856346	11613	33769	672	223

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856378	11614	33770	480	159

Description

GTC ORF with score 116 to: (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172) (re:8392) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856387	11615	33771	288	95

Description

6500731549 hyfg:b2487 hypothetical protein:hydrogenase-4 component g (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2487 b2487 Escherichia coli 562 -11535407 1500687114 hyfg (ec:1.-.-.-) (de:hydrogenase-4 component g,) (db:swissprot) HYFG_ECOLI P77329 ESCHERICHIA COLI 562 -11535407 7000685590 hypothetical protein b2487 (db:pir2.dat) F65024 F65024 Escherichia coli 562 -11535407 7500883716 hyfg hyfg (db:genpept-bct1) (de:escherichia coli p177 (o177), bacterioferritin comigratory protein(bcp), putative hydrogenase-4 complex (hyfabcdefghijr), andputative formate transporter (focb) gene, complete cds and putativepermease p75 (perm) gene partial cds.)... ECOORF123 M63654 g1616956 Escherichia coli 562 -11535407 235291 hyfg hydrogenase 4 subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:o555; 73 pct identical (17 gaps) to 546 residues) (le:10793) (re:12460) (di:direct) AE000335 AE000335 g1788832 Escherichia coli 562 -11535407 5000692970 (de:(ecoli_2427) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2427 ECOLI_2427 Escherichia coli 562 10063757

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856394	11616	33772	498	165

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856409	11617	33773	1677	558

Description

6500731550 hyfh:b2488 hypothetical protein:hydrogenase-4 component h (gtcfc:14.1) (ec:1.-.-.) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2488 b2488 Escherichia coli 562 -11535408 1500686056 hyfh (de:hydrogenase-4 component h) (db:swissprot) HYFH_ECOLI P77423 ESCHERICHIA COLI 562 -11535408 7000685591 hypothetical protein b2488 (cl:formate hydrogenlyase protein 6:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) G65024 G65024 Escherichia coli 562 -11535408 225064 hev f formate hydrogenlyase subunit 6 fhl subunit (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #424(55.9-56.3 min.)) (nt:similar to (swissprot accession number p16432)) (le:13854) (re:14399) (di:direct) D90877 D90877 g1805547 Escherichia coli 562 -11535408 7500883717 hyfh hyfh (db:genpept-bct1) (de:escherichia coli p177 (o177), bacterioferritin comigratory protein(bcp), putative hydrogenase-4 complex (hyfabcddefghijr), andputative formate transporter (focb) gene, complete cds and putativepermease p75 (perm) gene partial cds.)... ECOORF123 M63654 g1616957 Escherichia coli 562 -11535408 235292 hyfh hydrogenase 4 fe-s subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:o181; this 181 aa orf is 45 pct identical (2 gaps)) (le:12470) (re:13015) (di:direct) AE000335 AE000335 g1788833 Escherichia coli 562 -11535408 5000692971 (de:(ecoli_2428) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2428 ECOLI_2428 Escherichia coli 562 10060245

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856411	11618	33774	456	151

Description

6500731551 hyfi:b2489 hypothetical protein:hydrogenase-4 component i (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2489 b2489 Escherichia coli 562 -11535409 1500687116 hyfi (ec:1.-.-.-) (de:hydrogenase-4 component i,) (db:swissprot) HYFI_ECOLI P77668 ESCHERICHIA COLI 562 -11535409 7000685592 psbg homolog protein b2489 (cl:psbg protein) (db:pir2.dat) H65024 H65024 Escherichia coli 562 -11535409 7000685593 hyfi hyfi (db:genpept-bct1) (de:escherichia coli p177 (o177), bacterioferritin comigratory protein(bcp), putative hydrogenase-4 complex (hyfabcdefghijr), andputative formate transporter (focb) gene, complete cds and putativepermease p75 (perm) gene partial cds.)... ECOORF123 M63654 g2668498 Escherichia coli 562 -11535409 235293 hyfi hydrogenase 4 fe-s subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completengenome.) (nt:o252; 60 pct identical (2 gaps) to) (le:13012) (re:13770) (di:direct) AE000335 AE000335 g1788834 Escherichia coli 562 -11535409 5000692972 (de:(ecoli_2429) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2429 ECOLI_2429 Escherichia coli 562 10063771

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856442	11619	33775	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856444	11620	33776	588	195

Description

5000692973 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2490 b2490 Escherichia coli 562 -11535410 7000691670 hypothetical protein b2490 (cl:formate hydrogenlyase maturation protein) (db:pir2.dat) A65025 A65025 Escherichia coli 562 -11535410 7500960216 b2490 putative protein processing element (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completengenome.) (nt:o158 was o130; 48 pct identical (1 gap) to) (le:13700) (re:14176) (di:direct) AE000335 AE000335 g1788835 Escherichia coli 562 -11535410 6500731552 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2490 b2490 Escherichia coli 562 -11535410

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856445	11621	33777	504	168

Description

5000692974 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2491 b2491 Escherichia coli 562 -11535411
7000691671 hypothetical protein b2491 (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) B65025 B65025 Escherichia coli 562 -11535411 7500960217 hyfr putative 2-component regulator:interaction with (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:o663; this 663 aa orf is 51 pct identical (19 gaps)) (le:14227) (re:16218) (di:direct) AE000335 AE000335 g1788836 Escherichia coli 562 -11535411 6500731553 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2491 b2491 Escherichia coli 562 -11535411

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856447	11622	33778	336	111

Description

6500731554 focb:b2492 hypothetical protein:probable formate transporter 2:formate channel 2 (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2492 b2492 Escherichia coli 562 -11535412
1500686091 focb (de:probable formate transporter 2 (formate channel 2)) (db:swissprot) FOCB_ECOLI P77733 ESCHERICHIA COLI 562 -11535412 7000685313 focb probable formate transport protein 2:probable formate channel protein 2 (cl:formate dehydrogenase focb) (db:pir2.dat) C65025 C65025 Escherichia coli 562 -11535412 225069 foca probable formate transporter formate channel . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #425(56.2-56.5 min.)) (nt:similar to (swissprot accession number p21501)) (le:1845) (re:2693) (di:direct) D90878 D90878 g1805553 Escherichia coli 562 -11535412
7500881696 focb formate channel b (db:genpept-bct1) (de:escherichia coli p177 (o177), bacterioferritin comigratory protein(bcp), putative hydrogenase-4 complex (hyfabcdefghijr), andputative formate transporter (focb) gene, complete cds and putativepermease p75 (perm) gene partial cds)... ECOORF123 M63654 g1616961 Escherichia coli 562 -11535412 235296 focb probable formate transporter formate channel (fn:putative transport; transport of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:o282; this 282 aa orf is 50 pct identical (1 gap)) (le:16240) (re:17088) (di:direct) AE000335 AE000335 g1788837 Escherichia coli 562 -11535412 5000692975 (de:(ecoli_2432) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2432 ECOLI_2432 Escherichia coli 562 10060366

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856448	11623	33779	714	237

Description

6500731555 perm:b2493 hypothetical protein:putative permease perm
(gtcfc:11.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2493
b2493 Escherichia coli 562 -11535413 1500687003 perm (de:putative permease
perm) (db:swissprot) PERM_ECOLI P77406 ESCHERICHIA COLI 562 -11535413
7000686115 hypothetical protein b2493 (db:pir2.dat) D65025 D65025
Escherichia coli 562 -11535413 225070 (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #425(56.2-56.5 min.)) (nt:similar to (swissprot accession
number p43970)) (le:2731) (re:3792) (di:complement) D90878 D90878 g1805554
Escherichia coli 562 -11535413 7500887838 perm putative permease
(fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:f353; this
353 aa orf is 69 pct identical (0 gaps)) (le:17126) (re:18187)
(di:complement) AE000335 AE000335 g1788838 Escherichia coli 562 -11535413
5000692976 (de:(ecoli_2433) (pn:function not assigned) (gtcfc:13.7:14.1)
(ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2433
ECOLI_2433 Escherichia coli 562 10063332

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856473	11624	33780	1818	605

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856476	11625	33781	600	200

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856506	11626	33782	2121	707

Description

5000692977 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2494 b2494 Escherichia coli 562 -11535414
 7000691672 hypothetical protein b2494 (db:pir2.dat) E65025 E65025
 Escherichia coli 562 -11535414 7500960218 b2494 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 226 of 400 of the completegenome.) (nt:o487; this 487 aa orf is 25 pct identical (24 gaps)) (le:137) (re:1600) (di:direct) AE000336 AE000336
 g1788840 Escherichia coli 562 -11535414 6500731556 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2494 b2494 Escherichia coli 562 -11535414

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856533	11627	33783	1638	545

Description

5000692978 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2495 b2495 Escherichia coli 562 -11535415
 7000691673 hypothetical protein b2495 (db:pir2.dat) F65025 F65025
 Escherichia coli 562 -11535415 7500960219 b2495 putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 226 of 400 of the completegenome.) (nt:o119; this 119 aa orf is 50 pct identical (0 gaps)) (le:1621) (re:1980) (di:direct) AE000336 AE000336
 g1788841 Escherichia coli 562 -11535415 6500731557 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2495 b2495 Escherichia coli 562 -11535415

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856545	11628	33784	2472	823

Description

GTC ORF with score 171 to: (fn:involved in heterokaryon incompatibility) (sr:podospira anserina dna) (db:genpept-vr1) (de:podospira anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856547	11629	33785	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856555	11630	33786	432	143

Description

5000692979 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2496 b2496 Escherichia coli 562 -11535416
 7000691674 hypothetical protein b2496 (db:pir2.dat) G65025 G65025 Escherichia coli 562 -11535416 7500960220 b2496 putative dna replication factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 226 of 400 of the completegenome.) (nt:f248; residues 73-246 are 51 pct identical to) (le:2118) (re:2864) (di:complement) AE000336 AE000336 g1788842 Escherichia coli 562 -11535416
 6500731558 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2496 b2496 Escherichia coli 562 -11535416

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856567	11631	33787	348	115

Description

5000692980 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2503 b2503 Escherichia coli 562 -11535417
 7000691675 hypothetical protein b2503 (db:pir2.dat) F65026 F65026 Escherichia coli 562 -11535417 225081 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #427(56.5-56.9 min.)) (nt:similar to (swissprot accession number q04855)) (le:1533) (re:3776) (di:complement) D90880 D90880 g1805566 Escherichia coli 562 -11535417 7500960221 b2503 putative cytochrome c-type biogenesis protein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 226 of 400 of the completegenome.) (nt:f747; this 747 aa orf is 31 pct identical (7 gaps)) (le:10738) (re:12981) (di:complement) AE000336 AE000336 g1788849 Escherichia coli 562 -11535417 6500731559 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2503 b2503 Escherichia coli 562 -11535417

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856569	11632	33788	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856571	11633	33789	1191	396

Description

5000692981 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2504 b2504 Escherichia coli 562 -11535418
 7000691676 hypothetical protein b2504 (db:pir2.dat) G65026 G65026
 Escherichia coli 562 -11535418 7500960222 b2504 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 227 of 400 of the completegenome.) (nt:o63; this 63 aa orf is 40 pct identical (1 gap)) (le:206) (re:397) (di:direct) AE000337 AE000337 g1788851 Escherichia coli 562 -11535418 6500731560 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2504 b2504 Escherichia coli 562 -11535418

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856576	11634	33790	519	172

Description

5000692982 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2505 b2505 Escherichia coli 562 -11535419
 7000691677 hypothetical protein b2505 (db:pir2.dat) H65026 H65026
 Escherichia coli 562 -11535419 7500960223 b2505 putative outer membrane lipoprotein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 227 of 400 of the completegenome.) (nt:o172; this 172 aa orf is 29 pct identical (15 gaps)) (le:708) (re:1226) (di:direct) AE000337 AE000337 g1788852 Escherichia coli 562 -11535419 6500731561 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2505 b2505 Escherichia coli 562 -11535419

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856580	11635	33791	1038	345

Description

5000692983 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2506 b2506 Escherichia coli 562 -11535420
 7000691678 hypothetical protein b2506 (db:pir2.dat) A65027 A65027
 Escherichia coli 562 -11535420 7500960224 b2506 putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 227 of 400 of the completegenome.) (nt:o179; this 179 aa orf is 30 pct identical (4 gaps)) (le:1242) (re:1781) (di:direct) AE000337 AE000337 g1788853 Escherichia coli 562 -11535420 6500731562 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2506 b2506 Escherichia coli 562 -11535420

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856601	11636	33792	1677	559

Description

5000692984 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2510 b2510 Escherichia coli 562 -11535421
 7502852267 yfgj (de:hypothetical 9.2 kd protein in xsea-hiss intergenic region) (db:swissprot) YFGJ_ECOLI P76575 ESCHERICHIA COLI 562 -11535421
 7000691679 hypothetical protein b2510 (db:pir2.dat) E65027 E65027 Escherichia coli 562 -11535421 7500960225 b2510 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 227 of 400 of the completegenome.) (nt:f83; this 83 aa orf is 28 pct identical (3 gaps)) (le:6515) (re:6766) (di:complement) AE000337 AE000337 g1788857 Escherichia coli 562 -11535421 6500731563 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2510 b2510 Escherichia coli 562 -11535421

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856629	11637	33793	375	124

Description

5000692985 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2511 b2511 Escherichia coli 562 -11535422
 7502852268 yfgk (de:hypothetical gtp-binding protein in xsea-hiss intergenic region) (db:swissprot) YFGK_ECOLI P77254 ESCHERICHIA COLI 562 -11535422 7000691680 hypothetical protein b2511 (cl:translation elongation factor tu homology) (db:pir2.dat) F65027 F65027 Escherichia coli 562 -11535422 225085 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #427(56.5-56.9 min.)) (nt:similar to (swissprot accession number p44536)) (le:10722) (re:12233) (di:complement) D90880 D90880 g1805570 Escherichia coli 562 -11535422 7500960226 b2511 putative gtp-binding factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 227 of 400 of the completegenome.) (nt:f503; this 503 aa orf is 72 pct identical (12 gaps)) (le:6800) (re:8311) (di:complement) AE000337 AE000337 g1788858 Escherichia coli 562 -11535422 6500731564 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2511 b2511 Escherichia coli 562 -11535422

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856634	11638	33794	204	67

Description

5000692986 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2512 b2512 Escherichia coli 562 -11535423
7500923464 yfgl (de:hypothetical 41.9 kd protein in xsea-hiss intergenic region) (db:swissprot) YFGL_ECOLI P77774 ESCHERICHIA COLI 562 -11535423
7000691681 hypothetical protein b2512 (db:pir2.dat) G65027 G65027 Escherichia coli 562 -11535423 225086 afsk serine/threonine protein kinase afsk ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #427(56.5-56.9 min.)) (nt:similar to (swissprot accession number p54741)) (le:12312) (re:13490) (di:complement) D90880 D90880 g1805571 Escherichia coli 562 -11535423 7500923467 b2512 putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 227 of 400 of the completegenome.) (nt:f392; this 392 aa orf is 27 pct identical (29 gaps)) (le:8390) (re:9568) (di:complement) AE000337 AE000337 g1788859 Escherichia coli 562 -11535423 6500731565 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2512 b2512 Escherichia coli 562 -11535423

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856639	11639	33795	1092	364

Description

5000692987 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2513 b2513 Escherichia coli 562 -11535424
7502852269 yfgm (de:hypothetical 22.2 kd protein in xsea-hiss intergenic region) (db:swissprot) YFGM_ECOLI P76576 ESCHERICHIA COLI 562 -11535424
7000691682 hypothetical protein b2513 (cl:hypothetical protein hi0370) (db:pir2.dat) H65027 H65027 Escherichia coli 562 -11535424 7500960227 b2513 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 227 of 400 of the completegenome.) (nt:f206; this 206 aa orf is 36 pct identical (2 gaps)) (le:9579) (re:10199) (di:complement) AE000337 AE000337 g1788860 Escherichia coli 562 -11535424
6500731566 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2513 b2513 Escherichia coli 562 -11535424

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856640	11640	33796	351	116

Description

6500731567 yfga:b2516 hypothetical 36.2 kd protein in ndk-gcpe intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2516 b2516 Escherichia coli 562 -11535425 111889 yfga (de:hypothetical 36.2 kd protein in ndk-gcpe intergenic region) (db:swissprot) YFGA_ECOLI P27434 ESCHERICHIA COLI 562 -11535425 7000687705 yfga hypothetical 36.2k protein ndk-gcpe intergenic region (db:pir2.dat) C65028 C65028 Escherichia coli 562 -11535425 225092 yfga (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #428(56.8-57.0 min.).) (nt:similar to (swissprot accession number p27434)) (le:737) (re:1750) (di:complement) D90881 D90881 g1799915 Escherichia coli 562 -11535425 7500923456 yfga putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 228 of 400 of the completegenome.) (nt:f337; 100 pct identical to yfga_ecoli sw: p27434) (le:1231) (re:2244) (di:complement) AE000338 AE000338 g1788864 Escherichia coli 562 -11535425 5000692989 (de:(ecoli_2456) (pn:hypothetical 36) (gn:yfga) (gtcfc:13.7:14.1) (ec:) (yfga_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2456 ECOLI_2456 Escherichia coli 562 10053617

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856643	11641	33797	432	143
<u>Description</u>				
<p>6500731568 yfgb:b2517 hypothetical 43.1 kd protein in ndk-gcpe intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2517 b2517 Escherichia coli 562 -11535426 111890 yfgb (de:hypothetical 43.1 kd protein in ndk-gcpe intergenic region) (db:swissprot) YFGB_ECOLI P36979 ESCHERICHIA COLI 562 -11535426 7000687706 yfgb hypothetical 43.1 kd protein in ndk-gcpe intergenic region (cl:conserved hypothetical protein hi0365) (db:pir2.dat) D65028 D65028 Escherichia coli 562 -11535426 225093 yfgb (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #428(56.8-57.0 min.)) (nt:similar to (swissprot accession number p36979)) (le:2035) (re:3189) (di:complement) D90881 D90881 g1799916 Escherichia coli 562 -11535426 225097 yfgb (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #429(56.9-57.2 min.)) (nt:similar to (swissprot accession number p36979)) (le:1039) (re:2193) (di:complement) D90882 D90882 g1799921 Escherichia coli 562 -11535426 7500923457 unknown (db:genpept-bct1) (de:escherichia coli k12 orf384 gene, complete cds, and orf337 gene,partial cds.) (nt:orf384) (le:235) (re:1389) (di:direct) ECU02965 U02965 g493519 Escherichia coli 562 -11535426 238455 yfgb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 228 of 400 of the completegenome.) (nt:f384; 100 pct identical to yfgb_ecoli sw: p36979) (le:2529) (re:3683) (di:complement) AE000338 AE000338 g1788865 Escherichia coli 562 -11535426 5000692990 (de:(ecoli_2457) (pn:hypothetical 43) (gn:yfgb) (gtcfc:13.7:14.1) (ec:) (yfgb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2457 ECOLI_2457 Escherichia coli 562 10053618</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856646	11642	33798	375	125

Description

6500731569 pbpc:b2519 hypothetical protein:bifunctional penicillin-binding protein 1c precursor:pbp-1c (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2519 b2519 Escherichia coli 562 -11535427
 1500686791 pbpc (de:bifunctional penicillin-binding protein 1c precursor (pbp-1c)) (db:swissprot) PBPC_ECOLI P76577 ESCHERICHIA COLI 562 -11535427
 7000686094 hypothetical protein b2519 (db:pir2.dat) F65028 F65028 Escherichia coli 562 -11535427 7500887706 pbpc bifunctional penicillin-binding protein 1c (fn:bifunctional murein) (db:genpept-bct1) (de:escherichia coli bifunctional penicillin-binding protein 1c (pbpc)gene, complete cds.) (nt:pbplc; similar to orf f770 encoded by sequence with) (le:89) (re:2401) (di:direct) ECU88571 U88571 g1850613 Escherichia coli 562 -11535427 295909 pbpc putative peptidoglycan enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 228 of 400 of the completegenome.) (nt:f770; this 770 aa orf is 31 pct identical (43 gaps)) (le:4413) (re:6725) (di:complement) AE000338 AE000338 g1788867 Escherichia coli 562 -11535427 5000692991 (de:(ecoli_2459) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2459 ECOLI_2459 Escherichia coli 562 10062583

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856652	11643	33799	687	228

Description

5000692992 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2520 b2520 Escherichia coli 562 -11535428
 7000691683 hypothetical protein b2520 (db:pir2.dat) G65028 G65028 Escherichia coli 562 -11535428 7500960228 b2520 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 228 of 400 of the completegenome.) (nt:f1653; f1653) (le:6726) (re:11687) (di:complement) AE000338 AE000338 g1788868 Escherichia coli 562 -11535428
 6500731570 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2520 b2520 Escherichia coli 562 -11535428

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856677	11644	33800	348	115

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856681	11645	33801	564	187

Description

6500731571 yfhi:b2523 hypothetical protein in fdx 3region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2523 b2523 Escherichia coli 562 -11535429 7000691829 yfhi hypothetical protein in fdx 3region (db:pir2.dat) B65029 B65029 Escherichia coli 562 -11535429 7500960346 pepb putative peptidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 229 of 400 of the completegenome.) (nt:f456; formerly designated yfhi) (le:1357) (re:2727) (di:complement) AE000339 AE000339 g1788872 Escherichia coli 562 -11535429 5000692994 (de:(ecoli_2463) (pn:hypothetical protein in fdx:3"region:fragment) (gn:yfhi) (gtcfc:13.7:14.1) (ec:) (yfhi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2463 ECOLI_2463 Escherichia coli 562 10123720

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856683	11646	33802	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856686	11647	33803	1104	368

Description

6500731572 yfhj:b2524 hypothetical 7.7 kd protein in fdx
3region:hypothetical 7.7 kd protein in ppeb-fdx intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2524
b2524 Escherichia coli 562 -11535430 111914 yfhj (de:hypothetical 7.7 kd
protein in ppeb-fdx intergenic region) (db:swissprot) YFHJ_ECOLI P37096
ESCHERICHIA COLI 562 -11535430 7000687710 yfhj hypothetical 7.7 kd protein
in fdx 3region (db:pir2.dat) C65029 C65029 Escherichia coli 562 -11535430
225103 yfhj (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#429(56.9-57.2 min.)) (nt:similar to (swissprot accession number p37096))
(le:14444) (re:14644) (di:complement) D90882 D90882 g1799927 Escherichia
coli 562 -11535430 225107 yfhj (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #430(57.2-57.5 min.)) (nt:similar to (swissprot accession
number p37096)) (le:299) (re:499) (di:complement) D90883 D90883 g1799932
Escherichia coli 562 -11535430 7500923486 yfhj orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
229 of 400 of the completegenome.) (nt:f66; 100 pct identical to yfhj_ecoli
sw: p37096) (le:2818) (re:3018) (di:complement) AE000339 AE000339 g1788873
Escherichia coli 562 -11535430 5000692995 (de:(ecoli_2464) (pn:hypothetical
7) (gn:yfhj) (gtcfc:13.7:14.1) (ec:) (yfhj_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2464 ECOLI_2464 Escherichia
coli 562 10053642

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856689	11648	33804	654	217

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856696	11649	33805	444	147

Description

6500731573 yfhe:b2527 hypothetical 20.1 kd protein in hsca
5region:hypothetical 20.1 kd protein in hsca-suhb intergenic region:orf-1
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2527
b2527 Escherichia coli 562 -11535431 111908 hscb (de:chaperone protein hscb
(hsc20)) (db:swissprot) HSCB_ECOLI P36540 ESCHERICHIA COLI 562 -11535431
162962 yfhe dnaj homolog hsca 5-region (db:pir2.dat) A36958 A36958
Escherichia coli 562 -11535431 225110 yfhe (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #430(57.2-57.5 min.)) (nt:similar to
(swissprot accession number p36540)) (le:2715) (re:3230) (di:complement)
D90883 D90883 g1799935 Escherichia coli 562 -11535431 7500883560 orf-1
(fn:unknown) (db:genpept-bct1) (de:escherichia coli k-12 heat shock protein
70 (hsca) gene, completecds.) (le:526) (re:1041) (di:direct) ECOHSCA U01827
g402674 Escherichia coli 562 -11535431 234688 yfhe orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
229 of 400 of the completegenome.) (nt:f171; 100 pct identical to yfhe_ecoli
sw: p36540) (le:5234) (re:5749) (di:complement) AE000339 AE000339 g1788876
Escherichia coli 562 -11535431 5000692996 (de:(ecoli_2467) (pn:hypothetical
20) (gn:yfhe) (gtcfc:13.7:14.1) (ec:) (yfhe_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2467 ECOLI_2467 Escherichia
coli 562 10053636

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856706	11650	33806	363	120

Description

6500731574 yfhf:b2528 hypothetical protein in hscA 5region:hypothetical 11.5 kd protein in hscA-suhb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2528 b2528 Escherichia coli 562 -11535432 111909 yfhf (de:hypothetical 11.5 kd protein in hscA-suhb intergenic region) (db:swissprot) YFHF_ECOLI P36539 ESCHERICHIA COLI 562 -11535432 7000687709 yfhf hypothetical protein in hscA 5region (cl:conserved hypothetical protein hi0376) (db:pir2.dat) G65029 G65029 Escherichia coli 562 -11535432 225111 yfhf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #430(57.2-57.5 min.)) (nt:similar to (swissprot accession number p36539)) (le:3326) (re:3649) (di:complement) D90883 D90883 g1799936 Escherichia coli 562 -11535432 7500923483 yfhf putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 229 of 400 of the completegenome.) (nt:f107; 91 pct identical to yfhf_ecoli sw: p36539) (le:5845) (re:6168) (di:complement) AE000339 AE000339 g1788877 Escherichia coli 562 -11535432 5000692997 (de:(ecoli_2468) (pn:hypothetical 11) (gn:yfhf) (gtcfc:13.7:14.1) (ec:) (yfhf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2468 ECOLI_2468 Escherichia coli 562 10120247

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856707	11651	33807	813	270

Description

5000692998 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2529 b2529 Escherichia coli 562 -11535433 7000691684 hypothetical protein b2529 (cl:yeast nitrogen fixation protein:nitrogen fixation protein homology) (db:pir2.dat) H65029 H65029 Escherichia coli 562 -11535433 225112 nifu nifu protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #430(57.2-57.5 min.)) (nt:similar to (swissprot accession number p05340)) (le:3666) (re:4052) (di:complement) D90883 D90883 g1799937 Escherichia coli 562 -11535433 7500953957 b2529 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 229 of 400 of the completegenome.) (nt:f128; this 128 aa orf is 50 pct identical (5 gaps)) (le:6185) (re:6571) (di:complement) AE000339 AE000339 g1788878 Escherichia coli 562 -11535433 6500731575 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2529 b2529 Escherichia coli 562 -11535433

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856712	11652	33808	474	157

Description

5000692999 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2530 b2530 Escherichia coli 562 -11535434
7000691685 hypothetical protein b2530 (cl:nitrogen fixation protein nifs) (db:pir2.dat) A65030 A65030 Escherichia coli 562 -11535434 7500960229 yfho putative aminotransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 229 of 400 of the completegenome.) (nt:f412; this 412 aa orf is 56 pct identical (2 gaps)) (le:6599) (re:7837) (di:complement) AE000339 AE000339 g1788879 Escherichia coli 562 -11535434 6500731576 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2530 b2530 Escherichia coli 562 -11535434

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856713	11653	33809	510	169

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856718	11654	33810	624	207

Description

5000693000 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2531 b2531 Escherichia coli 562 -11535435
7000691686 hypothetical protein b2531 (cl:hypothetical protein b2531) (db:pir2.dat) B65030 B65030 Escherichia coli 562 -11535435 225114 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #430(57.2-57.5 min.)) (nt:similar to (swissprot accession number p44675)) (le:5406) (re:5894) (di:complement) D90883 D90883 g1799939 Escherichia coli 562 -11535435 7500955874 b2531 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 229 of 400 of the completegenome.) (nt:f162; this 162 aa orf is 63 pct identical (0 gaps)) (le:7925) (re:8413) (di:complement) AE000339 AE000339 g1788880 Escherichia coli 562 -11535435 6500731577 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2531 b2531 Escherichia coli 562 -11535435

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856720	11655	33811	420	139

Description

5000693001 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2532 b2532 Escherichia coli 562 -11535436
7000691687 hypothetical protein b2532 (cl:conserved hypothetical protein mth1849) (db:pir2.dat) C65030 C65030 Escherichia coli 562 -11535436 225115 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #430(57.2-57.5 min.)) (nt:similar to (swissprot accession number p44676)) (le:6346) (re:7086) (di:complement) D90883 D90883 g1799940 Escherichia coli 562 -11535436 7500960230 b2532 putative atp synthase beta subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 229 of 400 of the completegenome.) (nt:f246; this 246 aa orf is 54 pct identical (6 gaps)) (le:8865) (re:9605) (di:complement) AE000339 AE000339 g1788881 Escherichia coli 562 -11535436 6500731578 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2532 b2532 Escherichia coli 562 -11535436

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856728	11656	33812	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856739	11657	33813	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856757	11658	33814	531	176

Description

5000693003 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2534 b2534 Escherichia coli 562 -11535437
7000691688 hypothetical protein b2534 (db:pir2.dat) E65030 E65030
Escherichia coli 562 -11535437 225117 bem46 bem46 protein fragment . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #430(57.2-57.5 min.)) (nt:similar to (swissprot accession number p54069)) (le:8126) (re:9007) (di:direct) D90883 D90883 g1799942 Escherichia coli 562 -11535437 225125 bem46 bem46 protein fragment . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p54069)) (le:1587) (re:2468) (di:direct) D90884 D90884 g1799951 Escherichia coli 562 -11535437 7500960231 b2534 putative enzyme 3.4.- (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:o293; this 293 aa orf is 30 pct identical (15 gaps)) (le:89) (re:970) (di:direct) AE000340 AE000340 g1788884 Escherichia coli 562 -11535437 6500731579 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2534 b2534 Escherichia coli 562 -11535437

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856761	11659	33815	576	191

Description

6500731580 yfhs:b2536 hypothetical protein:hypothetical 41.6 kd protein in csie-glya intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2536 b2536 Escherichia coli 562 -11535438
 4000708207 yfhs (de:hypothetical 41.6 kd protein in csie-glya intergenic region) (db:swissprot) YFHS_ECOLI Q47142 ESCHERICHIA COLI 562 -11535438
 7000687713 hypothetical protein b2536 (cl:conserved hypothetical protein hi0308) (db:pir2.dat) G65030 G65030 Escherichia coli 562 -11535438 225120 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #430(57.2-57.5 min.)) (nt:similar to (swissprot accession number p44629)) (le:10470) (re:11609) (di:complement) D90883 D90883 g1799945 Escherichia coli 562 -11535438 225128 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p44629)) (le:3931) (re:5070) (di:complement) D90884 D90884 g1799954 Escherichia coli 562 -11535438 7500923491 hcat mfs major facilitator superfamily transporter (fn:transport; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:f379; this 379 aa orf is 36 pct identical (5 gaps)) (le:2433) (re:3572) (di:complement) AE000340 AE000340 g1788886 Escherichia coli 562 -11535438 5000693005 (de:(ecoli_2476) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2476 ECOLI_2476 Escherichia coli 562 10120256

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856766	11660	33816	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856770	11661	33817	924	307

Description

6500731581 yfht:b2537 hypothetical protein:hypothetical transcriptional regulator in csie-glya intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2537 b2537 Escherichia coli 562 -11535439 4000708149 yfht (de:hypothetical transcriptional regulator in csie-glya intergenic region) (db:swissprot) YFHT_ECOLI Q47141 ESCHERICHIA COLI 562 -11535439 7000687714 hypothetical protein b2537 (cl:pseudomonas putida regulatory protein catr) (db:pir2.dat) H65030 H65030 Escherichia coli 562 -11535439 7500923493 hcar transcriptional activator of hca cluster (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:f327; 93 pct identical (1 gap) to unknown) (le:3732) (re:4622) (di:complement) AE000340 AE000340 g1788887 Escherichia coli 562 -11535439 5000693006 (de:(ecoli_2477) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2477 ECOLI_2477 Escherichia coli 562 10123723

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856779	11662	33818	609	202

Description

5000693009 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2540 b2540 Escherichia coli 562 -11535440
7500883072 hcac:hcaa3 (de:digoxigenin ferredoxin subunit) (db:swissprot) HCAC_ECOLI P77266 ESCHERICHIA COLI 562 -11535440 7000691689 hypothetical protein b2540 (cl:toluene dioxygenase ferredoxin component) (db:pir2.dat) C65031 C65031 Escherichia coli 562 -11535440 225132 bphf biphenyl dioxygenase system ferredoxin (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p37332)) (le:8132) (re:8452) (di:direct) D90884 D90884 g1799958 Escherichia coli 562 -11535440 7500883075 hcaa3 ferredoxin (db:genpept-bct1) (de:e.coli hcaa2, hcaa3, hcab, hcaa4 and yqjf genes.) (nt:part of multicomponent 3-phenylpropionate) (le:397) (re:717) (di:direct) ECHCAA234 Y11070 g2072111 Escherichia coli 562 -11535440 7500883074 hcac ferredoxin subunit of phenylpropionate (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:o106; this 106 aa orf is 44 pct identical (3 gaps)) (le:6634) (re:6954) (di:direct) AE000340 AE000340 g1788890 Escherichia coli 562 -11535440 1500689800 bphf biphenyl dioxygenase system ferredoxin (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p37332)) (le:8132) (re:8452) (di:direct) D90884 D90884 g1799958 Escherichia coli 562 -11535440 6500731582 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2540 b2540 Escherichia coli 562 -11535440

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856785	11663	33819	306	101

Description

5000693010 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2541 b2541 Escherichia coli 562 -11535441
7500923494 yfhx (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YFHX_ECOLI
P77646 ESCHERICHIA COLI 562 -11535441 7000691690 hypothetical protein b2541
(cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) D65031 D65031
Escherichia coli 562 -11535441 225133 bphb biphenyl-2:3-dihydro-2:3-diol
dehydrogenase ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p50206))
(le:8449) (re:9261) (di:direct) D90884 D90884 g1799959 Escherichia coli 562
-11535441 7500923497 hcab 2:3-dihydroxy-2:3-dihydrophenylpropionate
(fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.)
(nt:o270; this 270 aa orf is 47 pct identical (0 gaps)) (le:6951) (re:7763)
(di:direct) AE000340 AE000340 g1788891 Escherichia coli 562 -11535441
6500731583 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2541 b2541 Escherichia coli 562 -11535441

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856786	11664	33820	369	122

Description

5000693011 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2542 b2542 Escherichia coli 562 -11535442
7500883076 hcaa:hcaa4 (ec:1.18.1.3) (de:(ec 1.18.1.3)) (db:swissprot) HCAD_ECOLI P77650 ESCHERICHIA COLI 562 -11535442 7000691691 hypothetical protein b2542 (db:pir2.dat) E65031 E65031 Escherichia coli 562 -11535442
225134 bphg biphenyl dioxygenase system ferredoxin--nad + (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p37337)) (le:9271) (re:10473) (di:direct) D90884 D90884 g1799960 Escherichia coli 562 -11535442 1500689801 bphg biphenyl dioxygenase system ferredoxin--nad + (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #432(57.5-57.9 min.)) (nt:similar to (swissprot accession number p37337)) (le:77) (re:1279) (di:direct) D90885 D90885 g1799968 Escherichia coli 562 -11535442 7500883079 hcaa4 ferredoxin reductase (db:genpept-bct1) (de:e.coli hcaa2, hcaa3, hcaa4 and yqj genes.) (nt:part of multicomponent phenylpropionate) (le:1536) (re:2738) (di:direct) ECHCAA234 Y11070 g2072113 Escherichia coli 562 -11535442 7500883078 hcaa4 ferredoxin reductase subunit of phenylpropionate (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:o400; this 400 aa orf is 35 pct identical (5 gaps)) (le:7773) (re:8975) (di:direct) AE000340 AE000340 g1788892 Escherichia coli 562 -11535442 225141 bphg biphenyl dioxygenase system ferredoxin--nad + (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p37337)) (le:9271) (re:10473) (di:direct) D90884 D90884 g1799960 Escherichia coli 562 -11535442 6500731584 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2542 b2542 Escherichia coli 562 -11535442

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856787	11665	33821	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856790	11666	33822	249	82

Description

5000693012 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2543 b2543 Escherichia coli 562 -11535443
7500952203 ypha (de:hypothetical 17.9 kd protein in csie-glya intergenic region) (db:swissprot) YPHA_ECOLI P77751 ESCHERICHIA COLI 562 -11535443
7000691692 hypothetical protein b2543 (db:pir2.dat) F65031 F65031 Escherichia coli 562 -11535443 225135 yqjf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p42619)) (le:10498) (re:10992) (di:direct) D90884 D90884 g1799961 Escherichia coli 562 -11535443 1500689802 yqjf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #432(57.5-57.9 min.)) (nt:similar to (swissprot accession number p42619)) (le:1304) (re:1798) (di:direct) D90885 D90885 g1799969 Escherichia coli 562 -11535443 7500952206 yqjf (db:genpept-bct1) (de:e.coli hcaa2, hcaa3, hcab, hcaa4 and yqjf genes.) (le:2763) (re:3257) (di:direct) ECHCAA234 Y11070 g2072114 Escherichia coli 562 -11535443 7500952205 ypha orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:o164; this 164 aa orf is 43 pct identical (7 gaps)) (le:9000) (re:9494) (di:direct) AE000340 AE000340 g1788893 Escherichia coli 562 -11535443 225142 yqjf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p42619)) (le:10498) (re:10992) (di:direct) D90884 D90884 g1799961 Escherichia coli 562 -11535443 6500731585 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2543 b2543 Escherichia coli 562 -11535443

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856791	11667	33823	561	186

Description

5000693013 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2544 b2544 Escherichia coli 562 -11535444
7500952208 yphb (de:hypothetical 32.7 kd protein in csie-glya intergenic region) (db:swissprot) YPHB_ECOLI P76584 ESCHERICHIA COLI 562 -11535444
7000691693 hypothetical protein b2544 (db:pir2.dat) G65031 G65031 Escherichia coli 562 -11535444 7500952210 yphb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:f290; this 290 aa orf is 32 pct identical (4 gaps)) (le:9542) (re:10414) (di:complement) AE000340 AE000340 g1788894 Escherichia coli 562 -11535444 6500731586 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2544 b2544 Escherichia coli 562 -11535444

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856830	11668	33824	249	82

Description

5000693014 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2545 b2545 Escherichia coli 562 -11535445
7500952212 yphc (de:intergenic region) (db:swissprot) YPHC_ECOLI P77360
ESCHERICHIA COLI 562 -11535445 7000691694 hypothetical protein b2545
(cl:long-chain alcohol dehydrogenase homology) (db:pir2.dat) H65031 H65031
Escherichia coli 562 -11535445 225136 gutb sorbitol dehydrogenase ec
1.1.1.14 l-iditol (sr:escherichia coli (strain:k12) dna, clone_lib:kohara
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#431(57.3-57.7 min.)) (nt:similar to (swissprot accession number q06004))
(le:11924) (re:13018) (di:complement) D90884 D90884 g1799962 Escherichia
coli 562 -11535445 7500952214 gutb sorbitol dehydrogenase ec 1.1.1.14
l-iditol (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#432(57.5-57.9 min.)) (nt:similar to (swissprot accession number q06004))
(le:2730) (re:3824) (di:complement) D90885 D90885 g1799970 Escherichia coli
562 -11535445 7500952215 yphc putative oxidoreductase (fn:putative enzyme;
not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
230 of 400 of the completegenome.) (nt:f364; this 364 aa orf is 30 pct
identical (10 gaps)) (le:10426) (re:11520) (di:complement) AE000340 AE000340
g1788895 Escherichia coli 562 -11535445 225143 gutb sorbitol dehydrogenase
ec 1.1.1.14 l-iditol (sr:escherichia coli (strain:k12) dna, clone_lib:kohara
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#431(57.3-57.7 min.)) (nt:similar to (swissprot accession number q06004))
(le:11924) (re:13018) (di:complement) D90884 D90884 g1799962 Escherichia
coli 562 -11535445 6500731587 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2545 b2545
Escherichia coli 562 -11535445

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856834	11669	33825	378	126

Description

5000693015 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2546 b2546 Escherichia coli 562 -11535446
7500952216 yphd (de:hypothetical abc transporter permease protein yphd) (db:swissprot) YPHD_ECOLI P77315 ESCHERICHIA COLI 562 -11535446 7000691695 probable sugar transport permease protein b2546 (cl:l-arabinose transport system permease arah) (db:pir2.dat) A65032 A65032 Escherichia coli 562 -11535446 225137 arah l-arabinose transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p08532)) (le:13051) (re:14049) (di:complement) D90884 D90884 g1799963 Escherichia coli 562 -11535446 7500952218 arah l-arabinose transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #432(57.5-57.9 min.)) (nt:similar to (swissprot accession number p08532)) (le:3857) (re:4855) (di:complement) D90885 D90885 g1799971 Escherichia coli 562 -11535446 7500952219 yphd putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:f332; residues 173-318 are 45 pct identical to) (le:11553) (re:12551) (di:complement) AE000340 AE000340 g1788896 Escherichia coli 562 -11535446 225144 arah l-arabinose transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p08532)) (le:13051) (re:14049) (di:complement) D90884 D90884 g1799963 Escherichia coli 562 -11535446 6500731588 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2546 b2546 Escherichia coli 562 -11535446

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856836	11670	33826	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856847	11671	33827	303	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856848	11672	33828	978	325

Description

5000693016 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2547 b2547 Escherichia coli 562 -11535447
7500952221 yphe (de:hypothetical abc transporter atp-binding protein yphe) (db:swissprot) YPHE_ECOLI P77509 ESCHERICHIA COLI 562 -11535447 7000691696 hypothetical protein b2547 (cl:atp-binding cassette homology) (db:pir2.dat) B65032 B65032 Escherichia coli 562 -11535447 225138 mgla galactoside transport atp-binding protein mgla. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p23199)) (le:14074) (re:15585) (di:complement) D90884 D90884 g1799964 Escherichia coli 562 -11535447 7500952223 mgla galactoside transport atp-binding protein mgla. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #432(57.5-57.9 min.)) (nt:similar to (swissprot accession number p23199)) (le:4880) (re:6391) (di:complement) D90885 D90885 g1799972 Escherichia coli 562 -11535447 7500952224 yphe putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:f503; this 503 aa orf is 38 pct identical (9 gaps)) (le:12576) (re:14087) (di:complement) AE000340 AE000340 g1788897 Escherichia coli 562 -11535447 225145 mgla galactoside transport atp-binding protein mgla. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p23199)) (le:14074) (re:15585) (di:complement) D90884 D90884 g1799964 Escherichia coli 562 -11535447 6500731589 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2547 b2547 Escherichia coli 562 -11535447

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856880	11673	33829	786	261

Description

5000693017 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2548 b2548 Escherichia coli 562 -11535448
7500952226 yphf (de:abc transporter periplasmic binding protein yphf precursor) (db:swissprot) YPHF_ECOLI P77269 ESCHERICHIA COLI 562 -11535448
7000691697 hypothetical protein b2548 (db:pir2.dat) C65032 C65032 Escherichia coli 562 -11535448 225146 mglb d-galactose-binding periplasmic protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #432(57.5-57.9 min.)) (nt:similar to (swissprot accession number p23905)) (le:6414) (re:7397) (di:complement) D90885 D90885 g1799973 Escherichia coli 562 -11535448 7500952229 yphf putative lacI-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 230 of 400 of the completegenome.) (nt:f327) (le:14110) (re:15093) (di:complement) AE000340 AE000340 g1788898 Escherichia coli 562 -11535448 6500731590 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2548 b2548 Escherichia coli 562 -11535448

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856882	11674	33830	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856900	11675	33831	1053	350

Description

5000693018 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2549 b2549 Escherichia coli 562 -11535449
7500952230 yphg (de:hypothetical 127.3 kd protein in csie-glya intergenic region) (db:swissprot) YPHG_ECOLI P76585 ESCHERICHIA COLI 562 -11535449
7000691698 hypothetical protein b2549 (db:pir2.dat) D65032 D65032 Escherichia coli 562 -11535449 7500952232 yphg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 231 of 400 of the completegenome.) (nt:f1124; this 1124 aa orf is 26 pct identical (1) (le:79) (re:3453) (di:complement) AE000341 AE000341 g1788900 Escherichia coli 562 -11535449 6500731591 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2549 b2549 Escherichia coli 562 -11535449

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856901	11676	33832	285	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856907	11677	33833	366	121

Description

GTC ORF with score 129 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c3g6.) (nt:spac3g6.05, len:201aa, similar eg. to ylr251w,) (le:10647:11081:11217:11384) (re:11024:11152:11314:11456) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856913	11678	33834	348	115

Description

GTC ORF with score 155 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c3g6.) (nt:spac3g6.05, len:201aa, similar eg. to ylr251w,) (le:10647:11081:11217:11384) (re:11024:11152:11314:11456) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856915	11679	33835	291	96

Description

GTC ORF with score 104 to: (sr:aspergillus oryzae (strain:rib40) dna) (db:genpept-pln1) (ec:2.7.2.3) (de:aspergillus oryzae pgka gene for phosphoglycerate kinase, completedcds.) (le:1633:1771:2252) (re:1698:2191:3018) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856916	11680	33836	348	116

Description

5000693019 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2550 b2550 Escherichia coli 562 -11535450
7500952233 yphh (de:hypothetical 44.8 kd protein in csie-glya intergenic region) (db:swissprot) YPHH_ECOLI P76586 ESCHERICHIA COLI 562 -11535450
7000691699 hypothetical protein b2550 (cl:glucose kinase homology) (db:pir2.dat) E65032 E65032 Escherichia coli 562 -11535450 7500952235 yphh putative nagc-like transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 231 of 400 of the completengenome.) (nt:o399; this 399 aa orf is 23 pct identical (12 gaps)) (le:3472) (re:4671) (di:direct) AE000341 AE000341 g1788901 Escherichia coli 562 -11535450 6500731592 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2550 b2550 Escherichia coli 562 -11535450

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501856934	11681	33837	2121	706

Description

6500731593 yfha:b2554 hypothetical protein in glnb 5region:hypothetical 49.1 kd protein in glnb-purl intergenic region:orfbx:orf-2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2554 b2554 Escherichia coli 562 -11535451 111900 yfha (de:(orf-2)) (db:swissprot) YFHA_ECOLI P21712 ESCHERICHIA COLI 562 -11535451 7000687707 yfha hypothetical protein xb glnb 5 region (cl:nitrogen assimilation regulatory protein ntrc:response regulator homology:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) A65033 A65033 Escherichia coli 562 -11535451 225151 nitrogen regulator i homolog (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #432(57.5-57.9 min.)) (nt:similar to (pir accession number b49940)) (le:15498) (re:16832) (di:complement) D90885 D90885 g1799978 Escherichia coli 562 -11535451 7500923478 yfha putative 2-component transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 231 of 400 of the completengenome.) (nt:f444; orf2 of gb: s67014 and orf_f28p of gb:) (le:8084) (re:9418) (di:complement) AE000341 AE000341 g1788905 Escherichia coli 562 -11535451 5000693020 (de:(ecoli_2494) (pn:hypothetical 48) (gn:yfha) (gtcfc:13.7:14.1) (ec:) (yfha_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2494 ECOLI_2494 Escherichia coli 562 10120273

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856950	11682	33838	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856951	11683	33839	717	238

Description

6500731594 yfhg:b2555 hypothetical 27.3 kd protein in glnb
5region:hypothetical 27.3 kd protein in glnb-purl intergenic
region:orf-1:f239 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2555 b2555 Escherichia coli 562 -11535452 111911
yfhg (de:(f239)) (db:swissprot) YFHG_ECOLI P37328 ESCHERICHIA COLI 562
-11535452 164191 yfhg hypothetical 27.3k protein glnb 5region (db:pir2.dat)
A49940 A49940 Escherichia coli 562 -11535452 7500923485 orf1 5 of::glnb
(db:genpept-bct1) (de:glnb region: nitrogen regulator i homolog, glnb=small
protein pii(escherichia coli, genomic, 3 genes, 2641 nt).)
(nt:glutamine-leucine-rich polypeptide. this sequence) (le:128) (re:841)
(di:direct) S67014 S67014 g455661 Escherichia coli 562 -11535452 258594
yfhg putative alpha helix protein (fn:phenotype; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 231 of 400 of the
completegenome.) (nt:f239; 100 pct identical to yfhg_ecoli sw:) (le:9408)
(re:10121) (di:complement) AE000341 AE000341 g1788906 Escherichia coli 562
-11535452 5000693021 (de:(ecoli_2495) (pn:hypothetical 27) (gn:yfhg)
(gtcfc:13.7:14.1) (ec:) (yfhg_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2495 ECOLI_2495 Escherichia coli 562
10053639

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856952	11684	33840	204	68

Description

6500731595 yfhk:b2556 hypothetical protein:probable sensor protein yfhk
(gtcfc:14.1) (ec:2.7.3.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia
coli) b2556 b2556 Escherichia coli 562 -11535453 111916 yfhk (ec:2.7.3.-)
(de:probable sensor protein yfhk,) (db:swissprot) YFHK_ECOLI P52101
ESCHERICHIA COLI 562 -11535453 7000687711 hypothetical protein b2556
(db:pir2.dat) C65033 C65033 Escherichia coli 562 -11535453 7500923488 yfhk
putative 2-component sensor protein (fn:putative regulator; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 232 of 400 of the
completegenome.) (nt:f496; f496 (ttg start); orf_f460 gb: u36841 uses)
(le:113) (re:1603) (di:complement) AE000342 AE000342 g1788908 Escherichia
coli 562 -11535453 5000693022 (de:(ecoli_2496) (pn:function not assigned)
(gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia
coli)) ECOLI_2496 ECOLI_2496 Escherichia coli 562 10123727

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856959	11685	33841	471	157

Description

6500731596 yfhd:b2558 hypothetical 53.2 kd protein in purl-dpj intergenic region:o472 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2558 b2558 Escherichia coli 562 -11535454 7000690957 yfhd hypothetical 53.2 kd protein in purl-dpj intergenic region (cl:hypothetical protein hi0232) (db:pir2.dat) E65033 E65033 Escherichia coli 562 -11535454 7500959819 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 55 minutes.) (nt:alternate name yfhd; orf360 of genbank accession) (le:7183) (re:8601) (di:direct) ECU36841 U36841 g1033147 Escherichia coli 562 -11535454 239512 yfhd putative periplasmic binding transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 232 of 400 of the completegenome.) (nt:o472; 99 pct identical to yfhd_ecoli sw:) (le:6381) (re:7799) (di:direct) AE000342 AE000342 g1788910 Escherichia coli 562 -11535454 5000693023 (de:(ecoli_2498) (pn:hypothetical 53) (gn:yfhd) (gtcfc:13.7:14.1) (ec:) (yfhd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2498 ECOLI_2498 Escherichia coli 562 10123729

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856962	11686	33842	396	131

Description

GTC ORF with score 222 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0679.) (nt:similar to saccharomyces cerevisiae scd6 protein,) (le:32) (re:1144) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856976	11687	33843	1299	432

Description

6500731597 yfhc:b2559 hypothetical 20.0 kd protein in purl-dpj intergenic region:orf178 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2559 b2559 Escherichia coli 562 -11535455 111904 yfhc (de:hypothetical 20.0 kd protein in purl-dpj intergenic region (orf178)) (db:swissprot) YFHC_ECOLI P30134 ESCHERICHIA COLI 562 -11535455 7000687708 yfhc hypothetical 20.0 kd protein in purl-dpj intergenic region (cl:hypothetical protein yaaj) (db:pir2.dat) F65033 F65033 Escherichia coli 562 -11535455 234887 (db:genpept-bct1) (de:e.coli mutant strain sequence with orf 178, orf 190 and orf 360.) (nt:orf 178, gef-resistance, put. membrane protein) (le:1141) (re:1677) (di:direct) ECMUTORFS X72336 g296183 Escherichia coli 562 -11535455 239513 yfhc-ecoli protein (sr:escherichia coli (strain k12) (library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli ribonuclease iii and other genes, complete cds.) (le:4820) (re:5356) (di:complement) ECOK12RIII D64044 g987637 Escherichia coli 562 -11535455 7500923480 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 55 minutes.) (nt:alternate name yfhc; orf178 of genbank accession) (le:8598) (re:9134) (di:complement) ECU36841 U36841 g1033148 Escherichia coli 562 -11535455 233440 yfhc putative deaminase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 232 of 400 of the completegenome.) (nt:f178; 100 pct identical to yfhc_ecoli sw:) (le:7796) (re:8332) (di:complement) AE000342 AE000342 g1788911 Escherichia coli 562 -11535455 5000693024 (db:genpept) (de:e.coli mutant strain sequence with orf 178, orf 190 and orf 360.) (nt:orf 178, gef-resistance, put. membrane protein) (le:1141) (re:1677) (di:direct) ECMUTORFS X72336 g296183 Escherichia coli 562 -11535455

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856998	11688	33844	204	67

Description

6500731598 yfhh:b2560 hypothetical 21.9 kd protein in purl-dpj intergenic region:orf190:f204 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2560 b2560 Escherichia coli 562 -11535456 7500923479 yfhh (de:(f204)) (db:swissprot) YFHB_ECOLI P30133 ESCHERICHIA COLI 562 -11535456 163451 yfhh hypothetical 21.9k protein purl-dpj intergenic region:hypothetical protein 190 (db:pir2.dat) S20973 S20973 Escherichia coli 562 -11535456 5000693025 (db:genpept-bct1) (de:e.coli mutant strain sequence with orf 178, orf 190 and orf 360.) (nt:orf 190) (le:544) (re:1116) (di:direct) ECMUTORFS X72336 g296182 Escherichia coli 562 -11535456 233439 yfhh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 232 of 400 of the completegenome.) (nt:f190; 100 pct identical to yfhh_ecoli sw:) (le:8357) (re:8929) (di:complement) AE000342 AE000342 g1788912 Escherichia coli 562 -11535456 7502852270 (db:genpept) (de:e.coli mutant strain sequence with orf 178, orf 190 and orf 360.) (nt:orf 190) (le:544) (re:1116) (di:direct) ECMUTORFS X72336 g296182 Escherichia coli 562 -11535456 111903 yfhh (de:(f204)) (db:swissprot) YFHB_ECOLI P30133 ESCHERICHIA COLI 562 -11535456

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501856999	11689	33845	666	221

Description

6500731599 yfhh:b2561 hypothetical protein in purl-dpj intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2561 b2561 Escherichia coli 562 -11535457 7000691839 yfhh hypothetical protein in purl-dpj intergenic region (cl:hypothetical protein ybbh) (db:pir2.dat) H65033 H65033 Escherichia coli 562 -11535457 239515 yfhh-ecoli protein similarity (sr:escherichia coli (strain k12) (library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli ribonuclease iii and other genes, complete cds.) (le:6153) (re:7073) (di:direct) ECOK12RIII D64044 g987639 Escherichia coli 562 -11535457 7500955862 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 55 minutes.) (nt:alternate name yfhh) (le:9931) (re:10851) (di:direct) ECU36841 U36841 g1033150 Escherichia coli 562 -11535457 234889 yfhh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 232 of 400 of the completegenome.) (nt:o306; 100 pct identical to fragment yfhh_ecoli) (le:9129) (re:10049) (di:direct) AE000342 AE000342 g1788913 Escherichia coli 562 -11535457 5000693026 (de:(ecoli_2501) (pn:hypothetical 30) (gn:yfhh) (gtcfc:13.7:14.1) (ec:) (yfhh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2501 ECOLI_2501 Escherichia coli 562 10123730

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857000	11690	33846	801	266

Description

6500731600 yfhl:b2562 hypothetical protein:putative ferredoxin-like protein in purl-dpj intergenic region:o86 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2562 b2562 Escherichia coli 562 -11535458 111917 yfhl (de:putative ferredoxin-like protein in purl-dpj intergenic region (o86)) (db:swissprot) YFHL_ECOLI P52102 ESCHERICHIA COLI 562 -11535458 7000687712 hypothetical protein b2562 (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) A65034 A65034 Escherichia coli 562 -11535458 7500923489 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 55 minutes.) (nt:orf_o86) (le:10907) (re:11167) (di:direct) ECU36841 U36841 g1033151 Escherichia coli 562 -11535458 239516 yfhl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 232 of 400 of the completegenome.) (nt:o86; this 86 aa orf is 59 pct identical (1 gap)) (le:10105) (re:10365) (di:direct) AE000342 AE000342 g1788914 Escherichia coli 562 -11535458 5000693027 (de:(ecoli_2502) (pn:putative ferredoxin-like protein in purl-dpj intergenic region:o86) (gtcfc:13.7:14.1) (ec:) (yfhl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2502 ECOLI_2502 Escherichia coli 562 10053645

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857001	11691	33847	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857008	11692	33848	1275	424

Description

6500731601 yfic:b2575 hypothetical protein in nadb-srmb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2575 b2575 Escherichia coli 562 -11535459 7000691838 yfic hypothetical protein in nadb-srmb intergenic region (cl:hypothetical protein hi0423) (db:pir2.dat) F65035 F65035 Escherichia coli 562 -11535459 7500960352 yfic putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 234 of 400 of the completegenome.) (nt:f285; 99 pct identical to 210 residues of a 220 aa) (le:1841) (re:2698) (di:complement) AE000344 AE000344 g1788929 Escherichia coli 562 -11535459 5000693031 (de:(ecoli_2515) (pn:hypothetical 24) (gn:yfic) (gtcfc:13.7:14.1) (ec:) (yfic_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2515 ECOLI_2515 Escherichia coli 562 10123735

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857012	11693	33849	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857020	11694	33850	1278	425

Description

6500731602 yfie:b2577 hypothetical protein in the srmb-ung intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2577 b2577 Escherichia coli 562 -11535460 7000691842 yfie hypothetical protein in the srmb-ung intergenic region (db:pir2.dat) H65035 H65035 Escherichia coli 562 -11535460 7500960354 yfie putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 234 of 400 of the completegenome.) (nt:f308; 100 pct identical to 208 residues of a 215) (le:4253) (re:5179) (di:complement) AE000344 AE000344 g1788931 Escherichia coli 562 -11535460 5000693032 (de:(ecoli_2517) (pn:hypothetical transcriptional regulator in srmb-ung intergenic region) (gn:yfie) (gtcfc:13.7:14.1) (ec:)) (yfie_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2517 ECOLI_2517 Escherichia coli 562 10123736

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857026	11695	33851	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857027	11696	33852	324	107

Description

6500731603 yfik:b2578 hypothetical 21.2 kd protein in srmb-ung intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2578 b2578 Escherichia coli 562 -11535461 111955 yfik (de:hypothetical 21.2 kd protein in srmb-ung intergenic region) (db:swissprot) YFIK_ECOLI P38101 ESCHERICHIA COLI 562 -11535461 7000687729 yfik hypothetical 21.2 kd protein in srmb-ung intergenic region (db:pir2.dat) A65036 A65036 Escherichia coli 562 -11535461 225154 yfik (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #436(58.4-58.8 min.)) (nt:similar to (swissprot accession number p38101)) (le:726) (re:1313) (di:direct) D90886 D90886 g1799982 Escherichia coli 562 -11535461 7500923525 yfik orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 234 of 400 of the completegenome.) (nt:o195; 100 pct identical to yfik_ecoli sw: p38101) (le:5237) (re:5824) (di:direct) AE000344 AE000344 g1788932 Escherichia coli 562 -11535461 5000693033 (de:(ecoli_2518) (pn:hypothetical 21) (gn:yfik) (gtcfc:13.7:14.1) (ec:) (yfik_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2518 ECOLI_2518 Escherichia coli 562 10053683

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857028	11697	33853	981	326

Description

6500731604 yfid:b2579 hypothetical 14.3 kd protein in srmb-ung intergenic region:14.3 kd protein in srmb-ung intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2579 b2579 Escherichia coli 562 -11535462 111935 yfid (de:14.3 kd protein in srmb-ung intergenic region) (db:swissprot) YFID_ECOLI P33633 ESCHERICHIA COLI 562 -11535462 7000687720 yfid probable glycyl radical protein yfid:hypothetical 14.3kd protein srmb-ung intergenic region (cl:probable glycyl radical protein yfid:glycyl radical homology) (db:pir1.dat) B65036 B65036 Escherichia coli 562 -11535462 225155 yfid (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #436(58.4-58.8 min.)) (nt:similar to (swissprot accession number p33633)) (le:1369) (re:1752) (di:complement) D90886 D90886 g1799983 Escherichia coli 562 -11535462 7500923515 yfid putative formate acetyltransferase (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 234 of 400 of the completegenome.) (nt:f127; 100 pct identical to yfid_ecoli sw: p33633) (le:5880) (re:6263) (di:complement) AE000344 AE000344 g1788933 Escherichia coli 562 -11535462 5000693034 (de:(ecoli_2519) (pn:hypothetical 14) (gn:yfid) (gtcfc:13.7:14.1) (ec:) (yfid_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2519 ECOLI_2519 Escherichia coli 562 10053663

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857030	11698	33854	240	79

Description

6500731605 yfif:b2581 hypothetical 37.8 kd protein in ung 3 region:hypothetical 37.8 kd protein in ung-pssa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2581 b2581 Escherichia coli 562 -11535463 111941 yfif (ec:2.1.1.-) (de:hypothetical trna/rRNA methyltransferase yfif,) (db:swissprot) YFIF_ECOLI P33635 ESCHERICHIA COLI 562 -11535463 7000687723 yfif hypothetical 37.8 kd protein in ung 3 region (cl:hypothetical protein hi0424) (db:pir2.dat) D65036 D65036 Escherichia coli 562 -11535463 7500923519 yfif orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 234 of 400 of the completegenome.) (nt:f345; 100 pct identical to yfif_ecoli sw: p33635) (le:7305) (re:8342) (di:complement) AE000344 AE000344 g1788935 Escherichia coli 562 -11535463 5000693035 (de:(ecoli_2521) (pn:hypothetical 37) (gn:yfif) (gtcfc:13.7:14.1) (ec:) (yfif_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2521 ECOLI_2521 Escherichia coli 562 10053669

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857031	11699	33855	327	109

Description

6500731606 yfig:b2582 hypothetical protein in the ung 3 region:hypothetical thioredoxin-like protein in ung-pssa intergenic region (gtcfc:9.13) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2582 b2582 Escherichia coli 562 -11535464 111944 trxc (de:thioredoxin 2 (trx2)) (db:swissprot) THI2_ECOLI P33636 ESCHERICHIA COLI 562 -11535464 7000687725 yfig hypothetical protein in the ung 3 region (cl:thioredoxin:thioredoxin homology) (db:pir2.dat) E65036 E65036 Escherichia coli 562 -11535464 7500893033 thioredoxin 2 (db:genpept-bct1) (de:escherichia coli thioredoxin 2 gene, complete cds.) (le:31) (re:450) (di:direct) ECU85942 U85942 g2668567 Escherichia coli 562 -11535464 7000687726 trxc putative thioredoxin-like protein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 234 of 400 of the completegenome.) (nt:o139; formerly designated yfig) (le:8549) (re:8968) (di:direct) AE000344 AE000344 g1788936 Escherichia coli 562 -11535464 5000693036 (de:(ecoli_2522) (pn:hypothetical thioredoxin-like protein in ung:3"region:fragment) (gn:yfig) (gtcfc:13.7:14.1) (ec:) (yfig_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2522 ECOLI_2522 Escherichia coli 562 10123737

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857045	11700	33856	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857046	11701	33857	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857063	11702	33858	477	158

Description

6500731607 yfip:b2583 hypothetical protein:hypothetical 27.0 kd protein in ung-pssa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2583 b2583 Escherichia coli 562 -11535465 7000687733 hypothetical protein b2583 (db:pir2.dat) F65036 F65036 Escherichia coli 562 -11535465 7500923529 hypothtcal protein in ung 3 region (sr:escherichia coli (strain k12) (library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli ribonuclease iii and other genes, complete cds.) (le:26664) (re:27386) (di:direct) ECOK12RIII D64044 g987652 Escherichia coli 562 -11535465 234902 yfip orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 234 of 400 of the completegenome.) (nt:o240; this 240 aa orf is 32 pct identical (2 gaps)) (le:9013) (re:9735) (di:direct) AE000344 AE000344 g1788937 Escherichia coli 562 -11535465 4000708208 yfip (de:hypothetical 27.0 kd protein in ung-pssa intergenic region) (db:swissprot) YFIP_ECOLI Q47319 ESCHERICHIA COLI 562 -11535465 5000693037 (de:(ecoli_2523) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2523 ECOLI_2523 Escherichia coli 562 10123738

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857064	11703	33859	1368	455

Description

6500731608 yfiq:b2584 hypothetical protein:hypothetical 98.0 kd protein in ung-pssa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2584 b2584 Escherichia coli 562 -11535466
4000708209 yfiq (de:hypothetical 98.0 kd protein in ung-pssa intergenic region) (db:swissprot) YFIQ_ECOLI P76594 ESCHERICHIA COLI 562 -11535466
7000687734 hypothetical protein b2584 (db:pir2.dat) G65036 G65036 Escherichia coli 562 -11535466 7500923530 yfiq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 234 of 400 of the completegenome.) (nt:o886; this 886 aa orf is 25 pct identical (10 gaps)) (le:9767) (re:12427) (di:direct) AE000344 AE000344 g1788938 Escherichia coli 562 -11535466 5000693038 (de:(ecoli_2524) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2524 ECOLI_2524 Escherichia coli 562 10123739

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857083	11704	33860	1491	496

Description

GTC ORF with score 635 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome ii bac f12c20 genomic sequence,complete sequence.) (nt:unknown protein) (le:45171:46239:46705) (re:45637:46611:47409) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857084	11705	33861	582	193

Description

6500731609 yfim:b2586 hypothetical 9.9 kd protein in pss-kgtp intergenic region:hypothetical 9.9 kd protein in pssa-kgtp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2586 b2586 Escherichia coli 562 -11535467 111957 yfim (de:hypothetical 9.9 kd protein in pssa-kgtp intergenic region) (db:swissprot) YFIM_ECOLI P46126 ESCHERICHIA COLI 562 -11535467 7000687731 yfim hypothetical 9.9 kd protein in pss-kgtp intergenic region (db:pir2.dat) A65037 A65037 Escherichia coli 562 -11535467 225161 yfim (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #436(58.4-58.8 min.)) (nt:similar to (swissprot accession number p46126)) (le:9482) (re:9754) (di:direct) D90886 D90886 g1799989 Escherichia coli 562 -11535467 225164 yfim (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #437(58.6-59.0 min.)) (nt:similar to (swissprot accession number p46126)) (le:2329) (re:2601) (di:direct) D90887 D90887 g1799993 Escherichia coli 562 -11535467 7500923527 yfim orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 235 of 400 of the completegenome.) (nt:o90; 100 pct identical to yfim_ecoli sw: p46126) (le:1541) (re:1813) (di:direct) AE000345 AE000345 g1788941 Escherichia coli 562 -11535467 5000693039 (de:(ecoli_2526) (pn:hypothetical 9) (gn:yfim) (gtcfc:13.7:14.1) (ec:) (yfim_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2526 ECOLI_2526 Escherichia coli 562 10053685

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857087	11706	33862	363	120

Description

GTC ORF with score 142 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds; coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666) (re:27323:27486:27619:27751) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857089	11707	33863	417	138
<u>Description</u>				
6500731610 yfih:b2593 hypothetical 26.3 kd protein in clpb 5region:hypothetical 26.3 kd protein in sfhb-clpb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2593 b2593 Escherichia coli 562 -11535468 111946 yfih (de:hypothetical 26.3 kd protein in sfhb-clpb intergenic region) (db:swissprot) YFIH_ECOLI P33644 ESCHERICHIA COLI 562 -11535468 7000687728 yfih hypothetical 26.3 kd protein in clpb 5region (db:pir2.dat) D65037 D65037 Escherichia coli 562 -11535468 225167 yfih (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #437(58.6-59.0 min.)) (nt:similar to (swissprot accession number p33644)) (le:12452) (re:13183) (di:complement) D90887 D90887 g1799996 Escherichia coli 562 -11535468 7500923523 yfih orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:f243; 100 pct identical to yfih_ecoli sw: p33644) (le:95) (re:826) (di:complement) AE000346 AE000346 g1788945 Escherichia coli 562 -11535468 5000693040 (de:(ecoli_2529) (pn:hypothetical 26) (gn:yfih) (gtcfc:13.7:14.1) (ec:) (yfih_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2529 ECOLI_2529 Escherichia coli 562 10053674				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857110	11708	33864	957	318
<u>Description</u>				
5000693042 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2595 b2595 Escherichia coli 562 -11535469 7000691700 hypothetical protein b2595 (cl:conserved hypothetical protein hi0177) (db:pir2.dat) F65037 F65037 Escherichia coli 562 -11535469 225170 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #437(58.6-59.0 min.)) (nt:similar to (swissprot accession number p44553)) (le:14297) (re:15034) (di:direct) D90887 D90887 g1799999 Escherichia coli 562 -11535469 7500960232 b2595 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:o245; 42 pct identical to y177_haein sw: p44553) (le:1938) (re:2675) (di:direct) AE000346 AE000346 g1788947 Escherichia coli 562 -11535469 6500731611 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2595 b2595 Escherichia coli 562 -11535469				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857121	11709	33865	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857137	11710	33866	279	92

Description

5000693043 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2596 b2596 Escherichia coli 562 -11535470
7000691701 hypothetical protein b2596 (db:pir2.dat) G65037 G65037 Escherichia coli 562 -11535470 7500960233 b2596 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:o68; ttg start) (le:2705) (re:2911) (di:direct) AE000346 AE000346 g1788948 Escherichia coli 562 -11535470
6500731612 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2596 b2596 Escherichia coli 562 -11535470

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857138	11711	33867	378	125

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857144	11712	33868	1119	372

Description

GTC ORF with score 276 to: (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f319; 100 pct identical amino acid sequence and) (le:7415) (re:8374) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857146	11713	33869	258	86

Description

6500731613 yfil:b2602 hypothetical protein in arof-rpls intergenic region:hypothetical 14.8 kd protein in arof-rpls intergenic region:urf2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2602 b2602 Escherichia coli 562 -11535471 111956 yfil (de:hypothetical 14.8 kd protein in arof-rpls intergenic region (urf2)) (db:swissprot) YFIL_ECOLI P11289 ESCHERICHIA COLI 562 -11535471 7000687730 yfil hypothetical protein in arof-rpls intergenic region (db:pir1.dat) (mp:57 min) QQEC89 E65038 Escherichia coli 562 -11535471 7500923526 yfil orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:ol34; 100 pct identical to 89 aa fragment) (le:7113) (re:7517) (di:direct) AE000346 AE000346 g1788954 Escherichia coli 562 -11535471 5000693045 (de:(ecoli_2538) (pn:hypothetical protein in arof-rpls intergenic region:urf2:fragment) (gn:yfil) (gtcfc:13.7:14.1) (ec:) (yfil_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2538 ECOLI_2538 Escherichia coli 562 10123743

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857151	11714	33870	369	122

Description

5000693046 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2603 b2603 Escherichia coli 562 -11535472 7502852271 yfir (de:hypothetical 19.0 kd protein in arof-rpls intergenic region precursor) (db:swissprot) YFIR_ECOLI P76597 ESCHERICHIA COLI 562 -11535472 7000691702 hypothetical protein b2603 (db:pir2.dat) F65038 F65038 Escherichia coli 562 -11535472 7500960234 b2603 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:ol72; this 172 aa orf is 28 pct identical (1 gap)) (le:7667) (re:8185) (di:direct) AE000346 AE000346 g1788955 Escherichia coli 562 -11535472 6500731614 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2603 b2603 Escherichia coli 562 -11535472

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857158	11715	33871	483	160

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857165	11716	33872	402	133

Description

6500731615 yfin:b2604 hypothetical protein in rpls 5region:hypothetical 46.0 kd protein in arof-rpls intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2604 b2604 Escherichia coli 562 -11535473 111958 yfin (de:hypothetical 46.0 kd protein in arof-rpls intergenic region) (db:swissprot) YFIN_ECOLI P46139 ESCHERICHIA COLI 562 -11535473 7000687732 yfin hypothetical protein in rpls 5region (db:pir2.dat) G65038 G65038 Escherichia coli 562 -11535473 7500923528 yfin orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:o408; 100 pct identical to 79 aa fragment) (le:8175) (re:9401) (di:direct) AE000346 AE000346 g1788956 Escherichia coli 562 -11535473 5000693047 (de:(ecoli_2540) (pn:hypothetical protein in rpls 5"region:fragment) (gn:yfin) (gtcfc:13.7:14.1) (ec:) (yfin_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2540 ECOLI_2540 Escherichia coli 562 10123745

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857166	11717	33873	348	115

Description

6500731616 yfib:b2605 hypothetical 17.2 kd protein in rpls 5region:putative 15.3 kd lipoprotein in arof-rpls intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2605 b2605 Escherichia coli 562 -11535474 111929 yfib (de:putative 15.3 kd lipoprotein in arof-rpls intergenic region precursor) (db:swissprot) YFIB_ECOLI P07021 ESCHERICHIA COLI 562 -11535474 7000687717 yfib hypothetical 17.2k protein rpls 5region (db:pir2.dat) (mp:57 min) H65038 H65038 Escherichia coli 562 -11535474 225180 yfib (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #438(58.9-59.3 min.)) (nt:similar to (swissprot accession number p07021)) (le:6512) (re:6994) (di:direct) D90888 D90888 g1800010 Escherichia coli 562 -11535474 7500923511 yfib putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:o160; 100 pct identical to yfib_ecoli sw:) (le:9417) (re:9899) (di:direct) AE000346 AE000346 g1788957 Escherichia coli 562 -11535474 5000693048 (de:(ecoli_2541) (pn:hypothetical 17) (gn:yfib) (gtcfc:13.7:14.1) (ec:) (yfib_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2541 ECOLI_2541 Escherichia coli 562 10053657

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857173	11718	33874	366	121

Description

6500731617 yfja:b2608 hypothetical 21.0 kd protein in trmd-rpsp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2608 b2608 Escherichia coli 562 -11535475 111967 rimm (de:16s rrna processing protein rimm) (db:swissprot) RIMM_ECOLI P21504 ESCHERICHIA COLI 562 -11535475 7000687735 yfja hypothetical 21k protein trmd-rpsp intergenic region (db:pir2.dat) (mp:57 min) C65039 C65039 Escherichia coli 562 -11535475 225183 yfja (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #438(58.9-59.3 min.)) (nt:similar to (swissprot accession number p21504)) (le:8256) (re:8813) (di:complement) D90888 D90888 g1800013 Escherichia coli 562 -11535475 7500889791 yfja orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:f185; 100 pct identical to yfja_ecoli sw: p21504) (le:11162) (re:11719) (di:complement) AE000346 AE000346 g1788960 Escherichia coli 562 -11535475 5000693049 (de:(ecoli_2544) (pn:hypothetical 21) (gn:yfja) (gtcfc:13.7:14.1) (ec:) (yfja_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2544 ECOLI_2544 Escherichia coli 562 10053695

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857176	11719	33875	411	136

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857178	11720	33876	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857184	11721	33877	663	220

Description

GTC ORF with score 337 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f53f10.) (nt:strong similarity to the ypt1 sub-family of ras) (le:9628:9799:10438) (re:9745:10042:10720) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857187	11722	33878	1452	484

Description

5000693050 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2611 b2611 Escherichia coli 562 -11535476
7000691703 hypothetical protein b2611 (db:pir2.dat) F65039 F65039
Escherichia coli 562 -11535476 7500960235 b2611 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the completegenome.) (nt:o288; this 288 aa orf is 26 pct identical (8 gaps)) (le:1608) (re:2474) (di:direct) AE000347 AE000347 g1788964 Escherichia coli 562 -11535476 6500731618 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2611 b2611 Escherichia coli 562 -11535476

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857188	11723	33879	369	122

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857189	11724	33880	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857204	11725	33881	1317	439

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857209	11726	33882	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857220	11727	33883	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857228	11728	33884	429	142

Description

6500731619 ypje:b2612 hypothetical protein:hypothetical 21.8 kd protein in ffh-grpe intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2612 b2612 Escherichia coli 562 -11535477
7000688235 hypothetical protein b2612 (db:pir2.dat) G65039 G65039
Escherichia coli 562 -11535477 7500952248 ypje orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the completegenome.) (nt:o196; uug start; this 196 aa orf is 27 pct) (le:2519) (re:3109) (di:direct) AE000347 AE000347 g1788965
Escherichia coli 562 -11535477 4000708210 ypje (de:hypothetical 21.8 kd protein in ffh-grpe intergenic region) (db:swissprot) YPJE_ECOLI P76600
ESCHERICHIA COLI 562 -11535477 5000693051 (de:(ecoli_2548) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2548 ECOLI_2548 Escherichia coli 562
10123747

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857229	11729	33885	798	265

Description

6500731620 yfjd:b2613 hypothetical protein in grpe 3 region:hypothetical 25.7 kd protein in ffh-grpe intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2613 b2613 Escherichia coli 562 -11535478 7000687736 yfjd hypothetical protein in grpe 3 region (cl:yfjd protein) (db:pir2.dat) H65039 H65039 Escherichia coli 562 -11535478
7500923543 yfjd putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the completegenome.) (nt:o227; 85 pct identical to 70 aa fragment) (le:3099) (re:3782) (di:direct) AE000347 AE000347 g1788966 Escherichia coli 562 -11535478 111973 yfjd (de:hypothetical 25.7 kd protein in ffh-grpe intergenic region) (db:swissprot) YFJD_ECOLI P37908 ESCHERICHIA COLI 562 -11535478 5000693052 (de:(ecoli_2549) (pn:hypothetical 8) (gn:yfjd) (gtcfc:13.7:14.1) (ec:) (yfjd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2549 ECOLI_2549 Escherichia coli 562
10123748

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857231	11730	33886	195	64
<u>Description</u>				
5000693054 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2618 b2618 Escherichia coli 562 -11535479				
7000691704 hypothetical protein b2618 (db:pir2.dat) E65040 E65040 Escherichia coli 562 -11535479 7500960236 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_f102) (le:2962) (re:3270) (di:complement) ECU36840 U36840 g1033114 Escherichia coli 562 -11535479 239480 b2618 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the completegenome.) (nt:f102; this 102 aa orf is 55 pct identical (1 gap)) (le:7730) (re:8038) (di:complement) AE000347 AE000347 g1788971 Escherichia coli 562 -11535479 6500731621 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2618 b2618 Escherichia coli 562 -11535479				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857234	11731	33887	1011	336
<u>Description</u>				
6500731622 yfjg:b2619 hypothetical protein:hypothetical 17.8 kd protein in smpa-smpb intergenic region:f158 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2619 b2619 Escherichia coli 562 -11535480 111977 yfjg (de:hypothetical 17.8 kd protein in smpa-smpb intergenic region (f158)) (db:swissprot) YFJG_ECOLI P52121 ESCHERICHIA COLI 562 -11535480 7000687737 hypothetical protein b2619 (db:pir2.dat) F65040 F65040 Escherichia coli 562 -11535480 225194 yfjg (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #438(58.9-59.3 min.)) (nt:similar to (swissprot accession number p52121)) (le:17172) (re:17648) (di:complement) D90888 D90888 g1800024 Escherichia coli 562 -11535480 7500923548 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_f158) (le:3242) (re:3718) (di:complement) ECU36840 U36840 g1033115 Escherichia coli 562 -11535480 239481 b2619 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the completegenome.) (nt:f158) (le:8010) (re:8486) (di:complement) AE000347 AE000347 g1788972 Escherichia coli 562 -11535480 5000693055 (de:(ecoli_2555) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2555 ECOLI_2555 Escherichia coli 562 10053705				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857236	11732	33888	258	85

Description

6500731623 yfjh:b2623 hypothetical protein:hypothetical 37.1 kd protein in inta-alpa intergenic region:f358 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2623 b2623 Escherichia coli 562 -11535481 111979 yfjh (de:hypothetical 37.1 kd protein in inta-alpa intergenic region (f358)) (db:swissprot) YFJH_ECOLI P52123 ESCHERICHIA COLI 562 -11535481 7000687738 hypothetical protein b2623 (db:pir2.dat) A65041 A65041 Escherichia coli 562 -11535481 7500923549 yfjh putative histone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 238 of 400 of the completegenome.) (nt:f318; 31 pct identical (5 gaps) to 87 residues) (le:152) (re:1108) (di:complement) AE000348 AE000348 g1788976 Escherichia coli 562 -11535481 5000693058 (de:(ecoli_2558) (pn:hypothetical 37) (gtcfc:13.7:14.1) (ec:) (yfjh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2558 ECOLI_2558 Escherichia coli 562 10053707

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857239	11733	33889	1566	521

Description

6500731624 yfji:b2625 hypothetical protein:hypothetical 54.0 kd protein in alpa-gabd intergenic region:o469 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2625 b2625 Escherichia coli 562 -11535482 111980 yfji (de:hypothetical 54.0 kd protein in alpa-gabd intergenic region (o469)) (db:swissprot) YFJI_ECOLI P52124 ESCHERICHIA COLI 562 -11535482 7000687739 hypothetical protein b2625 (db:pir2.dat) C65041 C65041 Escherichia coli 562 -11535482 7500923550 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_o469) (le:7939) (re:9348) (di:direct) ECU36840 U36840 g1033120 Escherichia coli 562 -11535482 239486 yfji orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 238 of 400 of the completegenome.) (nt:o469; this 469 aa orf is 26 pct identical (2 gaps)) (le:1493) (re:2902) (di:direct) AE000348 AE000348 g1788978 Escherichia coli 562 -11535482 5000693059 (de:(ecoli_2560) (pn:hypothetical 54) (gtcfc:13.7:14.1) (ec:) (yfji_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2560 ECOLI_2560 Escherichia coli 562 10053708

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857242	11734	33890	450	149

Description

6500731625 yfjj:b2626 hypothetical protein:hypothetical 24.6 kd protein in alpa-gabd intergenic region:o208 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2626 b2626 Escherichia coli 562 -11535483 111981 yfjj (de:hypothetical 24.6 kd protein in alpa-gabd intergenic region (o208)) (db:swissprot) YFJJ_ECOLI P52125 ESCHERICHIA COLI 562 -11535483 7000687740 hypothetical protein b2626 (cl:yagk protein) (db:pir2.dat) D65041 D65041 Escherichia coli 562 -11535483 7500923551 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_o208) (le:9501) (re:10127) (di:direct) ECU36840 U36840 g1033121 Escherichia coli 562 -11535483 239487 yfjj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 238 of 400 of the completegenome.) (nt:o208; this 208 aa orf is 24 pct identical (4 gaps)) (le:3055) (re:3681) (di:direct) AE000348 AE000348 g1788979 Escherichia coli 562 -11535483 5000693060 (de:(ecoli_2561) (pn:hypothetical 24) (gtcfc:13.7:14.1) (ec:) (yfjj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2561 ECOLI_2561 Escherichia coli 562 10053709

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857269	11735	33891	354	117

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857282	11736	33892	405	134

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857289	11737	33893	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857290	11738	33894	669	223

Description

6500731626 yfjk:b2627 hypothetical protein:hypothetical 83.1 kd protein in alpa-gabd intergenic region:f729 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2627 b2627 Escherichia coli 562 -11535484 111982 yfjk (de:hypothetical 83.1 kd protein in alpa-gabd intergenic region (f729)) (db:swissprot) YFJK_ECOLI P52126 ESCHERICHIA COLI 562 -11535484 7000687741 hypothetical protein b2627 (db:pir2.dat) E65041 E65041 Escherichia coli 562 -11535484 7500923552 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_f729) (le:10305) (re:12494) (di:complement) ECU36840 U36840 g1033122 Escherichia coli 562 -11535484 239488 yfjk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 238 of 400 of the completgenome.) (nt:f729; this 729 aa orf is 32 pct identical (4 gaps)) (le:3859) (re:6048) (di:complement) AE000348 AE000348 g1788980 Escherichia coli 562 -11535484 5000693061 (de:(ecoli_2562) (pn:hypothetical 83) (gtcfc:13.7:14.1) (ec:) (yfjk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2562 ECOLI_2562 Escherichia coli 562 10053710

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857308	11739	33895	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857320	11740	33896	339	112

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857328	11741	33897	300	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857362	11742	33898	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857377	11743	33899	3102	1034

Description

6500731627 yfjl:b2628 hypothetical protein:hypothetical 62.0 kd protein in alpa-gabd intergenic region:f358 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2628 b2628 Escherichia coli 562 -11535485 111983 yfjl (de:hypothetical 62.0 kd protein in alpa-gabd intergenic region (f358)) (db:swissprot) YFJL_ECOLI P52127 ESCHERICHIA COLI 562 -11535485 7000687742 hypothetical protein b2628 (db:pir2.dat) F65041 F65041 Escherichia coli 562 -11535485 7500923553 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_f538) (le:12491) (re:14107) (di:complement) ECU36840 U36840 g1033123 Escherichia coli 562 -11535485 239489 yfjl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 238 of 400 of the completegenome.) (nt:f538; this 538 aa orf is 26 pct identical (10 gaps)) (le:6045) (re:7661) (di:complement) AE000348 AE000348 g1788981 Escherichia coli 562 -11535485 5000693062 (de:(ecoli_2563) (pn:hypothetical 62) (gtcfc:13.7:14.1) (ec:) (yfjl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2563 ECOLI_2563 Escherichia coli 562 10053711

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857381	11744	33900	624	207

Description

6500731628 yfjm:b2629 hypothetical protein:hypothetical 10.0 kd protein in alpa-gabd intergenic region:f87 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2629 b2629 Escherichia coli 562 -11535486 111984 yfjm (de:hypothetical 10.0 kd protein in alpa-gabd intergenic region (f87)) (db:swissprot) YFJM_ECOLI P52128 ESCHERICHIA COLI 562 -11535486 7000687743 hypothetical protein b2629 (db:pir2.dat) G65041 G65041 Escherichia coli 562 -11535486 7500923554 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_f87) (le:14467) (re:14730) (di:complement) ECU36840 U36840 g1033124 Escherichia coli 562 -11535486 239490 yfjm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 238 of 400 of the completegenome.) (nt:f87; this 87 aa orf is 31 pct identical (6 gaps) to) (le:8021) (re:8284) (di:complement) AE000348 AE000348 g1788982 Escherichia coli 562 -11535486 5000693063 (de:(ecoli_2564) (pn:hypothetical 10) (gtcfc:13.7:14.1) (ec:) (yfjm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2564 ECOLI_2564 Escherichia coli 562 10053712

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857382	11745	33901	294	97

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857386	11746	33902	720	239

Description

6500731629 yfjn:b2630 hypothetical protein:hypothetical 40.1 kd protein in alpa-gabd intergenic region:o357 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2630 b2630 Escherichia coli 562 -11535487 111985 yfjn (de:hypothetical 40.1 kd protein in alpa-gabd intergenic region (o357)) (db:swissprot) YFJN_ECOLI P52129 ESCHERICHIA COLI 562 -11535487 7000687744 hypothetical protein b2630 (db:pir2.dat) H65041 H65041 Escherichia coli 562 -11535487 7500923555 yfjn putative cell division protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 238 of 400 of the completegenome.) (nt:o357; this 357 aa orf is 23 pct identical (1 gap)) (le:8426) (re:9499) (di:direct) AE000348 AE000348 g1788983 Escherichia coli 562 -11535487 5000693064 (de:(ecoli_2565) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2565 ECOLI_2565 Escherichia coli 562 10123752

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857399	11747	33903	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857400	11748	33904	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857401	11749	33905	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857406	11750	33906	354	117

Description

6500731630 yfjo:b2631 hypothetical protein:hypothetical 11.9 kd protein in alpa-gabd intergenic region:o106 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2631 b2631 Escherichia coli 562 -11535488 111986 yfjo (de:hypothetical 11.9 kd protein in alpa-gabd intergenic region (o106)) (db:swissprot) YFJO_ECOLI P52130 ESCHERICHIA COLI 562 -11535488 7000687745 hypothetical protein b2631 (db:pir2.dat) A65042 A65042 Escherichia coli 562 -11535488 7500923556 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_o106) (le:15989) (re:16309) (di:direct) ECU36840 U36840 g1033126 Escherichia coli 562 -11535488 239492 yfjo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 238 of 400 of the completegenome.) (nt:o106; this 106 aa orf is 28 pct identical (3 gaps)) (le:9543) (re:9863) (di:direct) AE000348 AE000348 g1788984 Escherichia coli 562 -11535488 5000693065 (de:(ecoli_2566) (pn:hypothetical 11) (gtcfc:13.7:14.1) (ec:) (yfjo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2566 ECOLI_2566 Escherichia coli 562 10053714

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857409	11751	33907	960	319

Description

GTC ORF with score 110 to: (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:f286; 100 pct identical amino acid sequence and) (le:5736) (re:6596) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857420	11752	33908	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857430	11753	33909	486	161

Description

6500731631 yfjp:b2632 hypothetical protein:hypothetical 32.5 kd protein in alpa-gabd intergenic region:o289 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2632 b2632 Escherichia coli 562 -11535489 111987 yfjp (de:hypothetical 32.5 kd protein in alpa-gabd intergenic region (o289)) (db:swissprot) YFJP_ECOLI P52131 ESCHERICHIA COLI 562 -11535489 7000687746 yfjp yfjp protein (cl:ykfa protein:translation elongation factor tu homology) (db:pir2.dat) B65042 B65042 Escherichia coli 562 -11535489 7500923557 yfjp putative gtp-binding protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:o289; this 289 aa orf is 24 pct identical (3 gaps)) (le:205) (re:1074) (di:direct) AE000349 AE000349 g1788986 Escherichia coli 562 -11535489 5000693066 (de:(ecoli_2567) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2567 ECOLI_2567 Escherichia coli 562 10123753

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857438	11754	33910	1191	396

Description

GTC ORF with score 843 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c3e7.) (nt:spbc3e7.10, putative methionine aminopeptidase 1,) (le:23540:23709:23779:23885) (re:23656:23729:23824:24840) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857444	11755	33911	300	99

Description

6500731632 yfjq:b2633 hypothetical protein:hypothetical 31.3 kd protein in alpa-gabd intergenic region:o273 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2633 b2633 Escherichia coli 562 -11535490 111988 yfjq (de:hypothetical 31.3 kd protein in alpa-gabd intergenic region (o273)) (db:swissprot) YFJQ_ECOLI P52132 ESCHERICHIA COLI 562 -11535490 7000687747 yfjq yfjq protein (db:pir2.dat) C65042 C65042 Escherichia coli 562 -11535490 7500923558 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_o273) (le:17619) (re:18440) (di:direct) ECU36840 U36840 g1033128 Escherichia coli 562 -11535490 239494 yfjq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:o273; this 273 aa orf is 67 pct identical (1 gap)) (le:1166) (re:1987) (di:direct) AE000349 AE000349 g1788987 Escherichia coli 562 -11535490 5000693067 (de:(ecoli_2568) (pn:hypothetical 31) (gtcfc:13.7:14.1) (ec:) (yfjq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2568 ECOLI_2568 Escherichia coli 562 10053716

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857459	11756	33912	462	153

Description

6500731633 yfjr:b2634 hypothetical protein:hypothetical transcriptional regulator in alpa-gabd intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2634 b2634 Escherichia coli 562 -11535491 111989 yfjr (de:hypothetical transcriptional regulator in alpa-gabd intergenic region) (db:swissprot) YFJR_ECOLI P52133 ESCHERICHIA COLI 562 -11535491 7000687748 hypothetical protein b2634 (db:pir2.dat) D65042 D65042 Escherichia coli 562 -11535491 7500923563 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_o233) (le:18657) (re:19358) (di:direct) ECU36840 U36840 g1033129 Escherichia coli 562 -11535491 239495 yfjr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:o233; 29 pct identical (9 gaps) to 116 residues) (le:2204) (re:2905) (di:direct) AE000349 AE000349 g1788988 Escherichia coli 562 -11535491 5000693068 (de:(ecoli_2569) (pn:hypothetical transcriptional regulator in alpa-gabd intergenic region:o233) (gtcfc:13.7:14.1) (ec:)) (yfjr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2569 ECOLI_2569 Escherichia coli 562 10053717

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857461	11757	33913	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857493	11758	33914	636	211

Description

6500731634 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2635 b2635 Escherichia coli 562 -11535492 7000691705 hypothetical protein b2635 (db:pir2.dat) E65042 E65042 Escherichia coli 562 -11535492 7500960237 b2635 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:o130; sequence change split orf of earlier version;) (le:2790) (re:3182) (di:direct) AE000349 AE000349 g2367144 Escherichia coli 562 -11535492

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857494	11759	33915	837	278

Description

6500731635 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2636 b2636 Escherichia coli 562 -11535493
7000691706 probable membrane protein b2636 (db:pir2.dat) F65042 F65042 Escherichia coli 562 -11535493 7500960429 b2636 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:o230; sequence change split orf of earlier version;) (le:2933) (re:3625) (di:direct) AE000349 AE000349 g2367145 Escherichia coli 562 -11535493

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857495	11760	33916	1617	538

Description

6500731636 yfjt:b2637 hypothetical protein:hypothetical 17.1 kd protein in alpa-gabd intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2637 b2637 Escherichia coli 562 -11535494 111991 yfjt (de:hypothetical 17.1 kd protein in alpa-gabd intergenic region precursor) (db:swissprot) YFJT_ECOLI P52135 ESCHERICHIA COLI 562 -11535494 7000687749 yfjt yfjt protein (db:pir2.dat) G65042 G65042 Escherichia coli 562 -11535494 7500923564 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_o155) (le:20103) (re:20570) (di:direct) ECU36840 U36840 g1033131 Escherichia coli 562 -11535494 239497 yfjt orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:o155; this 155 aa orf is 22 pct identical (3 gaps)) (le:3649) (re:4116) (di:direct) AE000349 AE000349 g1788990 Escherichia coli 562 -11535494 5000693070 (de:(ecoli_2571) (pn:hypothetical 17) (gtcfc:13.7:14.1) (ec:) (yfjt_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2571 ECOLI_2571 Escherichia coli 562 10053719

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857499	11761	33917	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857510	11762	33918	555	184

Description

GTC ORF with score 242 to: (sr:baker's yeast) (db:genpept-pln2)
(de:saccharomyces cerevisiae putative transmembrane protein hum1p(hum1)
gene, complete cds.) (nt:novel protein; putative transmembrane protein;)
(le:1) (re:1236) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857519	11763	33919	534	177

Description

5000693071 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2638 b2638 Escherichia coli 562 -11535495
7000691707 hypothetical protein b2638 (db:pir2.dat) H65042 H65042
Escherichia coli 562 -11535495 7500960238 (db:genpept-bct1) (de:escherichia
coli k-12 genome, approximately 57 minutes.) (nt:orf_f104) (le:20795)
(re:21109) (di:complement) ECU36840 U36840 g1033132 Escherichia coli 562
-11535495 239498 b2638 orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the
completengenome.) (nt:f104; this 104 aa orf is 80 pct identical (0 gaps))
(le:4341) (re:4655) (di:complement) AE000349 AE000349 g1788991 Escherichia
coli 562 -11535495 6500731637 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2638 b2638
Escherichia coli 562 -11535495

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857522	11764	33920	1494	497

Description

GTC ORF with score 566 to: (db:genpept-bct2) (de:vibrio cholerae galactosyl
transferase, gdp-mannosepyrophosphorylase, phosphomannomutase, udp-galactose
4-epimerase,galactosyl transferase, nucleotide sugar dehydrogenase,
nucleotidesugar epimerase, and ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857549	11765	33921	387	128

Description

5000693072 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2639 b2639 Escherichia coli 562 -11535496
 7000691708 hypothetical protein b2639 (db:pir2.dat) A65043 A65043
 Escherichia coli 562 -11535496 7500960239 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_f172) (le:21122) (re:21640) (di:complement) ECU36840 U36840 g1033133 Escherichia coli 562 -11535496 239499 b2639 putative pump protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:f172; this 172 aa orf is 89 pct identical (0 gaps)) (le:4668) (re:5186) (di:complement) AE000349 AE000349 g1788992
 Escherichia coli 562 -11535496 6500731638 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2639 b2639
 Escherichia coli 562 -11535496

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857550	11766	33922	567	188

Description

5000693073 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2640 b2640 Escherichia coli 562 -11535497
 7000691709 hypothetical protein b2640 (db:pir2.dat) B65043 B65043
 Escherichia coli 562 -11535497 7500960240 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:undetected frameshift would join with orf_f38) (le:21791) (re:21991) (di:complement) ECU36840 U36840 g1033134 Escherichia coli 562 -11535497 239500 b2640 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:f66) (le:5337) (re:5537) (di:complement) AE000349 AE000349 g1788993 Escherichia coli 562 -11535497
 6500731639 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2640 b2640 Escherichia coli 562 -11535497

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857552	11767	33923	1011	337

Description

GTC ORF with score 246 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f33g12.) (nt:contains similarity to g beta repeats) (le:7129:7328:7489) (re:7285:7432:7619) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857553	11768	33924	789	262
<u>Description</u>				
5000693074 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2641 b2641 Escherichia coli 562 -11535498				
7000691710 hypothetical protein b2641 (db:pir2.dat) C65043 C65043 Escherichia coli 562 -11535498 7500960241 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:undetected frameshift would join with orf_f66) (le:21931) (re:22047) (di:complement) ECU36840 U36840 g1033135 Escherichia coli 562 -11535498 239501 b2641 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:f38; this 38 aa orf is 29 pct identical (0 gaps)) (le:5477) (re:5593) (di:complement) AE000349 AE000349 g1788994 Escherichia coli 562 -11535498 6500731640 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2641 b2641 Escherichia coli 562 -11535498				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857576	11769	33925	201	66
<u>Description</u>				
6500731641 yfjw:b2642 hypothetical protein:hypothetical 64.2 kd protein in alpa-gabd intergenic region:o567 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2642 b2642 Escherichia coli 562 -11535499 111994 yfjw (de:hypothetical 64.2 kd protein in alpa-gabd intergenic region) (db:swissprot) YFJW_ECOLI P52138 ESCHERICHIA COLI 562 -11535499 7000687750 hypothetical protein b2642 (db:pir2.dat) D65043 D65043 Escherichia coli 562 -11535499 225201 yfjw (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #442(59.7-60.0 min.)) (nt:similar to (swissprot accession number p52138)) (le:1309) (re:3012) (di:direct) D90889 D90889 g1800032 Escherichia coli 562 -11535499 7500923565 yfjw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:o567; this 567 aa orf is 24 pct identical (7 gaps)) (le:5819) (re:7522) (di:direct) AE000349 AE000349 g2367146 Escherichia coli 562 -11535499				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857580	11770	33926	198	65
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857596	11771	33927	507	168

Description

6500731642 yfjx:b2643 hypothetical protein:hypothetical 17.3 kd protein in alpa-gabd intergenic region:o152 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2643 b2643 Escherichia coli 562 -11535500 111995 yfjx (de:hypothetical 17.3 kd protein in alpa-gabd intergenic region (o152)) (db:swissprot) YFJX_ECOLI P52139 ESCHERICHIA COLI 562 -11535500 7000687751 yfjx yfjx protein (cl:klca protein) (db:pir2.dat) E65043 E65043 Escherichia coli 562 -11535500 225202 yfjx (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #442(59.7-60.0 min.)) (nt:similar to (swissprot accession number p52139)) (le:3910) (re:4368) (di:direct) D90889 D90889 g1800033 Escherichia coli 562 -11535500 7500923566 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_o152) (le:24874) (re:25332) (di:direct) ECU36840 U36840 g1033137 Escherichia coli 562 -11535500 239503 yfjx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:o152; this 152 aa orf is 25 pct identical (1 gap)) (le:8420) (re:8878) (di:direct) AE000349 AE000349 g1788996 Escherichia coli 562 -11535500 5000693076 (de:(ecoli_2577) (pn:hypothetical 17) (gtcfc:13.7:14.1) (ec:) (yfjx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2577 ECOLI_2577 Escherichia coli 562 10053723

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857603	11772	33928	363	120

Description

6500731643 yfjy:b2644 hypothetical protein:hypothetical 18.0 kd protein in alpa-gabd intergenic region:ol60 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2644 b2644 Escherichia coli 562 -11535501 111996 yfjy (de:hypothetical 18.0 kd protein in alpa-gabd intergenic region) (db:swissprot) YFJY_ECOLI P52140 ESCHERICHIA COLI 562 -11535501 7000687752 yfjy yfjy protein (db:pir2.dat) F65043 F65043 Escherichia coli 562 -11535501 225203 yfjy (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #442(59.7-60.0 min.)) (nt:similar to (swissprot accession number p52140)) (le:4377) (re:4859) (di:direct) D90889 D90889 g1800034 Escherichia coli 562 -11535501 7500923567 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_ol60) (le:25341) (re:25823) (di:direct) ECU36840 U36840 g1033138 Escherichia coli 562 -11535501 239504 yfjy putative dna repair protein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 239 of 400 of the completgenome.) (nt:ol60) (le:8887) (re:9369) (di:direct) AE000349 AE000349 g1788997 Escherichia coli 562 -11535501 5000693077 (de:(ecoli_2578) (pn:hypothetical 18) (gtcfc:13.7:14.1) (ec:) (yfjy_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2578 ECOLI_2578 Escherichia coli 562 10053724

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857611	11773	33929	399	132

Description

6500731644 yfjz:b2645 hypothetical protein:hypothetical 11.7 kd protein in alpa-gabd intergenic region:o105 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2645 b2645 Escherichia coli 562 -11535502 111997 yfjz (de:hypothetical 11.7 kd protein in alpa-gabd intergenic region (o105)) (db:swissprot) YFJZ_ECOLI P52141 ESCHERICHIA COLI 562 -11535502 7000687753 yfiz yfiz protein (db:pir2.dat) G65043 G65043 Escherichia coli 562 -11535502 225204 yfjz (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #442(59.7-60.0 min.)) (nt:similar to (swissprot accession number p52141)) (le:5106) (re:5423) (di:direct) D90889 D90889 g1800035 Escherichia coli 562 -11535502 7500923568 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_o105) (le:26070) (re:26387) (di:direct) ECU36840 U36840 g1033139 Escherichia coli 562 -11535502 239505 yfjz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:o105; this 105 aa orf is 66 pct identical (0 gaps)) (le:9616) (re:9933) (di:direct) AE000349 AE000349 g1788998 Escherichia coli 562 -11535502 5000693078 (de:(ecoli_2579) (pn:hypothetical 11) (gtcfc:13.7:14.1) (ec:) (yfjz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2579 ECOLI_2579 Escherichia coli 562 10053725

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857612	11774	33930	648	215

Description

5000693079 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2646 b2646 Escherichia coli 562 -11535503 7500952249 ypjf (de:hypothetical 12.3 kd protein in alpa-gabd intergenic region) (db:swissprot) YPJF_ECOLI Q46953 ESCHERICHIA COLI 562 -11535503 7000691711 hypothetical protein b2646 (db:pir2.dat) H65043 H65043 Escherichia coli 562 -11535503 239506 (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:orf_o109) (le:26408) (re:26737) (di:direct) ECU36840 U36840 g1033140 Escherichia coli 562 -11535503 7500952251 ypjf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 239 of 400 of the completegenome.) (nt:o109; this 109 aa orf is 33 pct identical (0 gaps)) (le:9954) (re:10283) (di:direct) AE000349 AE000349 g1788999 Escherichia coli 562 -11535503 6500731645 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2646 b2646 Escherichia coli 562 -11535503

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857617	11775	33931	243	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857620	11776	33932	690	229

Description

6500731646 ypja:b2647 hypothetical protein:hypothetical 98.4 kd protein in alpa-gabd intergenic region:f949 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2647 b2647 Escherichia coli 562 -11535504 115614 ypja (de:hypothetical 98.4 kd protein in alpa-gabd intergenic region (f949)) (db:swissprot) YPJA_ECOLI P52143 ESCHERICHIA COLI 562 -11535504 7000688231 hypothetical protein b2647 (db:pir2.dat) A65044 A65044 Escherichia coli 562 -11535504 7500952244 ypja putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 240 of 400 of the completegenome.) (nt:f1569; this 1569 aa orf is 42 pct identical (65) (le:212) (re:4921) (di:complement) AE000350 AE000350 g1789001 Escherichia coli 562 -11535504 5000693080 (de:(ecoli_2581) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2581 ECOLI_2581 Escherichia coli 562 10123759

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857628	11777	33933	1158	385

Description

5000693081 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2648 b2648 Escherichia coli 562 -11535505 7000691712 hypothetical protein b2648 (db:pir2.dat) B65044 B65044 Escherichia coli 562 -11535505 7500960242 b2648 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 240 of 400 of the completegenome.) (nt:f47; this 47 aa orf is 76 pct identical (0 gaps)) (le:5130) (re:5273) (di:complement) AE000350 AE000350 g1789002 Escherichia coli 562 -11535505 6500731647 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2648 b2648 Escherichia coli 562 -11535505

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857631	11778	33934	585	195

Description

5000693082 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2649 b2649 Escherichia coli 562 -11535506
 7000691713 hypothetical protein b2649 (db:pir2.dat) C65044 C65044
 Escherichia coli 562 -11535506 7500960243 b2649 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 240 of 400 of the completegenome.) (nt:f263; this 263 aa orf is 26 pct identical (20 gaps)) (le:5703) (re:6494) (di:complement) AE000350 AE000350 g1789003 Escherichia coli 562 -11535506 6500731648 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2649 b2649 Escherichia coli 562 -11535506

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857649	11779	33935	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857672	11780	33936	234	77

Description

GTC ORF with score 106 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone f4d11 (essaiiproject).) (nt:similarity to protein kinase tmk1, arabidopsis) (le:33819:34133:34431) (re:34034:34294:34578) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857673	11781	33937	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857674	11782	33938	465	154

Description

5000693083 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2650 b2650 Escherichia coli 562 -11535507
 7000691714 hypothetical protein b2650 (db:pir2.dat) D65044 D65044
 Escherichia coli 562 -11535507 7500960244 b2650 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 240 of 400 of the completegenome.) (nt:f160) (le:6594) (re:7076) (di:complement) AE000350 AE000350 g1789004 Escherichia coli 562 -11535507
 6500731649 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2650 b2650 Escherichia coli 562 -11535507

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857683	11783	33939	303	100

Description

6500731650 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2651 b2651 Escherichia coli 562 -11535508
 7000691715 hypothetical protein b2651 (db:pir2.dat) E65044 E65044
 Escherichia coli 562 -11535508 7500960245 b2651 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 240 of 400 of the completegenome.) (nt:o43; c-terminal differs from earlier version) (le:7286) (re:7417) (di:direct) AE000350 AE000350 g2367148
 Escherichia coli 562 -11535508

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857705	11784	33940	1203	400

Description

5000693085 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2653 b2653 Escherichia coli 562 -11535509
 7000691716 hypothetical protein b2653 (db:pir2.dat) F65044 F65044
 Escherichia coli 562 -11535509 7500960246 b2653 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 240 of 400 of the completegenome.) (nt:f57; this 57 aa orf is 24 pct identical (0 gaps)) (le:7865) (re:8038) (di:complement) AE000350 AE000350 g1789006 Escherichia coli 562 -11535509 6500731651 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2653 b2653 Escherichia coli 562 -11535509

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857726	11785	33941	420	139
<u>Description</u>				
5000693086 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2654 b2654 Escherichia coli 562 -11535510				
7000691717 hypothetical protein b2654 (db:pir2.dat) G65044 G65044				
Escherichia coli 562 -11535510 7500960247 b2654 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 240 of 400 of the completegenome.) (nt:ol10; phage stats; this 110 aa orf is 31 pct) (le:8462) (re:8794) (di:direct) AE000350 AE000350 g1789007				
Escherichia coli 562 -11535510 6500731652 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2654 b2654				
Escherichia coli 562 -11535510				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857727	11786	33942	792	263
<u>Description</u>				
5000693087 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2655 b2655 Escherichia coli 562 -11535511				
7000691718 hypothetical protein b2655 (db:pir2.dat) H65044 H65044				
Escherichia coli 562 -11535511 7500960248 b2655 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 240 of 400 of the completegenome.) (nt:ol64; ol64; phage stats; this 164 aa orf is 30 pct) (le:8813) (re:9307) (di:direct) AE000350 AE000350 g1789008				
Escherichia coli 562 -11535511 6500731653 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2655 b2655				
Escherichia coli 562 -11535511				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857740	11787	33943	768	255
<u>Description</u>				
5000693088 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2656 b2656 Escherichia coli 562 -11535512				
7000691719 hypothetical protein b2656 (db:pir2.dat) A65045 A65045				
Escherichia coli 562 -11535512 7500960249 b2656 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 240 of 400 of the completegenome.) (nt:o62; o62; phage stats; this 62 aa orf is 29 pct) (le:9312) (re:9500) (di:direct) AE000350 AE000350 g1789009				
Escherichia coli 562 -11535512 6500731654 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2656 b2656				
Escherichia coli 562 -11535512				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857765	11788	33944	450	149

Description

GTC ORF with score 111 to: (sr:rabbit (strain new zealand white, adult) kidney, cdna to mrna) (db:genpept-mam) (de:rabbit cytochrome p450iva7 (cyp4a7) mrna, complete cds.) (nt:lauric acid omega-hydroxylase) (le:25) (re:1560) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857773	11789	33945	384	127

Description

5000693089 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2657 b2657 Escherichia coli 562 -11535513
7000691720 hypothetical protein b2657 (db:pir2.dat) B65045 B65045
Escherichia coli 562 -11535513 7500960250 b2657 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 240 of 400 of the completegenome.) (nt:o210; o210; phage stats; this 210 aa orf is 28 pct) (le:9672) (re:10304) (di:direct) AE000350 AE000350 g1789010 Escherichia coli 562 -11535513 6500731655 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2657 b2657 Escherichia coli 562 -11535513

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857774	11790	33946	588	195

Description

5000693090 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2658 b2658 Escherichia coli 562 -11535514
7000691721 hypothetical protein b2658 (db:pir2.dat) C65045 C65045
Escherichia coli 562 -11535514 7500960251 b2658 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 241 of 400 of the completegenome.) (nt:o90; o90; phage stats; this 90 aa orf is 32 pct) (le:100) (re:372) (di:direct) AE000351 AE000351 g1789012
Escherichia coli 562 -11535514 6500731656 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2658 b2658
Escherichia coli 562 -11535514

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857796	11791	33947	642	213

Description

5000693091 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2659 b2659 Escherichia coli 562 -11535515
7000691722 hypothetical protein b2659 (db:pir2.dat) D65045 D65045
Escherichia coli 562 -11535515 7500960252 b2659 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 241 of 400 of the completegenome.) (nt:o360; this 360 aa orf is 28 pct identical (5 gaps)) (le:603) (re:1685) (di:direct) AE000351 AE000351
g1789013 Escherichia coli 562 -11535515 6500731657 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2659 b2659 Escherichia coli 562 -11535515

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857804	11792	33948	2358	786

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857810	11793	33949	825	274

Description

6500731658 ygaf:b2660 hypothetical protein in gabp 3region:hypothetical 48.6 kd protein in alpa-gabp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2660 b2660 Escherichia coli 562 -11535516 112254 ygaf (de:hypothetical 48.6 kd protein in alpa-gabp intergenic region) (db:swissprot) YGAF_ECOLI P37339 ESCHERICHIA COLI 562 -11535516 7000687766 ygaf hypothetical protein in gabp 3region (db:pir2.dat) E65045 E65045 Escherichia coli 562 -11535516 7500924001 ygaf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 241 of 400 of the completegenome.) (nt:o444; 100 pct identical to 204 aa) (le:1639) (re:2973) (di:direct) AE000351 AE000351
g1789014 Escherichia coli 562 -11535516 5000693092 (de:(ecoli_2593) (pn:hypothetical protein in gabp:3"region:fragment) (gn:ygaf) (gtcfc:13.7:14.1) (ec:) (ygaf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2593 ECOLI_2593 Escherichia coli 562 10123771

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857814	11794	33950	519	172

Description

6500731659 ygae:b2664 hypothetical transcriptional regulator in gabp 3 region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2664 b2664 Escherichia coli 562 -11535517 7000691847 ygae hypothetical transcription regulator gabp 3 region (cl:probable transcription regulator gabp) (db:pir2.dat) A65046 A65046 Escherichia coli 562 -11535517 7500960364 ygae putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 241 of 400 of the completegenome.) (nt:o226; 100 pct identical to 114 aa) (le:7379) (re:8059) (di:direct) AE000351 AE000351 g1789018 Escherichia coli 562 -11535517 5000693093 (de:(ecoli_2597) (pn:hypothetical transcriptional regulator in gabp:3"region:fragment) (gn:ygae) (gtcfc:13.7:14.1) (ec:) (ygae_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2597 ECOLI_2597 Escherichia coli 562 10123772

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857815	11795	33951	318	105

Description

6500731660 ygau:b2665 hypothetical protein:unknown protein from 2d-page:spot lm6 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2665 b2665 Escherichia coli 562 -11535518 7000691723 hypothetical protein b2665 (db:pir2.dat) B65046 B65046 Escherichia coli 562 -11535518 7500960253 ygau orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 241 of 400 of the completegenome.) (nt:f149; this 149 aa orf is 42 pct identical (10 gaps)) (le:8060) (re:8509) (di:complement) AE000351 AE000351 g1789019 Escherichia coli 562 -11535518 5000693094 (de:(ecoli_2598) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2598 ECOLI_2598 Escherichia coli 562 10123773

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857820	11796	33952	990	329

Description

5000693095 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2666 b2666 Escherichia coli 562 -11535519
7500952327 ygae (de:hypothetical 5.9 kd protein in gabp-stpa intergenic region) (db:swissprot) YQAE_ECOLI P77240 ESCHERICHIA COLI 562 -11535519
7000691724 hypothetical protein b2666 (cl:conserved hypothetical protein b2666) (db:pir2.dat) C65046 C65046 Escherichia coli 562 -11535519 225220 zk632.10 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #443(59.8-60.2 min.)) (nt:similar to (swissprot accession number p34655)) (le:17039) (re:17197) (di:complement) D90890 D90890 g1800052 Escherichia coli 562 -11535519 7500952329 zk632.10 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6 min.)) (nt:similar to (swissprot accession number p34655)) (le:340) (re:498) (di:complement) D90891 D90891 g1800056 Escherichia coli 562 -11535519 7500952330 b2666 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 241 of 400 of the completegenome.) (nt:f52; this 52 aa orf is 52 pct identical (0 gaps)) (le:8593) (re:8751) (di:complement) AE000351 AE000351 g1789020 Escherichia coli 562 -11535519 225223 zk632.10 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #443(59.8-60.2 min.)) (nt:similar to (swissprot accession number p34655)) (le:17039) (re:17197) (di:complement) D90890 D90890 g1800052 Escherichia coli 562 -11535519 6500731661 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2666 b2666 Escherichia coli 562 -11535519

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857824	11797	33953	699	232
<u>Description</u>				
5000693096 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2667 b2667 Escherichia coli 562 -11535520				
7000691725 hypothetical protein b2667 (cl:arsenical resistance operon repressor) (db:pir2.dat) D65046 D65046 Escherichia coli 562 -11535520				
225221 hlyu transcriptional activator hlyu. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #443(59.8-60.2 min.)) (nt:similar to (swissprot accession number p52695)) (le:17380) (re:17679) (di:direct)				
D90890 D90890 g1800053 Escherichia coli 562 -11535520 225224 hlyu transcriptional activator hlyu. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6 min.)) (nt:similar to (swissprot accession number p52695)) (le:681) (re:980) (di:direct) D90891 D90891 g1800057				
Escherichia coli 562 -11535520 7500960254 b2667 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 241 of 400 of the completegenome.) (nt:o99; this 99 aa orf is 45 pct identical (1 gap)) (le:8934) (re:9233) (di:direct) AE000351 AE000351				
g1789021 Escherichia coli 562 -11535520 6500731662 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2667 b2667 Escherichia coli 562 -11535520				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857832	11798	33954	1083	360
<u>Description</u>				
6500731663 ygap:b2668 hypothetical protein:hypothetical 18.6 kd protein in gapb-stpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2668 b2668 Escherichia coli 562 -11535521 118680				
ygap (de:hypothetical 18.6 kd protein in gapb-stpa intergenic region) (db:swissprot) YGAP_ECOLI P55734 ESCHERICHIA COLI 562 -11535521 7000687769				
hypothetical protein b2668 (cl:hypothetical protein slr1261) (db:pir2.dat) E65046 E65046 Escherichia coli 562 -11535521 7500924005 ygap				
orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 241 of 400 of the completegenome.) (nt:o174; this 174 aa orf is 33 pct identical (4 gaps)) (le:9243) (re:9767) (di:direct)				
AE000351 AE000351 g1789022 Escherichia coli 562 -11535521 5000693097				
(de:(ecoli_2601) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2601				
ECOLI_2601 Escherichia coli 562 10061034				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857836	11799	33955	1227	408
<u>Description</u>				
5000693098 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2670 b2670 Escherichia coli 562 -11535522 7000691726 hypothetical protein b2670 (db:pir2.dat) G65046 G65046 Escherichia coli 562 -11535522 7500960255 b2670 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:ol49; this 149 aa orf is 28 pct identical (16 gaps)) (le:365) (re:814) (di:direct) AE000352 AE000352 g1789025 Escherichia coli 562 -11535522 6500731664 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2670 b2670 Escherichia coli 562 -11535522				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857841	11800	33956	219	72
<u>Description</u>				
6500731665 ygam:b2672 hypothetical protein:hypothetical 12.3 kd protein in stpa-nrdh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2672 b2672 Escherichia coli 562 -11535523 118676 ygam (de:hypothetical 12.3 kd protein in stpa-nrdh intergenic region) (db:swissprot) YGAM_ECOLI Q47413 ESCHERICHIA COLI 562 -11535523 7000687768 hypothetical protein b2672 (cl:conserved hypothetical protein b2672) (db:pir2.dat) A65047 A65047 Escherichia coli 562 -11535523 225227 yqjd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6 min.)) (nt:similar to (swissprot accession number p42617)) (le:3604) (re:3945) (di:direct) D90891 D90891 g1800060 Escherichia coli 562 -11535523 7500924004 ygam orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:ol13; this 113 aa orf is 41 pct identical (3 gaps)) (le:1335) (re:1676) (di:direct) AE000352 AE000352 g1789027 Escherichia coli 562 -11535523 5000693100 (de:(ecoli_2605) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2605 ECOLI_2605 Escherichia coli 562 10061033				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857848	11801	33957	306	101

Description

6500731666 nrdh:b2673 hypothetical protein:glutaredoxin-like protein nrdh (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2673 b2673 Escherichia coli 562 -11535524 118346 nrdh (de:glutaredoxin-like protein nrdh) (db:swissprot) NRDH_ECOLI Q47414 ESCHERICHIA COLI 562 -11535524 1500686128 hypothetical 9.1k protein b2673 (db:pir2.dat) S70891 S70891 Escherichia coli 562 -11535524 305935 9.1 kd protein (db:genpept-bct1) (de:e.coli nrdef operon (partial).) (nt:orfb) (le:595) (re:840) (di:direct) ECNRDE X79787 g1050470 Escherichia coli 562 -11535524 233502 nrdh glutaredoxin-like protein:hydrogen donor (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:o81; this 81 aa orf is 28 pct identical (2 gaps) to) (le:1924) (re:2169) (di:direct) AE000352 AE000352 g1789028 Escherichia coli 562 -11535524 5000693101 (de:(ecoli_2606) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2606 ECOLI_2606 Escherichia coli 562 10060496

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857849	11802	33958	1230	409

Description

6500731667 nrdb:b2674 hypothetical protein:nrdb protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2674 b2674 Escherichia coli 562 -11535525 118677 nrdb (de:nrdb protein) (db:swissprot) NRDI_ECOLI Q47415 ESCHERICHIA COLI 562 -11535525 1500686993 hypothetical protein b2674 (db:pir2.dat) S70890 S70890 Escherichia coli 562 -11535525 305936 (db:genpept-bct1) (de:e.coli nrdef operon (partial).) (nt:orfc) (le:837) (re:1247) (di:direct) ECNRDE X79787 g1050471 Escherichia coli 562 -11535525 233503 nrdb orf:hypothetical protein (fn:phenotype; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:o136; this 136 aa orf is 55 pct identical (2 gaps)) (le:2166) (re:2576) (di:direct) AE000352 AE000352 g1789029 Escherichia coli 562 -11535525 5000693102 (de:(ecoli_2607) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2607 ECOLI_2607 Escherichia coli 562 10063273

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857892	11803	33959	1389	463
<u>Description</u>				
5000693103 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2680 b2680 Escherichia coli 562 -11535526				
7000691727 hypothetical protein b2680 (db:pir2.dat) A65048 A65048				
Escherichia coli 562 -11535526 7500960256 b2680 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:o88; this 88 aa orf is 28 pct identical (1 gap)) (le:9517) (re:9783) (di:direct) AE000352 AE000352				
g1789035 Escherichia coli 562 -11535526 6500731668 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2680 b2680 Escherichia coli 562 -11535526				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857903	11804	33960	393	130
<u>Description</u>				
5000693104 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2681 b2681 Escherichia coli 562 -11535527				
7000691728 hypothetical protein b2681 (db:pir2.dat) B65048 B65048				
Escherichia coli 562 -11535527 7500960257 b2681 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:o305; this 305 aa orf is 20 pct identical (9 gaps)) (le:9777) (re:10694) (di:direct) AE000352 AE000352				
g1789036 Escherichia coli 562 -11535527 6500731669 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2681 b2681 Escherichia coli 562 -11535527				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501857919	11805	33961	1233	411
<u>Description</u>				
5000693105 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2682 b2682 Escherichia coli 562 -11535528				
7500924006 ygaz (de:hypothetical 26.1 kd protein in prox-mpira intergenic region) (db:swissprot) YGAZ_ECOLI P76630 ESCHERICHIA COLI 562 -11535528				
7000691729 hypothetical protein b2682 (cl:hypothetical protein b2682) (db:pir2.dat) C65048 C65048 Escherichia coli 562 -11535528 7500924008 b2682 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 243 of 400 of the completegenome.) (nt:o245; this 245 aa orf is 25 pct identical (8 gaps)) (le:92) (re:829) (di:direct) AE000353 AE000353				
g1789038 Escherichia coli 562 -11535528 6500731670 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2682 b2682 Escherichia coli 562 -11535528				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857928	11806	33962	438	145

Description

6500731671 ygah:b2683 hypothetical protein in emrr 5 region:hypothetical
12.0 kd protein in prox-emrr intergenic region (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b2683 b2683 Escherichia coli 562
-11535529 112258 ygah (de:hypothetical 12.0 kd protein in prox-emrr
intergenic region) (db:swissprot) YGAH_ECOLI P43667 ESCHERICHIA COLI 562
-11535529 7000687767 ygah hypothetical protein in emrr 5 region
(db:pir2.dat) D65048 D65048 Escherichia coli 562 -11535529 225235 ygah
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6
min.)) (nt:similar to (swissprot accession number p43667)) (le:13817)
(re:14152) (di:direct) D90891 D90891 g1800068 Escherichia coli 562 -11535529
7500924002 ygah orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 243 of 400 of the
completegenome.) (nt:o111; 94 pct identical to 50 residues of 58) (le:819)
(re:1154) (di:direct) AE000353 AE000353 g1789039 Escherichia coli 562
-11535529 5000693106 (de:(ecoli_2616) (pn:hypothetical protein in emrr
5"region:fragment) (gn:ygah) (gtcfc:13.7:14.1) (ec:) (ygah_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2616
ECOLI_2616 Escherichia coli 562 10120320

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857932	11807	33963	819	272

Description

6500731672 ygag:b2687 hypothetical protein in emrb 3 region:hypothetical
 19.4 kd protein in emrb-gsha intergenic region (gtcfc:14.1) (keggfc:14.2)
 (rileyfc:5.7.0) (db:gtc-escherichia coli) b2687 b2687 Escherichia coli 562
 -11535530 7000691827 ygag hypothetical protein in emrb 3 region
 (cl:conserved hypothetical protein hi0491) (db:pir2.dat) H65048 H65048
 Escherichia coli 562 -11535530 225239 ygag (sr:escherichia coli
 (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
 (de:e.coli genomic dna, kohara clone #445(60.2-60.6 min.)) (nt:similar to
 (swissprot accession number p45578)) (le:17691) (re:18206) (di:complement)
 D90891 D90891 g1800072 Escherichia coli 562 -11535530 225244 ygag
 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #446(60.5-60.9
 min.)) (nt:similar to (swissprot accession number p45578)) (le:3125)
 (re:3640) (di:complement) D90892 D90892 g1800078 Escherichia coli 562
 -11535530 7500960344 ygag orf:hypothetical protein (fn:orf; unknown)
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 243 of 400 of the
 completgenome.) (nt:f171; 100 pct identical to 119 aa) (le:4693) (re:5208)
 (di:complement) AE000353 AE000353 g1789043 Escherichia coli 562 -11535530
 5000693108 (de:(ecoli_2620) (pn:hypothetical protein in
 emrb:3"region:fragment) (gn:ygag) (gtcfc:13.7:14.1) (ec:) (ygag_ecoli)
 (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2620
 ECOLI_2620 Escherichia coli 562 10120323

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857944	11808	33964	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857949	11809	33965	441	146

Description

5000693109 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2689 b2689 Escherichia coli 562 -11535531
7502852272 yqaa (de:hypothetical 15.6 kd protein in gsha-csra intergenic region) (db:swissprot) YQAA_ECOLI P76631 ESCHERICHIA COLI 562 -11535531
7000691730 hypothetical protein b2689 (cl:hypothetical protein hi0489) (db:pir2.dat) B65049 B65049 Escherichia coli 562 -11535531 7500960258 b2689 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 243 of 400 of the completegenome.) (nt:f142; this 142 aa orf is 50 pct identical (8 gaps)) (le:6988) (re:7416) (di:complement) AE000353 AE000353 g1789045 Escherichia coli 562 -11535531 6500731673 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2689 b2689 Escherichia coli 562 -11535531

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857952	11810	33966	339	112

Description

5000693110 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2690 b2690 Escherichia coli 562 -11535532
7500952320 yqab (de:hypothetical 20.8 kd protein in gsha-csra intergenic region) (db:swissprot) YQAB_ECOLI P77475 ESCHERICHIA COLI 562 -11535532
7000691731 hypothetical protein b2690 (cl:hypothetical protein b2690) (db:pir2.dat) C65049 C65049 Escherichia coli 562 -11535532 225247 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #446(60.5-60.9 min.)) (nt:similar to (swissprot accession number p44004)) (le:5844) (re:6410) (di:complement) D90892 D90892 g1800081 Escherichia coli 562 -11535532 7500952323 yqab putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 243 of 400 of the completegenome.) (nt:f188; this 188 aa orf is 41 pct identical (1 gap)) (le:7413) (re:7979) (di:complement) AE000353 AE000353 g1789046 Escherichia coli 562 -11535532 6500731674 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2690 b2690 Escherichia coli 562 -11535532

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857965	11811	33967	753	250

Description

6500731675 ygad:b2700 hypothetical 17.6 kd protein in mltb-reca intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2700 b2700 Escherichia coli 562 -11535533 112250 ygad (de:hypothetical 17.6 kd protein in mltb-reca intergenic region) (db:swissprot) YGAD_ECOLI P41053 ESCHERICHIA COLI 562 -11535533 7000687765 ygad ygad protein (cl:conserved hypothetical protein aq_1996) (db:pir2.dat) H65049 H65049 Escherichia coli 562 -11535533 225252 ygad (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #446(60.5-60.9 min.)) (nt:similar to (swissprot accession number p41053)) (le:12755) (re:13252) (di:complement) D90892 D90892 g1800086 Escherichia coli 562 -11535533 7500924000 ygad ygad (db:genpept-bct1) (de:escherichia coli membrane-bound lytic transglycosylase (mltb) gene, and ygad (ygad) gene, complete cds.) (nt:putative) (le:1381) (re:1878) (di:direct) ECU18785 U18785 g642539 Escherichia coli 562 -11535533 238756 ygad orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 244 of 400 of the complete genome.) (nt:f165; 100 pct identical to ygad_ecoli sw: p41053) (le:1805) (re:2302) (di:complement) AE000354 AE000354 g1789052 Escherichia coli 562 -11535533 5000693112 (de:(ecoli_2628) (pn:hypothetical 17) (gn:ygad) (gtcfc:13.7:14.1) (ec:) (ygad_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2628 ECOLI_2628 Escherichia coli 562 10053978

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501857970	11812	33968	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858007	11813	33969	606	201

Description

5000693117 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2710 b2710 Escherichia coli 562 -11535534
7000691732 hypothetical protein b2710 (cl:escherichia coli hypothetical protein b2710:rubredoxin homology) (db:pir2.dat) B65051 B65051 Escherichia coli 562 -11535534 7500960259 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o479) (le:4780) (re:6219) (di:direct) ECU29579 U29579 g882603 Escherichia coli 562 -11535534 239284 b2710 putative flavodoxin (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 245 of 400 of the completegenome.) (nt:o479; this 479 aa orf is 34 pct identical (6 gaps)) (le:86) (re:1525) (di:direct) AE000355 AE000355 g1789064 Escherichia coli 562 -11535534 6500731676 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2710 b2710 Escherichia coli 562 -11535534

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858014	11814	33970	2889	962

Description

6500731677 ygbd:b2711 hypothetical protein in hyda 3region:hypothetical 41.4 kd protein in srlq-hypf intergenic region:orf4:orf2:o377 (gtcfc:14.1) (ec:1.18.1.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2711 b2711 Escherichia coli 562 -11535535 7000691833 ygbd rubredoxin--nad+ reductase::hypothetical protein hyda 3-region (cl:rubredoxin--nad+ reductase rubb) (ec:1.18.1.1) (db:pir2.dat) C65051 C65051 Escherichia coli 562 -11535535 7500960348 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o377) (le:6216) (re:7349) (di:direct) ECU29579 U29579 g882604 Escherichia coli 562 -11535535 239285 ygbd putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 245 of 400 of the completegenome.) (nt:o377; 99 pct identical to 235 aa fragment) (le:1522) (re:2655) (di:direct) AE000355 AE000355 g1789065 Escherichia coli 562 -11535535 5000693118 (de:(ecoli_2640) (pn:hypothetical 41) (gn:ygbd) (gtcfc:13.7:14.1) (ec:1.18.1.-) (ygbd_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2640 ECOLI_2640 Escherichia coli 562 10123788

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858016	11815	33971	543	180

Description

6500731678 ygba:b2732 hypothetical 13.9 kd protein in fhla-muts intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2732 b2732 Escherichia coli 562 -11535536 112264 ygba (de:hypothetical 13.9 kd protein in fhla-muts intergenic region) (db:swissprot) YGBA_ECOLI P25728 ESCHERICHIA COLI 562 -11535536 7000687770 ygba hypothetical 13.9 kd protein in fhla-muts intergenic region (db:pir2.dat) H65053 H65053 Escherichia coli 562 -11535536 7500924017 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:alternate gene name ygba; orf_f117) (le:28757) (re:29110) (di:complement) ECU29579 U29579 g882625 Escherichia coli 562 -11535536 239306 ygba orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 247 of 400 of the completegenome.) (nt:f117; 100 pct identical to ygba_ecoli sw: p25728) (le:2182) (re:2535) (di:complement) AE000357 AE000357 g1789088 Escherichia coli 562 -11535536 5000693121 (de:(ecoli_2661) (pn:hypothetical 13) (gn:ygba) (gtcfc:13.7:14.1) (ec:)) (ygba_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2661 ECOLI_2661 Escherichia coli 562 10053992

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858022	11816	33972	1404	467

Description

5000693122 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2734 b2734 Escherichia coli 562 -11535537 120876 pphb:prpb (ec:3.1.3.16) (de:serine/threonine protein phosphatase 2,) (db:swissprot) PRP2_ECOLI P55799 ESCHERICHIA COLI 562 -11535537 7000686185 probable multiple specificity phosphoprotein phosphatase:b2734:hypothetical protein b2734 (cl:phage lambda phosphoprotein phosphatase:phosphoesterase core homology) (ec:3.1.3.-) (db:pir1.dat) B65054 B65054 Escherichia coli 562 -11535537 1500689808 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o218) (le:32064) (re:32720) (di:direct) ECU29579 U29579 g882627 Escherichia coli 562 -11535537 7500888564 prpb prpb (db:genpept-bct1) (de:escherichia coli serine/threonine type phosphoprotein phosphatase(prpb) gene, complete cds.) (nt:allele: wild type; serine/threonine type) (le:202) (re:858) (di:direct) ECU51682 U51682 g2039139 Escherichia coli 562 -11535537 239308 pphb protein phosphatase 2 (fn:enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 247 of 400 of the completegenome.) (nt:o218; this 218 aa orf is 46 pct identical (1 gap)) (le:5489) (re:6145) (di:direct) AE000357 AE000357 g1789090 Escherichia coli 562 -11535537 6500731679 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2734 b2734 Escherichia coli 562 -11535537

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858023	11817	33973	261	86

Description

6500731680 ygbi:b2735 hypothetical protein:hypothetical transcriptional regulator in muts-rpos intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2735 b2735 Escherichia coli 562 -11535538 112271 ygbi (de:hypothetical transcriptional regulator in pphb-rpos intergenic region) (db:swissprot) YGBI_ECOLI P52598 ESCHERICHIA COLI 562 -11535538 7000687773 hypothetical protein b2735 (cl:regulatory protein gutr) (db:pir2.dat) C65054 C65054 Escherichia coli 562 -11535538 7500924022 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f265) (le:32771) (re:33568) (di:complement) ECU29579 U29579 g882628 Escherichia coli 562 -11535538 239309 ygbi putative deor-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 247 of 400 of the completegenome.) (nt:f265; this 265 aa orf is 50 pct identical (0 gaps)) (le:6196) (re:6993) (di:complement) AE000357 AE000357 g1789091 Escherichia coli 562 -11535538 5000693123 (de:(ecoli_2664) (pn:hypothetical transcriptional regulator in muts-rpos intergenic region:f265) (gtcfc:13.7:14.1) (ec:) (ygbi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2664 ECOLI_2664 Escherichia coli 562 10053999

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858026	11818	33974	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858030	11819	33975	540	179

Description

5000693124 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2736 b2736 Escherichia coli 562 -11535539
7500924024 ygbj (de:hypothetical 30.8 kd protein in pphb-rpos intergenic region) (db:swissprot) YGBJ_ECOLI Q46888 ESCHERICHIA COLI 562 -11535539
7000691733 hypothetical protein b2736 (cl:3-hydroxyisobutyrate dehydrogenase:3-hydroxyisobutyrate dehydrogenase homology) (db:pir2.dat) D65054 D65054 Escherichia coli 562 -11535539 239310 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o302) (le:33735) (re:34643) (di:direct) ECU29579 U29579 g882629 Escherichia coli 562 -11535539 7500924026 b2736 putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 247 of 400 of the completegenome.) (nt:o302; this 302 aa orf is 34 pct identical (2 gaps)) (le:7159) (re:8067) (di:direct) AE000357 AE000357 g1789092 Escherichia coli 562 -11535539 6500731681 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2736 b2736 Escherichia coli 562 -11535539

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858032	11820	33976	2001	666

Description

5000693125 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2737 b2737 Escherichia coli 562 -11535540
7500924029 ygbk (de:hypothetical 41.3 kd protein in pphb-rpos intergenic region) (db:swissprot) YGBK_ECOLI Q46889 ESCHERICHIA COLI 562 -11535540
7000691734 hypothetical protein b2737 (db:pir2.dat) E65054 E65054 Escherichia coli 562 -11535540 239311 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o388) (le:34640) (re:35806) (di:direct) ECU29579 U29579 g882630 Escherichia coli 562 -11535540 7500924031 b2737 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 247 of 400 of the completegenome.) (nt:o388; this 388 aa orf is 55 pct identical (6 gaps)) (le:8064) (re:9230) (di:direct) AE000357 AE000357 g1789093 Escherichia coli 562 -11535540 6500731682 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2737 b2737 Escherichia coli 562 -11535540

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858036	11821	33977	537	178

Description

5000693126 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2738 b2738 Escherichia coli 562 -11535541
 5500686584 ygb1 (de:hypothetical 23.2 kd protein in pphb-rpos intergenic region) (db:swissprot) YGBL_ECOLI Q46890 ESCHERICHIA COLI 562 -11535541
 7000687774 hypothetical protein b2738 (db:pir2.dat) F65054 F65054 Escherichia coli 562 -11535541 7500924034 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o212) (le:35898) (re:36536) (di:direct) ECU29579 U29579 g882631 Escherichia coli 562 -11535541 239312 ygb1 putative epimerase/aldolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 247 of 400 of the completegenome.) (nt:o212; this 212 aa orf is 34 pct identical (9 gaps)) (le:9322) (re:9960) (di:direct) AE000357 AE000357 g1789094 Escherichia coli 562 -11535541 6500731683 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2738 b2738 Escherichia coli 562 -11535541

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858037	11822	33978	477	158

Description

6500731684 ygbm:b2739 hypothetical protein:hypothetical 29.2 kd protein in muts-rpos intergenic region:o258 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2739 b2739 Escherichia coli 562 -11535542 118317 ygbm (de:hypothetical 29.2 kd protein in pphb-rpos intergenic region) (db:swissprot) YGBM_ECOLI Q46891 ESCHERICHIA COLI 562 -11535542 7000687775 hypothetical protein b2739 (cl:conserved hypothetical protein h1013) (db:pir2.dat) G65054 G65054 Escherichia coli 562 -11535542 7500924036 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o258) (le:36541) (re:37317) (di:direct) ECU29579 U29579 g882632 Escherichia coli 562 -11535542 239313 ygbm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 247 of 400 of the completegenome.) (nt:o258; 40 pct identical amino acid sequence and) (le:9965) (re:10741) (di:direct) AE000357 AE000357 g1789095 Escherichia coli 562 -11535542 5000693127 (de:(ecoli_2668) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2668 ECOLI_2668 Escherichia coli 562 10060451

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858044	11823	33979	429	143

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858045	11824	33980	387	128

Description

GTC ORF with score 121 to: (sr:neurospora crassa (strain arg-12-s, cpc-1(cd15)), cdna to mrna, an) (db:genpept-pln1) (de:n.crassa cpc-1 gene, encoding cross-pathway control protein,complete cds.) (nt:cross-pathway control protein 1) (le:1188:1255) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858046	11825	33981	312	103

Description

5000693128 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2740 b2740 Escherichia coli 562 -11535543
7000691735 hypothetical protein b2740 (cl:d-serine permease) (db:pir2.dat) H65054 H65054 Escherichia coli 562 -11535543 7500960260 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o454) (le:37406) (re:38770) (di:direct) ECU29579 U29579 g882633 Escherichia coli 562 -11535543 239314 b2740 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 248 of 400 of the completegenome.) (nt:o454; this 454 aa orf is 34 pct identical (9 gaps)) (le:75) (re:1439) (di:direct) AE000358 AE000358 g1789097 Escherichia coli 562 -11535543 6500731685 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2740 b2740 Escherichia coli 562 -11535543

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858053	11826	33982	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858059	11827	33983	429	142

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858070	11828	33984	345	114

Description

6500731686 ybgo:b2745 hypothetical protein:hypothetical 39.1 kd protein in sure-cysc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2745 b2745 Escherichia coli 562 -11535544
4000709970 ybgo (de:hypothetical 39.1 kd protein in sure-cysc intergenic region) (db:swissprot) YGBO_ECOLI Q57261 ESCHERICHIA COLI 562 -11535544
163356 hypothetical protein b2745 (cl:hypothetical protein hi0701) (db:pir2.dat) I69731 I69731 Escherichia coli 562 -11535544 239319 (sr:escherichia coli (strain mpl80) dna) (db:genpept-bct1) (de:escherichia coli sure gene, complete cds and l-isoaspartylproteinmethyltransferase (pcm) gene, partial cds.) (nt:orf1) (le:796) (re:1845) (di:direct) ECOPCMORFS L07942 g1036738 Escherichia coli 562 -11535544 7500924038 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:was orf_f292 and orf_f255 before splice; orf_f349) (le:42560) (re:43609) (di:complement) ECU29579 U29579 g882638 Escherichia coli 562 -11535544
235368 ybgo putative hydrogenase subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 248 of 400 of the completegenome.) (nt:f349; was f292 and f255 before splice; this 349 aa) (le:5229) (re:6278) (di:complement) AE000358 AE000358 g1789102 Escherichia coli 562 -11535544 5000693130 (de:(ecoli_2674) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2674 ECOLI_2674 Escherichia coli 562 10086883

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858072	11829	33985	426	141
<u>Description</u>				
<p>6500731687 ygbb:b2746 hypothetical 16.9 kd protein in sure-cysc intergenic region:orf0 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2746 b2746 Escherichia coli 562 -11535545 112265 ygbb (de:hypothetical 16.9 kd protein in sure-cysc intergenic region (orf0)) (db:swissprot) YGBB_ECOLI P36663 ESCHERICHIA COLI 562 -11535545 163301 ygbb hypothetical 16.9k protein sure-cysc intergenic region (cl:conserved hypothetical protein hi0671) (db:pir2.dat) I55083 I55083 Escherichia coli 562 -11535545 239320 (sr:escherichia coli (strain mp180) dna) (db:genpept-bct1) (de:escherichia coli sure gene, complete cds and l-isoaspartylproteinmethyltransferase (pcm) gene, partial cds.) (nt:orf0) (le:320) (re:799) (di:direct) ECOPCMORFS L07942 g433711 Escherichia coli 562 -11535545 7500924018 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:alternate gene name ygbb; orf0 of 107942; orf_f159) (le:43606) (re:44085) (di:complement) ECU29579 U29579 g882639 Escherichia coli 562 -11535545 235367 ygbb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 248 of 400 of the completegenome.) (nt:f159; 100 pct identical to ygbb_ecoli sw:) (le:6275) (re:6754) (di:complement) AE000358 AE000358 g1789103 Escherichia coli 562 -11535545 5000693131 (de:(ecoli_2675) (pn:hypothetical 16) (gn:ygbb) (gtcfc:13.7:14.1) (ec:) (ygbb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2675 ECOLI_2675 Escherichia coli 562 10053993</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858076	11830	33986	2457	818
<u>Description</u>				
<p>5000693132 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2747 b2747 Escherichia coli 562 -11535546 7000687776 ygbp (de:hypothetical 25.7 kd protein in sure-cysc intergenic region) (db:swissprot) YGBP_ECOLI Q46893 ESCHERICHIA COLI 562 -11535546 7000687777 hypothetical protein b2747 (db:pir2.dat) G65055 G65055 Escherichia coli 562 -11535546 7500924040 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f236) (le:44085) (re:44795) (di:complement) ECU29579 U29579 g882640 Escherichia coli 562 -11535546 239321 ygbp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 248 of 400 of the completegenome.) (nt:f236; this 236 aa orf is 36 pct identical (7 gaps)) (le:6754) (re:7464) (di:complement) AE000358 AE000358 g1789104 Escherichia coli 562 -11535546 6500731688 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2747 b2747 Escherichia coli 562 -11535546</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858084	11831	33987	885	294

Description

5000693133 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2748 b2748 Escherichia coli 562 -11535547
 7500924042 ygbq (de:hypothetical 11.6 kd protein in sure-cysc intergenic region) (db:swissprot) YGBQ_ECOLI Q46894 ESCHERICHIA COLI 562 -11535547
 7000691736 hypothetical protein b2748 (cl:hypothetical protein hi0673) (db:pir2.dat) H65055 H65055 Escherichia coli 562 -11535547 239322
 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f103) (le:44814) (re:45125) (di:complement) ECU29579
 U29579 g882641 Escherichia coli 562 -11535547 7500924044 b2748
 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 248 of 400 of the completegenome.) (nt:f103; this 103 aa orf is 42 pct identical (0 gaps)) (le:7483) (re:7794) (di:complement) AE000358 AE000358 g1789105 Escherichia coli 562 -11535547 6500731689
 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2748 b2748 Escherichia coli 562 -11535547

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858098	11832	33988	648	215

Description

6500731690 ygbe:b2749 hypothetical protein in sure-cysc intergenic region:hypothetical 12.0 kd protein in sure-cysc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2749 b2749 Escherichia coli 562 -11535548 112268 ygbe (de:hypothetical 12.0 kd protein in sure-cysc intergenic region) (db:swissprot) YGBE_ECOLI P46141 ESCHERICHIA COLI 562 -11535548 7000687771 ygbe hypothetical protein in sure-cysc intergenic region (db:pir2.dat) A65056 A65056 Escherichia coli 562 -11535548 7500924020 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f107) (le:45317) (re:45640) (di:complement) ECU29579 U29579 g882642 Escherichia coli 562 -11535548 239323 ygbe putative cytochrome oxidase subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 248 of 400 of the completegenome.) (nt:f107; 100 pct identical to 66 aa of ygbe_ecoli) (le:7988) (re:8311) (di:complement) AE000358 AE000358 g1789106 Escherichia coli 562 -11535548 5000693134 (de:(ecoli_2678) (pn:hypothetical protein in sure-cysc intergenic region:fragment) (gn:ygbe) (gtcfc:13.7:14.1) (ec:) (ygbe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2678 ECOLI_2678 Escherichia coli 562 10123803

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858099	11833	33989	903	300

Description

6500731691 ygbf:b2754 hypothetical protein in iap 3 region:hypothetical 13.2 kd protein in iap-cysh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2754 b2754 Escherichia coli 562 -11535549 112269 ygbf (de:hypothetical 13.2 kd protein in iap-cysh intergenic region) (db:swissprot) YGBF_ECOLI P45956 ESCHERICHIA COLI 562 -11535549 7000687772 ygbf hypothetical protein in iap 3 region (db:pir2.dat) F65056 F65056 Escherichia coli 562 -11535549 7500924021 ygbf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 249 of 400 of the completegenome.) (nt:f94; 100 pct identical to ygbf_ecoli sw: p45956) (le:2144) (re:2494) (di:complement) AE000359 AE000359 g1789112 Escherichia coli 562 -11535549 5000693135 (de:(ecoli_2683) (pn:hypothetical 13) (gn:ygbf) (gtcfc:13.7:14.1) (ec:) (ygbf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2683 ECOLI_2683 Escherichia coli 562 10053997

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858115	11834	33990	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858120	11835	33991	615	204

Description

5000693136 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2755 b2755 Escherichia coli 562 -11535550 7000691737 hypothetical protein b2755 (db:pir2.dat) G65056 G65056 Escherichia coli 562 -11535550 7500960261 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f305) (le:51158) (re:52075) (di:complement) ECU29579 U29579 g882648 Escherichia coli 562 -11535550 239329 b2755 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 249 of 400 of the completegenome.) (nt:f305; this 305 aa orf is 29 pct identical (5 gaps)) (le:2430) (re:3347) (di:complement) AE000359 AE000359 g1789113 Escherichia coli 562 -11535550 6500731692 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2755 b2755 Escherichia coli 562 -11535550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858128	11836	33992	918	305

Description

5000693137 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2756 b2756 Escherichia coli 562 -11535551
7000691738 hypothetical protein b2756 (db:pir2.dat) H65056 H65056
Escherichia coli 562 -11535551 7500960262 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f199) (le:52091) (re:52690) (di:complement) ECU29579 U29579 g882649 Escherichia coli 562 -11535551 239330 b2756 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 249 of 400 of the completegenome.) (nt:f199; this 199 aa orf is 25 pct identical (14 gaps)) (le:3363) (re:3962) (di:complement) AE000359 AE000359 g1789114 Escherichia coli 562 -11535551 6500731693 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2756 b2756
Escherichia coli 562 -11535551

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858129	11837	33993	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858161	11838	33994	195	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858171	11839	33995	636	211

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858172	11840	33996	399	132

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858176	11841	33997	576	191

Description

5000693138 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2757 b2757 Escherichia coli 562 -11535552
7000691739 hypothetical protein b2757 (db:pir2.dat) A65057 A65057
Escherichia coli 562 -11535552 7500960263 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f226) (le:52677) (re:53357) (di:complement) ECU29579 U29579 g882650 Escherichia coli 562 -11535552 239331 b2757 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 249 of 400 of the completegenome.) (nt:f226; this 226 aa orf is 31 pct identical (8 gaps)) (le:3949) (re:4629) (di:complement) AE000359 AE000359 g1789115 Escherichia coli 562 -11535552 6500731694 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2757 b2757
Escherichia coli 562 -11535552

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858177	11842	33998	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858202	11843	33999	489	162

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858221	11844	34000	537	178

Description

GTC ORF with score 373 to: (sr:neurospora crassa (strain:acr-2(kh2)) dna, clone_lib:cosmid pdc10) (db:genpept-pln1) (de:neurospora crassa dna for thiamine-4, partial cds.) (nt:protein sequence is in conflict with the conceptual) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858222	11845	34001	195	64

Description

GTC ORF with score 163 to: (sr:neurospora crassa (strain:acr-2(kh2)) dna, clone_lib:cosmid pdc10) (db:genpept-pln1) (de:neurospora crassa dna for thiamine-4, partial cds.) (nt:protein sequence is in conflict with the conceptual) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858223	11846	34002	456	151

Description

GTC ORF with score 264 to: (sr:neurospora crassa (strain:acr-2(kh2)) dna, clone_lib:cosmid pdc10) (db:genpept-pln1) (de:neurospora crassa dna for thiamine-4, partial cds.) (nt:protein sequence is in conflict with the conceptual) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858262	11847	34003	384	127

Description

5000693139 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2758 b2758 Escherichia coli 562 -11535553
7000691740 hypothetical protein b2758 (db:pir2.dat) B65057 B65057
Escherichia coli 562 -11535553 7500960264 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f363) (le:53354) (re:54445) (di:complement) ECU29579 U29579 g882651 Escherichia coli 562 -11535553 239332 b2758 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 249 of 400 of the completegenome.) (nt:f363; this 363 aa orf is 27 pct identical (0 gaps)) (le:4626) (re:5717) (di:complement) AE000359 AE000359 g1789116 Escherichia coli 562 -11535553 6500731695 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2758 b2758 Escherichia coli 562 -11535553

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858263	11848	34004	900	299

Description

5000693140 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2759 b2759 Escherichia coli 562 -11535554
7000687784 ygck (de:hypothetical 18.7 kd protein in iap-cysh intergenic region) (db:swissprot) YGCK_ECOLI P76632 ESCHERICHIA COLI 562 -11535554
7000687785 hypothetical protein b2759 (db:pir2.dat) C65057 C65057
Escherichia coli 562 -11535554 7500924064 ygck orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 249 of 400 of the completegenome.) (nt:f160; this 160 aa orf is 23 pct identical (6 gaps)) (le:5730) (re:6212) (di:complement) AE000359 AE000359 g1789117 Escherichia coli 562 -11535554 6500731696 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2759 b2759 Escherichia coli 562 -11535554

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858283	11849	34005	996	331
<u>Description</u>				
5000693141 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2760 b2760 Escherichia coli 562 -11535555				
7000691741 hypothetical protein b2760 (db:pir2.dat) D65057 D65057				
Escherichia coli 562 -11535555 7500960265 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f502) (le:54932) (re:56440) (di:complement) ECU29579 U29579 g882653 Escherichia coli 562 -11535555 239334 b2760 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 249 of 400 of the completegenome.) (nt:f502; this 502 aa orf is 29 pct identical (6 gaps)) (le:6205) (re:7713) (di:complement) AE000359 AE000359 g1789118 Escherichia coli 562 -11535555 6500731697 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2760 b2760 Escherichia coli 562 -11535555				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858286	11850	34006	1269	422
<u>Description</u>				
6500731698 ygcb:b2761 hypothetical protein in cysh 3 region:hypothetical 100.5 kd protein in iap-cysh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2761 b2761 Escherichia coli 562 -11535556 112281 ygcb (de:hypothetical 100.5 kd protein in iap-cysh intergenic region) (db:swissprot) YGCB_ECOLI P38036 ESCHERICHIA COLI 562 -11535556 7000687780 ygcb hypothetical protein in cysh 3 region (db:pir2.dat) E65057 E65057 Escherichia coli 562 -11535556 7500924059 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:alternate gene name ygcb; orf_f888) (le:56855) (re:59521) (di:complement) ECU29579 U29579 g882654 Escherichia coli 562 -11535556 239335 ygcb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 249 of 400 of the completegenome.) (nt:f888; 99 pct identical to fragment ygcb_ecoli) (le:8128) (re:10794) (di:complement) AE000359 AE000359 g1789119 Escherichia coli 562 -11535556 5000693142 (de:(ecoli_2690) (pn:hypothetical protein in cysh:3"region:fragment) (gn:ygcb) (gtcfc:13.7:14.1) (ec:) (ygcb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2690 ECOLI_2690 Escherichia coli 562 10123812				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858292	11851	34007	1296	431

Description

5000693143 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2765 b2765 Escherichia coli 562 -11535557
5500685786 ygcm (ec:4.6.1.10) (de:(ptp synthase)) (db:swissprot) PTPS_ECOLI
Q46903 ESCHERICHIA COLI 562 -11535557 7000686228 hypothetical protein b2765 (cl:hypothetical protein b2765) (db:pir2.dat) A65058 A65058 Escherichia coli 562 -11535557 7500888994 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o121) (le:64516) (re:64881) (di:direct) ECU29579 U29579 g882658 Escherichia coli 562 -11535557 239339 ygcm putative 6-pyruvoyl tetrahydrobiopterin (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 250 of 400 of the completegenome.) (nt:o121; this 121 aa orf is 37 pct identical (6 gaps)) (le:4846) (re:5211) (di:direct) AE000360 AE000360 g1789124 Escherichia coli 562 -11535557 6500731699 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2765 b2765 Escherichia coli 562 -11535557

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858317	11852	34008	984	327

Description

5000693144 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2766 b2766 Escherichia coli 562 -11535558
7000687786 ygcN (ec:1.5.5.-) (de:(ec 1.5.5.-)) (db:swissprot) YGCN_ECOLI
Q46904 ESCHERICHIA COLI 562 -11535558 7000687787 fixc protein homolog b2766 (cl:fixc protein) (db:pir2.dat) B65058 B65058 Escherichia coli 562 -11535558 7500924065 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o433) (le:64929) (re:66230) (di:direct) ECU29579 U29579 g882659 Escherichia coli 562 -11535558 239340 ygcN orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 250 of 400 of the completegenome.) (nt:o433; this 433 aa orf is 41 pct identical (10 gaps)) (le:5259) (re:6560) (di:direct) AE000360 AE000360 g1789125 Escherichia coli 562 -11535558 6500731700 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2766 b2766 Escherichia coli 562 -11535558

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858318	11853	34009	843	280

Description

5000693145 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2767 b2767 Escherichia coli 562 -11535559
7000687788 ygco (de:ferredoxin like protein ygco) (db:swissprot) YGCO_ECOLI Q46905 ESCHERICHIA COLI 562 -11535559 7000687789 hypothetical protein b2767 (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) C65058 C65058 Escherichia coli 562 -11535559 7500924066 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o98) (le:66185) (re:66481) (di:direct) ECU29579 U29579 g882660 Escherichia coli 562 -11535559 239341 ygco orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 250 of 400 of the completegenome.) (nt:o98; this 98 aa orf is 48 pct identical (0 gaps)) (le:6515) (re:6811) (di:direct) AE000360 AE000360 g1789126 Escherichia coli 562 -11535559 6500731701 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2767 b2767 Escherichia coli 562 -11535559

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858327	11854	34010	2295	765

Description

5000693146 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2768 b2768 Escherichia coli 562 -11535560
7000687790 ygcp (de:hypothetical 20.8 kd protein in cysj-eno intergenic region) (db:swissprot) YGCP_ECOLI Q46906 ESCHERICHIA COLI 562 -11535560
7000687791 hypothetical protein b2768 (db:pir2.dat) D65058 D65058 Escherichia coli 562 -11535560 7500924067 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_o191) (le:66498) (re:67073) (di:direct) ECU29579 U29579 g882661 Escherichia coli 562 -11535560 239342 ygcp putative anti-terminator regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 250 of 400 of the completegenome.) (nt:o191; this 191 aa orf is 28 pct identical (0 gaps)) (le:6828) (re:7403) (di:direct) AE000360 AE000360 g1789127 Escherichia coli 562 -11535560 6500731702 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2768 b2768 Escherichia coli 562 -11535560

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858338	11855	34011	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858339	11856	34012	282	93

Description

5000693147 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2769 b2769 Escherichia coli 562 -11535561
5500686586 ygcq (de:putative electron transfer flavoprotein subunit ygcq) (db:swissprot) YGCQ_ECOLI Q46907 ESCHERICHIA COLI 562 -11535561 7000687792 hypothetical protein b2769 (db:pir2.dat) E65058 E65058 Escherichia coli 562 -11535561 7500924068 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f297) (le:67221) (re:68114) (di:complement) ECU29579 U29579 g882662 Escherichia coli 562 -11535561
239343 ygcq putative flavoprotein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 250 of 400 of the completegenome.) (nt:f297; this 297 aa orf is 35 pct identical (6 gaps)) (le:7551) (re:8444) (di:complement) AE000360 AE000360 g1789128 Escherichia coli 562 -11535561 6500731703 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2769 b2769 Escherichia coli 562 -11535561

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858340	11857	34013	780	259

Description

6500731704 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2770 b2770 Escherichia coli 562 -11535562
7000691742 hypothetical protein b2770 (db:pir2.dat) F65058 F65058 Escherichia coli 562 -11535562 7500960266 ygcq putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 250 of 400 of the completegenome.) (nt:f261; c-terminal differs from earlier version;) (le:8408) (re:9193) (di:complement) AE000360 AE000360 g2367158 Escherichia coli 562 -11535562

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858351	11858	34014	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858353	11859	34015	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858361	11860	34016	717	238

Description

5000693149 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2771 b2771 Escherichia coli 562 -11535563
7000691743 hypothetical protein b2771 (cl:yaau protein) (db:pir2.dat)
G65058 G65058 Escherichia coli 562 -11535563 7500960267 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f469) (le:68836) (re:70245) (di:complement) ECU29579 U29579 g882664 Escherichia coli 562 -11535563 239345 ygcs putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 250 of 400 of the completgenome.) (nt:f469; this 469 aa orf is 26 pct identical (26 gaps)) (le:9165) (re:10574) (di:complement) AE000360 AE000360 g1789130 Escherichia coli 562 -11535563
6500731705 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2771 b2771 Escherichia coli 562 -11535563

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858367	11861	34017	1137	378

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858369	11862	34018	813	271

Description

5000693150 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2772 b2772 Escherichia coli 562 -11535564
7000691744 hypothetical protein b2772 (db:pir2.dat) H65058 H65058 Escherichia coli 562 -11535564 7500960268 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:orf_f264) (le:70267) (re:71061) (di:complement) ECU29579 U29579 g882665 Escherichia coli 562 -11535564 239346 b2772 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 250 of 400 of the completgenome.) (nt:f264; this 264 aa orf is 28 pct identical (3 gaps)) (le:10596) (re:11390) (di:complement) AE000360 AE000360 g1789131 Escherichia coli 562 -11535564 6500731706 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2772 b2772 Escherichia coli 562 -11535564

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858370	11863	34019	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858380	11864	34020	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858382	11865	34021	933	310

Description

6500731707 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b2773 b2773 Escherichia coli
562 -11535565 5500686587 ygcu (de:hypothetical 23.3 kd protein in cysj-eno
intergenic region) (db:swissprot) YGCU_ECOLI Q46911 ESCHERICHIA COLI 562
-11535565 7000687793 hypothetical protein b2773 (db:pir2.dat) A65059 A65059
Escherichia coli 562 -11535565 7500924069 ygcu putative oxidoreductase
subunit (fn:putative enzyme; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 250 of 400 of the completegenome.)
(nt:f218; sequence change joins 2 orfs from) (le:11393) (re:12049)
(di:complement) AE000360 AE000360 g2367159 Escherichia coli 562 -11535565

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858404	11866	34022	1344	447

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858410	11867	34023	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858412	11868	34024	186	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858417	11869	34025	606	201

Description

GTC ORF with score 161 to: (db:genpept-bct2) (de:acinetobacter sp. adp1 vanillate demethylase region, vanillatedemethylase (vanb) and vanillate demethylase (vana) genes, completecds.) (nt:similar to salicylate hydroxylase; orf7) (le:10288) (re:11433) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858422	11870	34026	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858436	11871	34027	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858440	11872	34028	855	285

Description

5000693153 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2774 b2774 Escherichia coli 562 -11535566
7000689022 hypothetical protein b2774 (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) B65059 B65059 Escherichia coli 562 -11535566 7500953787 ygcw putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 251 of 400 of the completegenome.) (nt:f286; this 286 aa orf is 45 pct identical (5 gaps)) (le:65) (re:925) (di:complement) AE000361 AE000361 g1789135 Escherichia coli 562 -11535566 6500731708 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2774 b2774 Escherichia coli 562 -11535566

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858449	11873	34029	306	101

Description

6500731709 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b2775 b2775 Escherichia coli 562 -11535567 5500686659 yqce (de:hypothetical 46.8 kd protein in cysj-eno intergenic region) (db:swissprot) YQCE_ECOLI P77031 ESCHERICHIA COLI 562 -11535567 7000688335 hypothetical protein b2775 (db:pir2.dat) C65059 C65059 Escherichia coli 562 -11535567 225261 yihm (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:e.coli genomic dna, 62.4-62.5 min.) (nt:similar to (swissprot accession number p32135)) (le:672) (re:1949) (di:direct) D90893 D90893 g1805578 Escherichia coli 562 -11535567 7500952381 yqce putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 251 of 400 of the completegenome.) (nt:o425; sequence change joins 2 orfs from earlier) (le:1169) (re:2446) (di:direct) AE000361 AE000361 g2367161 Escherichia coli 562 -11535567

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858462	11874	34030	1416	471

Description

6500731710 ygcf:b2777 hypothetical protein:hypothetical 25.0 kd protein in cysj-eno intergenic region:f223 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2777 b2777 Escherichia coli 562 -11535568 112284 ygcf (de:hypothetical 25.0 kd protein in cysj-eno intergenic region (f223)) (db:swissprot) YGCF_ECOLI P55139 ESCHERICHIA COLI 562 -11535568 7000687782 hypothetical protein b2777 (db:pir2.dat) E65059 E65059 Escherichia coli 562 -11535568 7500924061 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 62 minute region.) (nt:orf_f223) (le:2612) (re:3283) (di:complement) ECU29580 U29580 g882671 Escherichia coli 562 -11535568 239351 ygcf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 251 of 400 of the completegenome.) (nt:f223; this 223 aa orf is 33 pct identical (4 gaps)) (le:5324) (re:5995) (di:complement) AE000361 AE000361 g1789139 Escherichia coli 562 -11535568 5000693157 (de:(ecoli_2708) (pn:hypothetical 25) (gtcfc:13.7:14.1) (ec:) (ygcf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2708 ECOLI_2708 Escherichia coli 562 10054012

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858464	11875	34031	210	69

Description

6500731711 ygcg:b2778 hypothetical protein: hypothetical 34.9 kd protein in cysj-eno intergenic region: o313 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2778 b2778 Escherichia coli 562 -11535569 112286 ygcg (de: hypothetical 34.9 kd protein in cysj-eno intergenic region (o313)) (db:swissprot) YGCG_ECOLI P55140 ESCHERICHIA COLI 562 -11535569 7000687783 hypothetical protein b2778 (db:pir2.dat) F65059 F65059 Escherichia coli 562 -11535569 7500924063 (db:genpept-bct1) (de: escherichia coli k-12 genome; approximately 62 minute region.) (nt:orf_o313) (le:3507) (re:4448) (di:direct) ECU29580 U29580 g882672 Escherichia coli 562 -11535569 239352 ygcg orf: hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de: escherichia coli k-12 mg1655 section 251 of 400 of the complete genome.) (nt:o313; this 313 aa orf is 45 pct identical (0 gaps)) (le:6219) (re:7160) (di:direct) AE000361 AE000361 g1789140 Escherichia coli 562 -11535569 5000693158 (de: (ecoli_2709) (pn: hypothetical 34) (gtcfc:13.7:14.1) (ec: (ygcg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2709 ECOLI_2709 Escherichia coli 562 10054014

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858494	11876	34032	711	236

Description

5000693164 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2789 b2789 Escherichia coli 562 -11535570 7500882850 ygcg (de: probable glucarate transporter) (db:swissprot) GUDT_ECOLI Q46916 ESCHERICHIA COLI 562 -11535570 7000691745 hypothetical protein b2789 (cl: hexuronate transporter) (db:pir2.dat) A65061 A65061 Escherichia coli 562 -11535570 239363 (db:genpept-bct1) (de: escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_f450) (le:2303) (re:3655) (di:complement) ECU29581 U29581 g882684 Escherichia coli 562 -11535570 7500882852 b2789 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de: escherichia coli k-12 mg1655 section 252 of 400 of the complete genome.) (nt:f450; this 450 aa orf is 65 pct identical (2 gaps)) (le:10998) (re:12350) (di:complement) AE000362 AE000362 g1789152 Escherichia coli 562 -11535570 6500731712 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2789 b2789 Escherichia coli 562 -11535570

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858502	11877	34033	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858503	11878	34034	237	78

Description

5000693165 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2790 b2790 Escherichia coli 562 -11535571
 7000689458 hypothetical protein b2790 (cl:mioc protein:flavodoxin homology) (db:pir2.dat) B65061 B65061 Escherichia coli 562 -11535571 7500955732 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:corresponds to hypothetical protein from e.) (le:4090) (re:4539) (di:complement) ECU29581 U29581 g882685 Escherichia coli 562 -11535571 239364 b2790 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 253 of 400 of the completegenome.) (nt:f149; similar to genbank accession) (le:248) (re:697) (di:complement) AE000363 AE000363 g1789154 Escherichia coli 562 -11535571
 6500731713 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2790 b2790 Escherichia coli 562 -11535571

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858505	11879	34035	843	280

Description

6500731714 yqcb:b2791 hypothetical protein:hypothetical 29.7 kd protein in bara-syd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2791 b2791 Escherichia coli 562 -11535572
 4000709985 yqcb (de:hypothetical 29.7 kd protein in bara-syd intergenic region) (db:swissprot) YQCB_ECOLI Q46918 ESCHERICHIA COLI 562 -11535572
 7000688330 hypothetical protein b2791 (db:pir2.dat) C65061 C65061 Escherichia coli 562 -11535572 7500952368 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:corresponds to hypothetical protein from e.) (le:4557) (re:5339) (di:complement) ECU29581 U29581 g882686 Escherichia coli 562 -11535572 239365 yqcb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 253 of 400 of the completegenome.) (nt:f260; similar to genbank accession) (le:715) (re:1497) (di:complement) AE000363 AE000363 g1789155 Escherichia coli 562 -11535572 5000693166 (de:(ecoli_2722) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2722 ECOLI_2722 Escherichia coli 562 10123835

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858510	11880	34036	420	139

Description

5000693167 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2792 b2792 Escherichia coli 562 -11535573
 7500952370 yqcc (de:hypothetical 12.8 kd protein in bara-syd intergenic region) (db:swissprot) YQCC_ECOLI Q46919 ESCHERICHIA COLI 562 -11535573
 7000691746 hypothetical protein b2792 (cl:hypothetical protein hi1436) (db:pir2.dat) D65061 D65061 Escherichia coli 562 -11535573 239366
 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:corresponds to hypothetical protein from e.) (le:5339) (re:5668) (di:complement) ECU29581 U29581 g882687 Escherichia coli 562 -11535573 7500952372 b2792 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 253 of 400 of the completegenome.) (nt:f109; similar to genbank accession) (le:1497) (re:1826) (di:complement) AE000363 AE000363 g1789156 Escherichia coli 562 -11535573
 6500731715 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2792 b2792 Escherichia coli 562 -11535573

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858512	11881	34037	510	169

Description

GTC ORF with score 148 to: (fn:unknown) (db:genpept-bct1) (de:bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.) (nt:similar to hypothetical proteins from b. subtilis) (le:150701) (re:151063) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858537	11882	34038	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858547	11883	34039	687	228

Description

6500731716 yqcd:b2794 hypothetical protein:hypothetical 32.6 kd protein in syd-sdac intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2794 b2794 Escherichia coli 562 -11535574
5500686658 yqcd (de:hypothetical 32.6 kd protein in syd-sdac intergenic region) (db:swissprot) YQCD_ECOLI Q46920 ESCHERICHIA COLI 562 -11535574
7000688333 hypothetical protein b2794 (cl:hypothetical protein ykvm) (db:pir2.dat) F65061 F65061 Escherichia coli 562 -11535574 7500952378 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_o282) (le:6903) (re:7751) (di:direct) ECU29581 U29581 g882689 Escherichia coli 562 -11535574 239368 yqcd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 253 of 400 of the completgenome.) (nt:o282; this 282 aa orf is 62 pct identical (3 gaps)) (le:3061) (re:3909) (di:direct) AE000363 AE000363 g1789158 Escherichia coli 562 -11535574 5000693169 (de:(ecoli_2725) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2725 ECOLI_2725 Escherichia coli 562 10123837

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858558	11884	34040	282	93

Description

GTC ORF with score 107 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0438.) (nt:unnamed protein product) (le:141) (re:1340) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858562	11885	34041	429	142

Description

GTC ORF with score 201 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0438.) (nt:unnamed protein product) (le:141) (re:1340) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858576	11886	34042	696	232

Description

6500731717 ygdh:b2795 hypothetical protein in sdac 5region:hypothetical 51.0 kd protein in bara-sdac intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2795 b2795 Escherichia coli 562 -11535575 112298 ygdh (de:hypothetical 51.0 kd protein in bara-sdac intergenic region) (db:swissprot) YGDH_ECOLI P37350 ESCHERICHIA COLI 562 -11535575 7000687794 ygdh hypothetical protein in sdac 5region (db:pir2.dat) G65061 G65061 Escherichia coli 562 -11535575 7500924083 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:ttg start; alternate gene name ygdh; orf_o455) (le:7863) (re:9227) (di:direct) ECU29581 U29581 g882690 Escherichia coli 562 -11535575 239369 ygdh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 253 of 400 of the completegenome.) (nt:o454; 98 pct identical to fragment ygdh_ecoli) (le:4021) (re:5385) (di:direct) AE000363 AE000363 g1789159 Escherichia coli 562 -11535575 5000693170 (de:(ecoli_2726) (pn:hypothetical protein in sdac 5"region:fragment) (gn:ygdh) (gtcfc:13.7:14.1) (ec:) (ygdh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2726 ECOLI_2726 Escherichia coli 562 10123838

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858586	11887	34043	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858592	11888	34044	549	182

Description

6500731718 ygde:b2806 hypothetical 41.9 kd protein in fucr-gcva intergenic region:orf3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2806 b2806 Escherichia coli 562 -11535576 239380 ygde (de:hypothetical 41.9 kd protein in fucr-gcva intergenic region (orf3)) (db:swissprot) YGDE_ECOLI P32066 ESCHERICHIA COLI 562 -11535576 163484 ygde hypothetical 41.9k protein fucr-gcva intergenic region (db:pir2.dat) I41067 I41067 Escherichia coli 562 -11535576 5000693173 (db:genpept-bct1) (de:e.coli gene for glycine cleavage activator protein and orf 2 and 3.) (nt:orf3) (le:1367) (re:2467) (di:direct) ECGCVA X73413 g312768 Escherichia coli 562 -11535576 7500924082 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:alternate name orf2 of x73413 and u01030; orf_f366) (le:21698) (re:22798) (di:complement) ECU29581 U29581 g882701 Escherichia coli 562 -11535576 232980 ygde orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the completegenome.) (nt:f366; 100 pct identical to ygde_ecoli sw: p32066;) (le:6212) (re:7312) (di:complement) AE000364 AE000364 g1789171 Escherichia coli 562 -11535576 112296 ygde (de:hypothetical 41.9 kd protein in fucr-gcva intergenic region (orf3)) (db:swissprot) YGDE_ECOLI P32066 ESCHERICHIA COLI 562 -11535576

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858597	11889	34045	348	115

Description

6500731719 ygdd:b2807 hypothetical 14.3 kd protein in fucr-gcva intergenic region:orf2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2807 b2807 Escherichia coli 562 -11535577 239381 ygdd (de:hypothetical 14.3 kd protein in fucr-gcva intergenic region (orf2)) (db:swissprot) YGDD_ECOLI P32065 ESCHERICHIA COLI 562 -11535577 163456 ygdd hypothetical 14.3k protein fucr-gcva intergenic region (db:pir2.dat) I41066 I41066 Escherichia coli 562 -11535577 5000693174 (db:genpept-bct1) (de:e.coli gene for glycine cleavage activator protein and orf 2 and 3.) (nt:orf2) (le:979) (re:1374) (di:direct) ECGCVA X73413 g312767 Escherichia coli 562 -11535577 7500924080 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:alternate name orf3 of x73413; orf_f131) (le:22791) (re:23186) (di:complement) ECU29581 U29581 g882702 Escherichia coli 562 -11535577 232979 ygdd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the completegenome.) (nt:f131; 100 pct identical to ygdd_ecoli sw: p32065;) (le:7305) (re:7700) (di:complement) AE000364 AE000364 g1789172 Escherichia coli 562 -11535577 112294 ygdd (de:hypothetical 14.3 kd protein in fucr-gcva intergenic region (orf2)) (db:swissprot) YGDD_ECOLI P32065 ESCHERICHIA COLI 562 -11535577

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858599	11890	34046	1350	449

Description

5000693175 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2809 b2809 Escherichia coli 562 -11535578
 7500924084 ygdi (de:precursor) (db:swissprot) YGDI_ECOLI Q46924 ESCHERICHIA COLI 562 -11535578 7000691747 hypothetical protein b2809 (db:pir2.dat) E65063 E65063 Escherichia coli 562 -11535578 239383 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_f76) (le:24473) (re:24703) (di:complement) ECU29581 U29581 g882704 Escherichia coli 562 -11535578 7500924086 b2809 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the completegenome.) (nt:f76; this 76 aa orf is 34 pct identical (1 gap)) (le:8987) (re:9217) (di:complement) AE000364 AE000364 g1789174 Escherichia coli 562 -11535578 6500731720 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2809 b2809 Escherichia coli 562 -11535578

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858615	11891	34047	501	166

Description

5000693176 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2810 b2810 Escherichia coli 562 -11535579 7000691748 hypothetical protein b2810 (cl:nifs protein) (db:pir2.dat) F65063 F65063 Escherichia coli 562 -11535579 7500960269 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_o401) (le:24892) (re:26097) (di:direct) ECU29581 U29581 g882705 Escherichia coli 562 -11535579 239384 b2810 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the completegenome.) (nt:o401; this 401 aa orf is 29 pct identical (36 gaps)) (le:9406) (re:10611) (di:direct) AE000364 AE000364 g1789175 Escherichia coli 562 -11535579 6500731721 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2810 b2810 Escherichia coli 562 -11535579

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858617	11892	34048	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858619	11893	34049	375	124

Description

6500731722 ygdK:b2811 hypothetical protein:hypothetical 15.9 kd protein in gcva-metz intergenic region:ol47 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2811 b2811 Escherichia coli 562 -11535580 118681 ygdK (de:hypothetical 15.9 kd protein in gcva-metz intergenic region (ol47)) (db:swissprot) YGDK_ECOLI Q46926 ESCHERICHIA COLI 562 -11535580 7000687795 hypothetical protein b2811 (cl:hypothetical protein b2811) (db:pir2.dat) G65063 G65063 Escherichia coli 562 -11535580 7500924088 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_ol47) (le:26097) (re:26540) (di:direct) ECU29581 U29581 g882706 Escherichia coli 562 -11535580 239385 ygdK orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the completegenome.) (nt:ol47; this 147 aa orf is 35 pct identical (0 gaps)) (le:10611) (re:11054) (di:direct) AE000364 AE000364 g1789176 Escherichia coli 562 -11535580 5000693177 (de:(ecoli_2742) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2742 ECOLI_2742 Escherichia coli 562 10061035

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858621	11894	34050	645	214

Description

6500731723 ygdL:b2812 hypothetical protein:hypothetical 28.6 kd protein in gcva-mlta intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2812 b2812 Escherichia coli 562 -11535581 4000708115 ygdL (de:hypothetical 28.6 kd protein in gcva-mlta intergenic region) (db:swissprot) YGDL_ECOLI Q46927 ESCHERICHIA COLI 562 -11535581 7000687796 hypothetical protein b2812 (db:pir2.dat) H65063 H65063 Escherichia coli 562 -11535581 7500924089 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_f268) (le:26591) (re:27397) (di:complement) ECU29581 U29581 g882707 Escherichia coli 562 -11535581 239386 ygdL putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the completegenome.) (nt:f268; this 268 aa orf is 31 pct identical (11 gaps)) (le:11105) (re:11911) (di:complement) AE000364 AE000364 g1789177 Escherichia coli 562 -11535581 5000693178 (de:(ecoli_2743) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2743 ECOLI_2743 Escherichia coli 562 10123844

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858623	11895	34051	444	147

Description

5000693179 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2817 b2817 Escherichia coli 562 -11535582
7000691749 hypothetical protein b2817 (db:pir2.dat) B65064 B65064
Escherichia coli 562 -11535582 239388 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_f447) (le:29312) (re:30655) (di:complement) ECU29581 U29581 g882709 Escherichia coli 562 -11535582 7500876802 b2817 putative amidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 255 of 400 of the completegenome.) (nt:f447; this 447 aa orf is 47 pct identical (4 gaps)) (le:1826) (re:3169) (di:complement) AE000365 AE000365 g1789180 Escherichia coli 562 -11535582 7500876800 amic (ec:3.5.1.28) (de:n-acetylmuramoyl-l-alanine amidase amic precursor,) (db:swissprot) AMIC_ECOLI Q46929 ESCHERICHIA COLI 562 -11535582 6500731724 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2817 b2817 Escherichia coli 562 -11535582

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858628	11896	34052	465	154

Description

6500731725 ygdb:b2824 hypothetical 13.5 kd protein in ppdc-ppdb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2824 b2824 Escherichia coli 562 -11535583 239395 ygdb (de:hypothetical 13.5 kd protein in ppdc-ppdb intergenic region) (db:swissprot) YGDB_ECOLI P08370 ESCHERICHIA COLI 562 -11535583 135186 ygdb hypothetical 13.5k protein ppdc-ppdb intergenic region (db:pir1.dat) (mp:61 min) QQEC13 D24137 Escherichia coli 562 -11535583 5000693182 (db:genpept-bct1) (de:e. coli recc gene and thya-recc intergenic region including urf1-3.) (nt:urf2 (aa 1-121)) (le:1856) (re:2221) (di:direct) ECRECC X03966 g42687 Escherichia coli 562 -11535583 7500924079 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:alternate name ygdb, urf2; orf of x03966; 2nd) (le:44304) (re:44669) (di:complement) ECU29581 U29581 g882716 Escherichia coli 562 -11535583 238032 ygdb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 256 of 400 of the completegenome.) (nt:f121; 100 pct identical to ygdb_ecoli sw: p08370;) (le:3807) (re:4172) (di:complement) AE000366 AE000366 g1789188 Escherichia coli 562 -11535583 112293 ygdb (de:hypothetical 13.5 kd protein in ppdc-ppdb intergenic region) (db:swissprot) YGDB_ECOLI P08370 ESCHERICHIA COLI 562 -11535583

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858650	11897	34053	366	121

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858651	11898	34054	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858653	11899	34055	237	78

Description

6500731726 ygdP:b2830 hypothetical protein: hypothetical 20.8 kd protein in ptph-muth intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2830 b2830 Escherichia coli 562 -11535584
4000708953 ygdP (de: hypothetical 20.8 kd protein in ptph-muth intergenic region) (db:swissprot) YGDP_ECOLI Q46930 ESCHERICHIA COLI 562 -11535584
7000687797 hypothetical protein b2830 (cl: invasion-associated protein: mutt domain homology) (db:pir2.dat) G65065 G65065 Escherichia coli 562 -11535584
7500924091 (db:genpept-bct1) (de: escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_f176) (le:50002) (re:50532) (di:complement) ECU29581 U29581 g882723 Escherichia coli 562 -11535584
239401 ygdP putative invasion protein (fn:putative factor; not classified) (db:genpept-bct2) (de: escherichia coli k-12 mg1655 section 256 of 400 of the complete genome.) (nt:f176; this 176 aa orf is 37 pct identical (16 gaps)) (le:9505) (re:10035) (di:complement) AE000366 AE000366 g1789194 Escherichia coli 562 -11535584 5000693186 (de:(ecoli_2758) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2758 ECOLI_2758 Escherichia coli 562 10123850

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858662	11900	34056	1125	374

Description

5000693187 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2832 b2832 Escherichia coli 562 -11535585
7500924093 ygdq (de:hypothetical 26.2 kd protein in muth-tas intergenic region) (db:swissprot) YGDQ_ECOLI Q46931 ESCHERICHIA COLI 562 -11535585
7000691750 hypothetical protein b2832 (cl:conserved hypothetical protein hi0056) (db:pir2.dat) A65066 A65066 Escherichia coli 562 -11535585 239403 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_o237) (le:51975) (re:52688) (di:direct) ECU29581 U29581 g882725 Escherichia coli 562 -11535585 7500924095 b2832 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 257 of 400 of the completgenome.) (nt:o237; this 237 aa orf is 61 pct identical (3 gaps)) (le:1131) (re:1844) (di:direct) AE000367 AE000367 g1789197 Escherichia coli 562 -11535585
6500731727 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2832 b2832 Escherichia coli 562 -11535585

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858663	11901	34057	231	77

Description

5000693188 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2833 b2833 Escherichia coli 562 -11535586
7500924098 ygdr (de:precursor) (db:swissprot) YGDR_ECOLI Q46932 ESCHERICHIA COLI 562 -11535586 7000691751 hypothetical protein b2833 (db:pir2.dat) B65066 B65066 Escherichia coli 562 -11535586 239404 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_o72) (le:52826) (re:53044) (di:direct) ECU29581 U29581 g882726 Escherichia coli 562 -11535586 7500924100 b2833 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 257 of 400 of the completgenome.) (nt:o72; this 72 aa orf is 30 pct identical (8 gaps)) (le:1982) (re:2200) (di:direct) AE000367 AE000367 g1789198 Escherichia coli 562 -11535586 6500731728 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2833 b2833 Escherichia coli 562 -11535586

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858673	11902	34058	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858679	11903	34059	1212	403

Description

5000693189 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2834 b2834 Escherichia coli 562 -11535587
7500892764 tas (de:tas protein) (db:swissprot) TAS_ECOLI Q46933 ESCHERICHIA
COLI 562 -11535587 7000691752 hypothetical protein b2834 (db:pir2.dat)
C65066 C65066 Escherichia coli 562 -11535587 239405 (db:genpept-bct1)
(de:escherichia coli k-12 genome; approximately 63 to 64 minutes.)
(nt:orf_o346) (le:53152) (re:54192) (di:direct) ECU29581 U29581 g882727
Escherichia coli 562 -11535587 5500687966 b2834 orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
257 of 400 of the completegenome.) (nt:o346; this 346 aa orf is 37 pct
identical (15 gaps)) (le:2308) (re:3348) (di:direct) AE000367 AE000367
g1789199 Escherichia coli 562 -11535587 7502852273 tas (db:genpept-bct2)
(de:escherichia coli tas gene.) (le:889) (re:1929) (di:complement) ECTAS
Y14609 g2342573 Escherichia coli 562 -11535587 7500892761 tas (de:tas
protein) (db:swissprot) TAS_ECOLI Q46933 ESCHERICHIA COLI 562 -11535587
6500731729 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b2834 b2834 Escherichia coli 562 -11535587

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858712	11904	34060	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858716	11905	34061	255	84

Description

6500731730 yged:b2835 hypothetical protein in muth-aas intergenic region:hypothetical 41.7 kd protein in muth-aas intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2835 b2835 Escherichia coli 562 -11535588 112307 yged (de:hypothetical 41.7 kd protein in muth-aas intergenic region) (db:swissprot) YGED_ECOLI P39196 ESCHERICHIA COLI 562 -11535588 7000687798 yged hypothetical protein in muth-aas intergenic region (db:pir2.dat) D65066 D65066 Escherichia coli 562 -11535588 7500924113 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_f397) (le:54224) (re:55417) (di:complement) ECU29581 U29581 g882728 Escherichia coli 562 -11535588 239406 yged putative resistance proteins (fn:orf; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 257 of 400 of the completegenome.) (nt:f397; 100 pct identical to yged_ecoli sw: p39196) (le:3380) (re:4573) (di:complement) AE000367 AE000367 g1789200 Escherichia coli 562 -11535588 5000693190 (de:(ecoli_2763) (pn:hypothetical 8) (gn:yged) (gtcfc:13.7:14.1) (ec:) (yged_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2763 ECOLI_2763 Escherichia coli 562 10123855

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858718	11906	34062	318	105

Description

6500731731 ygea:b2840 hypothetical 25.2 kd protein in lysr-arae intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2840 b2840 Escherichia coli 562 -11535589 112306 ygea (de:hypothetical 25.2 kd protein in lysr-arae intergenic region) (db:swissprot) YGEA_ECOLI P03813 ESCHERICHIA COLI 562 -11535589 135192 ygea hypothetical 25.2k lysr-arae intergenic region (db:pir1.dat) (mp:61 min) QQECK A04438 Escherichia coli 562 -11535589 234432 (sr:e.coli (strain jm2433) dna, clone pmm2(3,5)) (db:genpept-bct1) (de:e.coli arabinose-proton symporter (arae) gene, complete cds, and lysa activator protein (lysr) gene, 3' end.) (nt:orf x) (le:1981) (re:2673) (di:direct) ECOARAEA J03732 g145322 Escherichia coli 562 -11535589 239411 unknown protein (sr:escherichia coli (1): k-12 bmh71-18(lac-pro)-del/f' pro-laci-q-zml) (db:genpept-bct1) (de:e.coli galr, lysa, and lysr genes coding for galetk operon repressor protein (gal repressor), diaminopimelate decarboxylase and lysa activatory protein.) (nt:or... ECOGALLYYS J01614 g1128956 Escherichia coli 562 -11535589 7500924112 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:alternate name ygea; orfx of j03732; orf_f230) (le:61498) (re:62190) (di:complement) ECU29581 U29581 g882733 Escherichia coli 562 -11535589 233829 ygea putative resistance proteins (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 257 of 400 of the complete genome.) (nt:f230; 100 pct identical to ygea_ecoli sw: p03813;) (le:10654) (re:11346) (di:complement) AE000367 AE000367 g1789205 Escherichia coli 562 -11535589 5000693191 (de:(ecoli_2768) (pn:hypothetical 25) (gn:ygea) (gtcfc:13.7:14.1) (ec:) (ygea_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2768 ECOLI_2768 Escherichia coli 562 10054034

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858720	11907	34063	888	295

Description

5000693194 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2844 b2844 Escherichia coli 562 -11535590
5500686660 yqef (ec:2.3.1.9) (de:thiolase)) (db:swissprot) YQEF_ECOLI
Q46939 ESCHERICHIA COLI 562 -11535590 7000688350 hypothetical protein b2844 (cl:acetyl-coa acetyltransferase) (db:pir2.dat) E65067 E65067 Escherichia coli 562 -11535590 7500952397 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_f394) (le:65966) (re:67150) (di:complement) ECU29581 U29581 g882737 Escherichia coli 562 -11535590
239415 yqef putative acyltransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 258 of 400 of the completegenome.) (nt:f394; this 394 aa orf is 61 pct identical (1 gap)) (le:3742) (re:4926) (di:complement) AE000368 AE000368 g1789210 Escherichia coli 562 -11535590 6500731732 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2844 b2844 Escherichia coli 562 -11535590

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858721	11908	34064	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858727	11909	34065	867	288

Description

5000693195 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2845 b2845 Escherichia coli 562 -11535591
7000691753 hypothetical protein b2845 (cl:threonine-serine permease) (db:pir2.dat) F65067 F65067 Escherichia coli 562 -11535591 7500960270 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_o409) (le:67402) (re:68631) (di:direct) ECU29581 U29581 g882738 Escherichia coli 562 -11535591 239416 b2845 putative transporter protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 258 of 400 of the completegenome.) (nt:o409; this 409 aa orf is 39 pct identical (14 gaps)) (le:5178) (re:6407) (di:direct) AE000368 AE000368 g1789211 Escherichia coli 562 -11535591
6500731733 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2845 b2845 Escherichia coli 562 -11535591

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858730	11910	34066	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858735	11911	34067	504	167

Description

5000693196 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2846 b2846 Escherichia coli 562 -11535592
7000688353 yqeh (de:hypothetical 26.6 kd protein in kdui-lyss intergenic region) (db:swissprot) YQEH_ECOLI Q46941 ESCHERICHIA COLI 562 -11535592
7000688354 hypothetical protein b2846 (db:pir2.dat) G65067 G65067 Escherichia coli 562 -11535592 7500952400 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:ttg start; orf_o230) (le:69031) (re:69723) (di:direct) ECU29581 U29581 g882739 Escherichia coli 562 -11535592 239417 yqeh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 258 of 400 of the completegenome.) (nt:o230; this 230 aa orf is 30 pct identical (1 gap)) (le:6807) (re:7499) (di:direct) AE000368 AE000368 g1789212 Escherichia coli 562 -11535592 6500731734 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2846 b2846 Escherichia coli 562 -11535592

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858750	11912	34068	381	126

Description

5000693197 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2847 b2847 Escherichia coli 562 -11535593
7000688356 yqei (de:hypothetical 30.9 kd protein in kdui-lyss intergenic region) (db:swissprot) YQEI_ECOLI Q46942 ESCHERICHIA COLI 562 -11535593
7000688357 hypothetical protein b2847 (db:pir2.dat) H65067 H65067 Escherichia coli 562 -11535593 7500952402 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_o269) (le:70057) (re:70866) (di:direct) ECU29581 U29581 g882740 Escherichia coli 562 -11535593 239418 yqei putative sensory transducer (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 258 of 400 of the completegenome.) (nt:o269; this 269 aa orf is 24 pct identical (2 gaps)) (le:7833) (re:8642) (di:direct) AE000368 AE000368 g1789213 Escherichia coli 562 -11535593 6500731735 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2847 b2847 Escherichia coli 562 -11535593

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858751	11913	34069	573	190
<u>Description</u>				
5500686661 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2848 b2848 Escherichia coli 562 -11535594				
7000688359 hypothetical protein b2848 (db:pir2.dat) A65068 A65068 Escherichia coli 562 -11535594 7500960272 yqej orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 258 of 400 of the completegenome.) (nt:ol64; residues 1-94 are 100 pct identical to the) (le:8623) (re:9117) (di:direct) AE000368 AE000368 g2367166 Escherichia coli 562 -11535594 6500731736 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2848 b2848 Escherichia coli 562 -11535594				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858752	11914	34070	408	135
<u>Description</u>				
5500686662 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2849 b2849 Escherichia coli 562 -11535595				
7000688361 hypothetical protein b2849 (db:pir2.dat) B65068 B65068 Escherichia coli 562 -11535595 7500960274 yqek orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 258 of 400 of the completegenome.) (nt:fl45; 100 pct identical to gb: ecu83187 accession) (le:9266) (re:9703) (di:complement) AE000368 AE000368 g2367167 Escherichia coli 562 -11535595 6500731737 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2849 b2849 Escherichia coli 562 -11535595				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858756	11915	34071	867	288
<u>Description</u>				
6500731738 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2850 b2850 Escherichia coli 562 -11535596				
5500686589 ygef (de:hypothetical 16.9 kd protein in kdui-lyss intergenic region) (db:swissprot) YGEF_ECOLI Q46786 ESCHERICHIA COLI 562 -11535596				
7000687799 hypothetical protein b2850 (db:pir2.dat) C65068 C65068 Escherichia coli 562 -11535596 7500924114 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_ol48) (le:370) (re:816) (di:direct) ECU28375 U28375 g887801 Escherichia coli 562 -11535596 239064 ygef orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:ol48) (le:116) (re:562) (di:direct) AE000369 AE000369 g2367169 Escherichia coli 562 -11535596				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858757	11916	34072	348	115

Description

5000693198 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2851 b2851 Escherichia coli 562 -11535597
7000687800 ygeg (de:hypothetical 19.1 kd protein in kdui-lyss intergenic region) (db:swissprot) YGEG_ECOLI Q46787 ESCHERICHIA COLI 562 -11535597
7000687801 hypothetical protein b2851 (cl:ippi protein) (db:pir2.dat) D65068 D65068 Escherichia coli 562 -11535597 7500924115 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o163) (le:1084) (re:1575) (di:direct) ECU28375 U28375 g887802 Escherichia coli 562 -11535597 239065 ygeg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:o163; this 163 aa orf is 36 pct identical (1 gap)) (le:830) (re:1321) (di:direct) AE000369 AE000369 g1789215 Escherichia coli 562 -11535597 6500731739 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2851 b2851 Escherichia coli 562 -11535597

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858760	11917	34073	723	240

Description

5000693199 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2852 b2852 Escherichia coli 562 -11535598
7000687802 ygeh (de:hypothetical 52.8 kd protein in kdui-lyss intergenic region) (db:swissprot) YGEH_ECOLI P76639 ESCHERICHIA COLI 562 -11535598
7000687803 hypothetical protein b2852 (db:pir2.dat) E65068 E65068 Escherichia coli 562 -11535598 7500924116 ygeh putative invasion protein (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:o458; this 458 aa orf is 28 pct identical (6 gaps)) (le:1656) (re:3032) (di:direct) AE000369 AE000369 g1789216 Escherichia coli 562 -11535598 6500731740 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2852 b2852 Escherichia coli 562 -11535598

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858762	11918	34074	237	78

Description

5000693200 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2853 b2853 Escherichia coli 562 -11535599
7500924117 ygei (de:hypothetical 8.1 kd protein in kdai-pbl intergenic region) (db:swissprot) YGEI_ECOLI Q46789 ESCHERICHIA COLI 562 -11535599
7000691754 hypothetical protein b2853 (db:pir2.dat) F65068 F65068 Escherichia coli 562 -11535599 239067 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o72) (le:3454) (re:3672) (di:direct) ECU28375 U28375 g887804 Escherichia coli 562 -11535599
7500924119 b2853 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:o72; this 72 aa orf is 33 pct identical (1 gap)) (le:3200) (re:3418) (di:direct) AE000369 AE000369 g1789217 Escherichia coli 562 -11535599 6500731741 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2853 b2853 Escherichia coli 562 -11535599

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858767	11919	34075	405	134

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858773	11920	34076	327	108

Description

5000693201 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2854 b2854 Escherichia coli 562 -11535600
7000691755 hypothetical protein b2854 (db:pir2.dat) G65068 G65068 Escherichia coli 562 -11535600 7500960275 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o138) (le:3816) (re:4232) (di:direct) ECU28375 U28375 g887805 Escherichia coli 562 -11535600
239068 b2854 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:o138; this 138 aa orf is 39 pct identical (7 gaps)) (le:3561) (re:3977) (di:direct) AE000369 AE000369 g1789218 Escherichia coli 562 -11535600
6500731742 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2854 b2854 Escherichia coli 562 -11535600

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858777	11921	34077	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858787	11922	34078	942	313

Description

6500731743 ygek:b2855 hypothetical protein:hypothetical transcriptional regulator in kdui-lyss intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2855 b2855 Escherichia coli 562 -11535601 5500686590 ygek (de:hypothetical transcriptional regulator in kdui-lyss intergenic region) (db:swissprot) YGEK_ECOLI Q46791 ESCHERICHIA COLI 562 -11535601 7000687804 hypothetical protein b2855 (db:pir2.dat) H65068 H65068 Escherichia coli 562 -11535601 7500924121 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f148) (le:4277) (re:4723) (di:complement) ECU28375 U28375 g887806 Escherichia coli 562 -11535601 239069 ygek putative 2-component transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completgenome.) (nt:f148) (le:4022) (re:4468) (di:complement) AE000369 AE000369 g1789219 Escherichia coli 562 -11535601 5000693202 (de:(ecoli_2780) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2780 ECOLI_2780 Escherichia coli 562 10123866

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858798	11923	34079	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858816	11924	34080	303	100

Description

GTC ORF with score 106 to: (sr:neurospora crassa strain=74-or23-1va) (db:genpept-pln1) (de:neurospora crassa two-component histidine kinase (nik-1) gene, 5'region and partial cds.) (nt:two-component histidine kinase) (le:1619:2488:3404:3732) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858826	11925	34081	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858832	11926	34082	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858849	11927	34083	702	233

Description

5000693203 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2856 b2856 Escherichia coli 562 -11535602
7000691756 hypothetical protein b2856 (db:pir2.dat) A65069 A65069 Escherichia coli 562 -11535602 7500960276 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f51) (le:4754) (re:4909) (di:complement) ECU28375 U28375 g887807 Escherichia coli 562 -11535602 239070 b2856 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:f51; this 51 aa orf is 32 pct identical (3 gaps)) (le:4499) (re:4654) (di:complement) AE000369 AE000369 g1789220 Escherichia coli 562 -11535602 6500731744 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2856 b2856 Escherichia coli 562 -11535602

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858854	11928	34084	675	224

Description

5000693204 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2857 b2857 Escherichia coli 562 -11535603
7000691757 hypothetical protein b2857 (db:pir2.dat) B65069 B65069 Escherichia coli 562 -11535603 7500960277 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f143) (le:5131) (re:5562) (di:complement) ECU28375 U28375 g887808 Escherichia coli 562 -11535603 239071 b2857 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:f143; this 143 aa orf is 18 pct identical (0 gaps)) (le:4876) (re:5307) (di:complement) AE000369 AE000369 g1789221 Escherichia coli 562 -11535603 6500731745 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2857 b2857 Escherichia coli 562 -11535603

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858855	11929	34085	186	61

Description

5000693205 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2858 b2858 Escherichia coli 562 -11535604
7000691758 hypothetical protein b2858 (db:pir2.dat) C65069 C65069
Escherichia coli 562 -11535604 7500960278 b2858 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:f73; 27 pct identical to 70 residues) (le:5310) (re:5531) (di:complement) AE000369 AE000369 g1789222 Escherichia coli 562 -11535604 6500731746 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2858 b2858 Escherichia coli 562 -11535604

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858857	11930	34086	219	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858859	11931	34087	771	256

Description

GTC ORF with score 684 to: (sr:fission yeast) (db:genpept) (de:schizosaccharomyces pombe putative transcription factor fet5(fet5+) gene, complete cds.) (nt:putative atp/gtp binding protein) (le:163:874) (re:828:1038) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858866	11932	34088	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858886	11933	34089	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858890	11934	34090	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858892	11935	34091	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858894	11936	34092	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858901	11937	34093	1614	537

Description

5000693206 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2859 b2859 Escherichia coli 562 -11535605
7000691759 hypothetical protein b2859 (db:pir2.dat) D65069 D65069
Escherichia coli 562 -11535605 7500960279 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f141) (le:5779) (re:6204) (di:complement) ECU28375 U28375 g887810 Escherichia coli 562 -11535605 239073 b2859 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:f141) (le:5524) (re:5949) (di:complement) AE000369 AE000369 g1789223 Escherichia coli 562 -11535605 6500731747 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2859 b2859 Escherichia coli 562 -11535605

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858902	11938	34094	801	266

Description

5000693207 yi21_4:yi21_5:b2861 insertion element is2 hypothetical 13.4 kd protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2861 b2861 Escherichia coli 562 -11535606 7500937246

b0360:b1403:b1997:b2861:b3044:b4272 (de:insertion element is2 hypothetical 13.4 kd protein (orf1)) (db:swissprot) YI21_ECOLI P19776 ESCHERICHIA COLI 562 -11535606 7502852274 (db:genpept-bct1) (de:e. coli gale gene with inserted is2 element.) (nt:orf 1 (aa 1-121)) (le:940) (re:1305) (di:complement) ECGALI V00279 g41529 Escherichia coli 562 -11535606 232961 yi21_4 is2 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:f121; 100 pct identical to yi21_ecoli sw: p19776) (le:6797) (re:7162) (di:complement) AE000369 AE000369 g1789225 Escherichia coli 562 -11535606 7500937245 yi21_5 is2 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 276 of 400 of the completegenome.) (nt:o121; 100 pct identical to yi21_ecoli sw: p19776) (le:3725) (re:4090) (di:direct) AE000386 AE000386 g1789423 Escherichia coli 562 -11535606 7502852275 int unknown (db:genpept) (de:bacteriophage x transposon is2, complete sequence.) (nt:orf1) (le:554) (re:919) (di:direct) BXU82084 U82084 g4099031 bacteriophage SfX 10874 -11535606 113070

b0360:b1403:b1997:b2861:b3044:b4272 (de:insertion element is2 hypothetical 13.4 kd protein (orf1)) (db:swissprot) YI21_ECOLI P19776 ESCHERICHIA COLI 562 -11535606 6500731748 yi21_4:yi21_5 insertion element is2 hypothetical 13.4 kd protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2861 b2861 Escherichia coli 562 -11535606

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858903	11939	34095	765	255

Description

5000693208 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2862 b2862 Escherichia coli 562 -11535607
 7500924122 ygep (de:hypothetical 11.3 kd protein in pbl-lyss intergenic region) (db:swissprot) YGEP_ECOLI Q46796 ESCHERICHIA COLI 562 -11535607
 7000691760 hypothetical protein b2862 (db:pir2.dat) G65069 G65069 Escherichia coli 562 -11535607 239076 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f99) (le:7506) (re:7805) (di:complement) ECU28375 U28375 g887813 Escherichia coli 562 -11535607 7500924124 b2862 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:f99; this 99 aa orf is 32 pct identical (0 gaps)) (le:7251) (re:7550) (di:complement) AE000369 AE000369 g1789226 Escherichia coli 562 -11535607 6500731749 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2862 b2862 Escherichia coli 562 -11535607

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858920	11940	34096	405	134

Description

5000693209 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2863 b2863 Escherichia coli 562 -11535608
 7000691761 hypothetical protein b2863 (db:pir2.dat) H65069 H65069 Escherichia coli 562 -11535608 7500960280 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:was f268 and f157p before splice) (le:7851) (re:8687) (di:complement) ECU28375 U28375 g887814 Escherichia coli 562 -11535608 239077 b2863 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:f278; this 278 aa orf is 28 pct identical (1 gap)) (le:7596) (re:8432) (di:complement) AE000369 AE000369 g1789227 Escherichia coli 562 -11535608 6500731750 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2863 b2863 Escherichia coli 562 -11535608

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858927	11941	34097	405	134

Description

5000693210 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2865 b2865 Escherichia coli 562 -11535609
7000691762 hypothetical protein b2865 (cl:lipoprotein d) (db:pir2.dat)
A65070 A65070 Escherichia coli 562 -11535609 7500960281 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:uug start) (le:8953) (re:9732) (di:complement) ECU28375 U28375 g887815
Escherichia coli 562 -11535609 239078 b2865 putative lipoprotein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 259 of 400 of the completegenome.) (nt:f259; this 259 aa orf is 48 pct identical (22 gaps)) (le:8698) (re:9477) (di:complement) AE000369 AE000369 g1789228 Escherichia coli 562 -11535609
6500731751 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2865 b2865 Escherichia coli 562 -11535609

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858935	11942	34098	429	142

Description

5000693211 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2866 b2866 Escherichia coli 562 -11535610
7000691763 xanthine dehydrogenase homolog (db:pir2.dat) B65070 B65070 Escherichia coli 562 -11535610 7500960282 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:possible start 13 codons upstream, for o765) (le:10162) (re:12420) (di:direct) ECU28375 U28375 g887816 Escherichia coli 562 -11535610 239079 b2866 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 260 of 400 of the completegenome.) (nt:o752; this 752 aa orf is 26 pct identical (41 gaps)) (le:245) (re:2503) (di:direct) AE000370 AE000370 g1789230 Escherichia coli 562 -11535610 6500731752 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2866 b2866 Escherichia coli 562 -11535610

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858939	11943	34099	693	230

Description

5000693212 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2867 b2867 Escherichia coli 562 -11535611
7000687805 yget (de:hypothetical 31.6 kd protein in kdui-lyss intergenic region) (db:swissprot) YGET_ECOLI Q46800 ESCHERICHIA COLI 562 -11535611
7000687806 hypothetical protein b2867 (db:pir2.dat) C65070 C65070 Escherichia coli 562 -11535611 7500924126 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o292) (le:12431) (re:13309) (di:direct) ECU28375 U28375 g887817 Escherichia coli 562 -11535611 239080 yget putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 260 of 400 of the completegenome.) (nt:o292; this 292 aa orf is 32 pct identical (22 gaps)) (le:2514) (re:3392) (di:direct) AE000370 AE000370 g1789231 Escherichia coli 562 -11535611 6500731753 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2867 b2867 Escherichia coli 562 -11535611

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858942	11944	34100	663	220

Description

5000693213 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2868 b2868 Escherichia coli 562 -11535612
7000691764 hypothetical protein b2868 (cl:isoquinoline 1-oxidoreductase alpha chain) (db:pir2.dat) D65070 D65070 Escherichia coli 562 -11535612
7500960283 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o159) (le:13306) (re:13785) (di:direct) ECU28375 U28375 g887818 Escherichia coli 562 -11535612 239081 b2868 putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 260 of 400 of the completegenome.) (nt:o159; 44 pct identical to 147 aa of gb: ptc2cutac_2) (le:3389) (re:3868) (di:direct) AE000370 AE000370 g1789232 Escherichia coli 562 -11535612 6500731754 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2868 b2868 Escherichia coli 562 -11535612

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501858943	11945	34101	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858949	11946	34102	1899	632

Description

6500731755 ygev:b2869 hypothetical protein:hypothetical sigma-54-dependent transcriptional regulator in kdui-lyss intergenic region (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2869 b2869 Escherichia coli 562 -11535613 5500686591 ygev (de:intergenic region) (db:swissprot) YGEV_ECOLI Q46802 ESCHERICHIA COLI 562 -11535613 7000687807 hypothetical protein b2869 (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) E65070 E65070 Escherichia coli 562 -11535613 7500924127 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f592) (le:13825) (re:15603) (di:complement) ECU28375 U28375 g887819 Escherichia coli 562 -11535613 239082 ygev putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 260 of 400 of the completegenome.) (nt:f592; this 592 aa orf is 45 pct identical (14 gaps)) (le:3908) (re:5686) (di:complement) AE000370 AE000370 g1789233 Escherichia coli 562 -11535613 5000693214 (de:(ecoli_2793) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2793 ECOLI_2793 Escherichia coli 562 10123877

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858953	11947	34103	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858969	11948	34104	1434	478

Description

5000693215 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2870 b2870 Escherichia coli 562 -11535614
 7000687808 ygew (de:hypothetical 40.2 kd protein in kdui-lyss intergenic region) (db:swissprot) YGEW_ECOLI Q46803 ESCHERICHIA COLI 562 -11535614
 7000687809 hypothetical protein b2870 (cl:aspartate/ornithine carbamoyltransferase homology) (db:pir2.dat) F65070 F65070 Escherichia coli 562 -11535614 7500924128 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:uug start; possible frameshift at end?) (le:16150) (re:17241) (di:direct) ECU28375 U28375 g887820 Escherichia coli 562 -11535614 239083 ygew putative carbamoyl transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 260 of 400 of the completegenome.) (nt:o363; this 363 aa orf is 27 pct identical (43 gaps)) (le:6234) (re:7325) (di:direct) AE000370 AE000370 g1789234 Escherichia coli 562 -11535614 6500731756 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2870 b2870 Escherichia coli 562 -11535614

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858971	11949	34105	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501858990	11950	34106	516	171

Description

5000693216 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2871 b2871 Escherichia coli 562 -11535615
 5500685119 ygex (ec:4.3.1.15) (de:(diaminopropionatase) (alpha,beta-diaminopropionate ammonia-lyase)) (db:swissprot) DPAL_ECOLI Q46804 ESCHERICHIA COLI 562 -11535615 7000685087 hypothetical protein b2871 (db:pir2.dat) G65070 G65070 Escherichia coli 562 -11535615 7500880560 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o398) (le:17325) (re:18521) (di:direct) ECU28375 U28375 g887821 Escherichia coli 562 -11535615 239084 ygex putative dehydratase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 260 of 400 of the completegenome.) (nt:o398; this 398 aa orf is 27 pct identical (19 gaps)) (le:7409) (re:8605) (di:direct) AE000370 AE000370 g1789235 Escherichia coli 562 -11535615 6500731757 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2871 b2871 Escherichia coli 562 -11535615

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859007	11951	34107	183	60
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859024	11952	34108	189	62
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859032	11953	34109	1290	429
<u>Description</u>				

GTC ORF with score 222 to: (or:Homo sapiens) (sr:human salivary) (db:genpept-pri1) (de:prb11=prb1 large length copy {exon 3} (human, salivary, genomicmutant, 1107 nt).) (nt:basic proline rich proteins (ps, pmf, pms, and pe)) (le:13) (re:1089) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859033	11954	34110	654	217
<u>Description</u>				

6500731758 ygey:b2872 hypothetical protein:hypothetical 44.8 kd protein in kdui-lyss intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2872 b2872 Escherichia coli 562 -11535616 5500686592 ygey (de:hypothetical 44.8 kd protein in kdui-lyss intergenic region) (db:swissprot) YGEY_ECOLI Q46805 ESCHERICHIA COLI 562 -11535616 7000687810 hypothetical protein b2872 (db:pir2.dat) H65070 H65070 Escherichia coli 562 -11535616 7500924129 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:possible frameshift at end to join to next orf?) (le:18579) (re:19790) (di:direct) ECU28375 U28375 g887822 Escherichia coli 562 -11535616 239085 ygey putative deacetylase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 260 of 400 of the complete genome.) (nt:o403; this 403 aa orf is 30 pct identical (44 gaps)) (le:8663) (re:9874) (di:direct) AE000370 AE000370 gl789236 Escherichia coli 562 -11535616 5000693217 (de:(ecoli_2796) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2796 ECOLI_2796 Escherichia coli 562 10123880

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859055	11955	34111	390	130

Description

5000693218 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2873 b2873 Escherichia coli 562 -11535617
 7500924130 ygez (de:hypothetical 51.5 kd protein in pbl-lyss intergenic region) (db:swissprot) YGEZ_ECOLI Q46806 ESCHERICHIA COLI 562 -11535617
 7000691765 hypothetical protein b2873 (cl:allantoinase:bacillus dihydroorotase homology) (db:pir2.dat) A65071 A65071 Escherichia coli 562 -11535617 239086 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:uug start) (le:19831) (re:21228) (di:direct) ECU28375 U28375 g887823 Escherichia coli 562 -11535617
 7500924132 b2873 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 260 of 400 of the completegenome.) (nt:o465; this 465 aa orf is 36 pct identical (12 gaps)) (le:9915) (re:11312) (di:direct) AE000370 AE000370 g1789237 Escherichia coli 562 -11535617 6500731759 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2873 b2873 Escherichia coli 562 -11535617

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859062	11956	34112	1128	375

Description

6500731760 ygea:b2874 hypothetical protein:carbamate kinase-like protein 1 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2874 b2874 Escherichia coli 562 -11535618 117484 ygea (de:carbamate kinase-like protein 1) (db:swissprot) ARCL_ECOLI Q46807 ESCHERICHIA COLI 562 -11535618
 7000684606 hypothetical protein b2874 (cl:carbamate kinase) (db:pir2.dat) B65071 B65071 Escherichia coli 562 -11535618 7500877081 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o310) (le:21276) (re:22208) (di:direct) ECU28375 U28375 g887824 Escherichia coli 562 -11535618 239087 ygea putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 260 of 400 of the completegenome.) (nt:o310; this 310 aa orf is 45 pct identical (21 gaps)) (le:11360) (re:12292) (di:direct) AE000370 AE000370 g1789238 Escherichia coli 562 -11535618 5000693219 (de:(ecoli_2798) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2798 ECOLI_2798 Escherichia coli 562 10059308

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859069	11957	34113	333	110
<u>Description</u>				
5000693220 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2875 b2875 Escherichia coli 562 -11535619				
7000691766 hypothetical protein b2875 (db:pir2.dat) C65071 C65071 Escherichia coli 562 -11535619 7500960284 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f541) (le:22429) (re:24054) (di:complement) ECU28375 U28375 g887825 Escherichia coli 562 -11535619 239088 b2875 putative synthases (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 261 of 400 of the completegenome.) (nt:f541; this 541 aa orf is 28 pct identical (7 gaps)) (le:141) (re:1766) (di:complement) AE000371 AE000371 g1789240 Escherichia coli 562 -11535619 6500731761 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2875 b2875 Escherichia coli 562 -11535619				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859073	11958	34114	570	189
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859077	11959	34115	189	62
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859085	11960	34116	345	114
<u>Description</u>				
5000693221 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2876 b2876 Escherichia coli 562 -11535620				
7000691767 hypothetical protein b2876 (db:pir2.dat) D65071 D65071 Escherichia coli 562 -11535620 7500960285 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:gug start) (le:24102) (re:24809) (di:complement) ECU28375 U28375 g887826 Escherichia coli 562 -11535620 239089 b2876 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 261 of 400 of the completegenome.) (nt:f235; this 235 aa orf is 24 pct identical (6 gaps)) (le:1814) (re:2521) (di:complement) AE000371 AE000371 g1789241 Escherichia coli 562 -11535620 6500731762 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2876 b2876 Escherichia coli 562 -11535620				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859091	11961	34117	264	87
<u>Description</u>				
5000693222 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2877 b2877 Escherichia coli 562 -11535621				
7000687816 ygfj (de:hypothetical 21.5 kd protein in kdui-lyss intergenic region) (db:swissprot) YGFJ_ECOLI Q46810 ESCHERICHIA COLI 562 -11535621				
7000687817 hypothetical protein b2877 (db:pir2.dat) E65071 E65071 Escherichia coli 562 -11535621 7500924156 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o192) (le:24975) (re:25553) (di:direct) ECU28375 U28375 g887827 Escherichia coli 562 -11535621 239090 ygfj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 261 of 400 of the completegenome.) (nt:o192; this 192 aa orf is 22 pct identical (12 gaps)) (le:2687) (re:3265) (di:direct) AE000371 AE000371 g1789242 Escherichia coli 562 -11535621 6500731763 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2877 b2877 Escherichia coli 562 -11535621				
<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859092	11962	34118	594	197
<u>Description</u>				
5000693223 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2878 b2878 Escherichia coli 562 -11535622				
7000691768 hypothetical protein b2878 (db:pir2.dat) F65071 F65071 Escherichia coli 562 -11535622 7500960286 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:was o492p and o826p before splice) (le:25875) (re:28973) (di:direct) ECU28375 U28375 g887828 Escherichia coli 562 -11535622 239091 b2878 putative oxidoreductase:fe-s subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 261 of 400 of the completegenome.) (nt:o1032; this 1032 aa orf is 35 pct identical (36) (le:3587) (re:6685) (di:direct) AE000371 AE000371 g1789243 Escherichia coli 562 -11535622 6500731764 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2878 b2878 Escherichia coli 562 -11535622				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501859093	11963	34119	246	81

Description

5000693224 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2879 b2879 Escherichia coli 562 -11535623

7000691769 hypothetical protein b2879 (db:pir2.dat) G65071 G65071 Escherichia coli 562 -11535623 7500960287 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:d21141 uses 2nd start; frame determined by lac) (le:28910) (re:30304) (di:direct) ECU28375 U28375 g887829 Escherichia coli 562 -11535623 239092 b2879 putative proteoglycan (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 261 of 400 of the completegenome.) (nt:o464; this 464 aa orf is 25 pct identical (12 gaps)) (le:6622) (re:8016) (di:direct) AE000371 AE000371 g1789244 Escherichia coli 562 -11535623

6500731765 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2879 b2879 Escherichia coli 562 -11535623

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501859095	11964	34120	450	149

Description

5000693225 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2880 b2880 Escherichia coli 562 -11535624

7500924157 ygfm (de:hypothetical 28.6 kd protein in pbl-lyss intergenic region) (db:swissprot) YGFM_ECOLI Q46813 ESCHERICHIA COLI 562 -11535624

7000691770 hypothetical protein b2880 (db:pir2.dat) H65071 H65071 Escherichia coli 562 -11535624 239093 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o259) (le:30355) (re:31134) (di:direct) ECU28375 U28375 g887830 Escherichia coli 562 -11535624 7500924159 b2880 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 261 of 400 of the completegenome.) (nt:o259; this 259 aa orf is 39 pct identical (4 gaps)) (le:8067) (re:8846) (di:direct) AE000371 AE000371 g1789245 Escherichia coli 562 -11535624 6500731766 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2880 b2880 Escherichia coli 562 -11535624

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859100	11965	34121	297	98
<u>Description</u>				
5000693226 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2881 b2881 Escherichia coli 562 -11535625				
7000691771 hypothetical protein b2881 (db:pir2.dat) A65072 A65072 Escherichia coli 562 -11535625 7500960288 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o956) (le:31131) (re:34001) (di:direct) ECU28375 U28375 g887831 Escherichia coli 562 -11535625 239094 b2881 putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 261 of 400 of the completegenome.) (nt:o956; this 956 aa orf is 24 pct identical (26 gaps)) (le:8843) (re:11713) (di:direct) AE000371 AE000371 g1789246 Escherichia coli 562 -11535625 6500731767 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2881 b2881 Escherichia coli 562 -11535625				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859104	11966	34122	579	192
<u>Description</u>				
6500731768 ygfo:b2882 hypothetical protein: hypothetical 51.4 kd protein in kdai-lyss intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2882 b2882 Escherichia coli 562 -11535626				
5500686593 ygfo (de: hypothetical 51.4 kd protein in kdai-lyss intergenic region) (db:swissprot) YGFO_ECOLI Q46815 ESCHERICHIA COLI 562 -11535626				
7000687818 hypothetical protein b2882 (cl: hypothetical protein b2882) (db:pir2.dat) B65072 B65072 Escherichia coli 562 -11535626 7500924161 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o485) (le:34109) (re:35566) (di:direct) ECU28375 U28375 g887832 Escherichia coli 562 -11535626 239095 ygfo putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 262 of 400 of the completegenome.) (nt:o485; this 485 aa orf is 44 pct identical (2 gaps)) (le:84) (re:1541) (di:direct) AE000372 AE000372 g1789248 Escherichia coli 562 -11535626				
5000693227 (de:(ecoli_2806) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2806 ECOLI_2806 Escherichia coli 562 10123889				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859106	11967	34123	369	122

Description

5000693228 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2883 b2883 Escherichia coli 562 -11535627
7000687819 ygfp (de:hypothetical 50.2 kd protein in kdui-lyss intergenic region) (db:swissprot) YGFP_ECOLI P76641 ESCHERICHIA COLI 562 -11535627
7000687820 hypothetical protein b2883 (db:pir2.dat) C65072 C65072 Escherichia coli 562 -11535627 7500924162 ygfp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 262 of 400 of the completegenome.) (nt:o439; this 439 aa orf is 22 pct identical (34 gaps)) (le:1556) (re:2875) (di:direct) AE000372 AE000372 g1789249 Escherichia coli 562 -11535627 6500731769 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2883 b2883 Escherichia coli 562 -11535627

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859113	11968	34124	387	129

Description

6500731770 ygfq:b2884 hypothetical protein:hypothetical 19.7 kd protein in kdui-lyss intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2884 b2884 Escherichia coli 562 -11535628
5500686594 ygfq (de:hypothetical 19.7 kd protein in kdui-lyss intergenic region) (db:swissprot) YGFQ_ECOLI Q46817 ESCHERICHIA COLI 562 -11535628
7000687821 hypothetical protein b2884 (db:pir2.dat) D65072 D65072 Escherichia coli 562 -11535628 7500924163 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o189) (le:36936) (re:37505) (di:direct) ECU28375 U28375 g887834 Escherichia coli 562 -11535628 239097 ygfq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 262 of 400 of the completegenome.) (nt:o189; this 189 aa orf is 83 pct identical (1 gap)) (le:2911) (re:3480) (di:direct) AE000372 AE000372 g1789250 Escherichia coli 562 -11535628 5000693229 (de:(ecoli_2808) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2808 ECOLI_2808 Escherichia coli 562 10123891

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859114	11969	34125	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859126	11970	34126	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859140	11971	34127	1794	597

Description

6500731771 ygfr:b2885 hypothetical protein:hypothetical 28.4 kd protein in kdui-lyss intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2885 b2885 Escherichia coli 562 -11535629 5500686595 ygfr (de:hypothetical 28.4 kd protein in kdui-lyss intergenic region) (db:swissprot) YGFR_ECOLI Q46818 ESCHERICHIA COLI 562 -11535629 7000687822 hypothetical protein b2885 (db:pir2.dat) E65072 E65072 Escherichia coli 562 -11535629 7500924164 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o276) (le:37472) (re:38302) (di:direct) ECU28375 U28375 g887835 Escherichia coli 562 -11535629 239098 ygfr putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 262 of 400 of the completegenome.) (nt:o276; this 276 aa orf is 81 pct identical (0 gaps)) (le:3447) (re:4277) (di:direct) AE000372 AE000372 g1789251 Escherichia coli 562 -11535629 5000693230 (de:(ecoli_2809) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2809 ECOLI_2809 Escherichia coli 562 10123892

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859152	11972	34128	351	116

Description

GTC ORF with score 223 to: (fn:converts chickpea phytoalexin, maackiain, to) (sr:nectria haematococca strain=156-30-6) (db:genpept-pln2) (de:nectria haematococca maackiain detoxification (mak1) gene, completecds.) (nt:predicted flavin-containing ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859159	11973	34129	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859165	11974	34130	588	195

Description

5000693231 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2886 b2886 Escherichia coli 562 -11535630
7000687823 ygfs (de:putative electron transport protein ygfs) (db:swissprot) YGFS_ECOLI Q46819 ESCHERICHIA COLI 562 -11535630 7000687824
hypothetical protein b2886 (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) F65072 F65072 Escherichia coli 562 -11535630 7500924165
(db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f163) (le:38338) (re:38829) (di:complement) ECU28375
U28375 g887836 Escherichia coli 562 -11535630 239099 ygfs putative oxidoreductase:fe-s subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 262 of 400 of the completegenome.) (nt:f163; residues 38-98 are 47 pct identical) (le:4313) (re:4804) (di:complement) AE000372 AE000372 g1789252 Escherichia coli 562 -11535630 6500731772 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2886 b2886 Escherichia coli 562 -11535630

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859208	11975	34131	1557	518

Description

6500731773 ygft:b2887 hypothetical protein:hypothetical 69.7 kd protein in kdui-lyss intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2887 b2887 Escherichia coli 562 -11535631
7000687825 hypothetical protein b2887 (db:pir2.dat) G65072 G65072 Escherichia coli 562 -11535631 7500924166 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f644) (le:38826) (re:40760) (di:complement) ECU28375 U28375 g887837 Escherichia coli 562 -11535631 239100 ygft putative oxidoreductase:fe-s subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 262 of 400 of the completegenome.) (nt:f644; this 644 aa orf is 53 pct identical (22 gaps)) (le:4801) (re:6735) (di:complement) AE000372 AE000372 g1789253 Escherichia coli 562 -11535631 5500686596 ygft (de:hypothetical 69.7 kd protein in kdui-lyss intergenic region) (db:swissprot) YGFT_ECOLI Q46820 ESCHERICHIA COLI 562 -11535631 5000693232 (de:(ecoli_2811) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2811 ECOLI_2811 Escherichia coli 562 10123894

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859240	11976	34132	285	94

Description

GTC ORF with score 141 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859243	11977	34133	273	90

Description

GTC ORF with score 134 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completecds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859258	11978	34134	555	185

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859261	11979	34135	1041	346

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859274	11980	34136	195	64

Description

6500731774 ygfu:b2888 hypothetical protein:hypothetical 54.4 kd protein in kdui-lyss intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2888 b2888 Escherichia coli 562 -11535632
5500686597 ygfu (de:hypothetical 54.4 kd protein in kdui-lyss intergenic region) (db:swissprot) YGFU_ECOLI_Q46821 ESCHERICHIA COLI 562 -11535632
7000687826 hypothetical protein b2888 (db:pir2.dat) H65072 H65072 Escherichia coli 562 -11535632 7500924167 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o505) (le:41112) (re:42629) (di:direct) ECU28375 U28375 g887838 Escherichia coli 562 -11535632 239101 ygfu putative permease (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 262 of 400 of the completegenome.) (nt:o505; this 505 aa orf is 41 pct identical (4 gaps)) (le:7087) (re:8604) (di:direct) AE000372 AE000372 g1789254 Escherichia coli 562 -11535632 5000693233 (de:(ecoli_2812) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2812 ECOLI_2812 Escherichia coli 562 10123895

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859280	11981	34137	1368	455

Description

5000693234 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2889 b2889 Escherichia coli 562 -11535633
7000691772 hypothetical protein b2889 (db:pir2.dat) A65073 A65073 Escherichia coli 562 -11535633 7500960289 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o182) (le:42879) (re:43427) (di:direct) ECU28375 U28375 g887839 Escherichia coli 562 -11535633 239102 b2889 putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 262 of 400 of the completegenome.) (nt:o182; this 182 aa orf is 34 pct identical (8 gaps)) (le:8854) (re:9402) (di:direct) AE000372 AE000372 g1789255 Escherichia coli 562 -11535633 6500731775 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2889 b2889 Escherichia coli 562 -11535633

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859282	11982	34138	699	232

Description

5000693236 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2896 b2896 Escherichia coli 562 -11535634
7500924168 ygfx (de:hypothetical 16.1 kd protein in fldb-bgla intergenic region) (db:swissprot) YGFX_ECOLI Q46824 ESCHERICHIA COLI 562 -11535634
7000691773 hypothetical protein b2896 (db:pir2.dat) H65073 H65073 Escherichia coli 562 -11535634 239109 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:gtg start) (le:50230) (re:50637) (di:complement) ECU28375 U28375 g887846 Escherichia coli 562 -11535634 7500924170 b2896 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.) (nt:f135; this 135 aa orf is 37 pct identical (3 gaps)) (le:4119) (re:4526) (di:complement) AE000373 AE000373 g1789263 Escherichia coli 562 -11535634 6500731776 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2896 b2896 Escherichia coli 562 -11535634

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859297	11983	34139	717	238

Description

6500731777 ygfy:b2897 hypothetical protein:hypothetical 10.5 kd protein in fldb-gcvp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2897 b2897 Escherichia coli 562 -11535635
1500686278 ygfy (de:hypothetical 10.5 kd protein in fldb-bgla intergenic region) (db:swissprot) YGFY_ECOLI Q46825 ESCHERICHIA COLI 562 -11535635
7000687827 hypothetical protein b2897 (db:pir2.dat) A65074 A65074 Escherichia coli 562 -11535635 7500924172 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f88) (le:50618) (re:50884) (di:complement) ECU28375 U28375 g887847 Escherichia coli 562 -11535635 239110 ygfy orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.) (nt:f88; this 88 aa orf is 54 pct identical (0 gaps)) (le:4507) (re:4773) (di:complement) AE000373 AE000373 g1789264 Escherichia coli 562 -11535635 5000693237 (de:(ecoli_2821) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2821 ECOLI_2821 Escherichia coli 562 10061036

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859313	11984	34140	453	150

Description

6500731778 ygfz:b2898 hypothetical protein:unknown protein from 2d-page:spot pr51 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2898 b2898 Escherichia coli 562 -11535636 7000691774 hypothetical protein b2898 (db:pir2.dat) B65074 B65074 Escherichia coli 562 -11535636 7500960290 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o326) (le:51127) (re:52107) (di:direct) ECU28375 U28375 g887848 Escherichia coli 562 -11535636 239111 ygfz orf: hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.) (nt:o326; this 326 aa orf is 38 pct identical (33 gaps)) (le:5016) (re:5996) (di:direct) AE000373 AE000373 g1789265 Escherichia coli 562 -11535636 5000693238 (de:(ecoli_2822) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2822 ECOLI_2822 Escherichia coli 562 10123902

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859317	11985	34141	204	67

Description

5000693239 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2899 b2899 Escherichia coli 562 -11535637 7000691775 hypothetical protein b2899 (cl:hemolysin iii yplq) (db:pir2.dat) C65074 C65074 Escherichia coli 562 -11535637 7500960291 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f219) (le:52303) (re:52962) (di:complement) ECU28375 U28375 g887849 Escherichia coli 562 -11535637 239112 b2899 putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.) (nt:f219; this 219 aa orf is 25 pct identical (14 gaps)) (le:6192) (re:6851) (di:complement) AE000373 AE000373 g1789266 Escherichia coli 562 -11535637 6500731779 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2899 b2899 Escherichia coli 562 -11535637

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859318	11986	34142	285	94

Description

6500731780 yqfb:b2900 hypothetical protein:hypothetical 11.9 kd protein in fldb-bgla intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2900 b2900 Escherichia coli 562 -11535638 1500686279 yqfb (de:hypothetical 11.9 kd protein in fldb-bgla intergenic region) (db:swissprot) YQFB_ECOLI Q46828 ESCHERICHIA COLI 562 -11535638 7000688372 hypothetical protein b2900 (db:pir2.dat) D65074 D65074 Escherichia coli 562 -11535638 7500952417 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_f103) (le:53126) (re:53437) (di:complement) ECU28375 U28375 g887850 Escherichia coli 562 -11535638 239113 yqfb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.) (nt:f103; this 103 aa orf is 69 pct identical (0 gaps)) (le:7015) (re:7326) (di:complement) AE000373 AE000373 g1789267 Escherichia coli 562 -11535638 5000693240 (de:(ecoli_2824) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2824 ECOLI_2824 Escherichia coli 562 10061037

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859322	11987	34143	426	142

Description

6500731781 ygff:b2902 hypothetical oxidoreductase:hypothetical oxidoreductase in bgla-gcvp intergenic region (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2902 b2902 Escherichia coli 562 -11535639 112323 ygff (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YGFF_ECOLI P52037 ESCHERICHIA COLI 562 -11535639 7000687813 ygff hypothetical oxidoreductase (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) F65074 F65074 Escherichia coli 562 -11535639 7500924153 ygff putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.) (nt:f247; 100 pct identical to fragment ygff_ecoli) (le:8861) (re:9604) (di:complement) AE000373 AE000373 g2367175 Escherichia coli 562 -11535639

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859325	11988	34144	327	108

Description

6500731782 ygfb:b2909 hypothetical 21.5 kd protein in pepp-ssr intergenic region:orf194:f194 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2909 b2909 Escherichia coli 562 -11535640 112318 ygfb (de:(f194)) (db:swissprot) YGFB_ECOLI P25533 ESCHERICHIA COLI 562 -11535640 163254 ygfb hypothetical 21.5k protein pepp-ssr intergenic region:orf 194 protein (db:pir2.dat) (mp:63 min) A47020 A47020 Escherichia coli 562 -11535640 239123 orf194 orf194 protein (sr:escherichia coli (strain:k12 ca274) dna) (db:genpept-bct1) (de:escherichia coli pepp, ubih (visb) and visc genes.) (le:477) (re:1061) (di:direct) ECOPUV D90281 g216626 Escherichia coli 562 -11535640 7500924148 ygfb (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f194) (le:9257) (re:9841) (di:complement) ECU28377 U28377 g882439 Escherichia coli 562 -11535640 235631 ygfb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 264 of 400 of the completegenome.) (nt:f194; 100 pct identical to ygfb_ecoli sw: p25533) (le:5796) (re:6380) (di:complement) AE000374 AE000374 g1789276 Escherichia coli 562 -11535640 5000693243 (de:(ecoli_2832) (pn:hypothetical 21) (gn:ygfb) (gtcfc:13.7:14.1) (ec:) (ygfb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2832 ECOLI_2832 Escherichia coli 562 10054046

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859342	11989	34145	417	138

Description

6500731783 ygfe:b2910 hypothetical 12.7 kd protein in pepp-ssr intergenic region:hypothetical 12.6 kd protein in pepp-ssr intergenic region:o109 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2910 b2910 Escherichia coli 562 -11535641 112321 ygfe (de:hypothetical 12.6 kd protein in pepp-ssr intergenic region (o109)) (db:swissprot) YGFE_ECOLI P45580 ESCHERICHIA COLI 562 -11535641 7000687812 ygfe hypothetical 12.7 kd protein in pepp-ssr intergenic region (cl:hypothetical protein hi0857) (db:pir2.dat) F65075 F65075 Escherichia coli 562 -11535641 7500924151 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o109) (le:10003) (re:10332) (di:direct) ECU28377 U28377 g882440 Escherichia coli 562 -11535641 239124 ygfe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 264 of 400 of the completegenome.) (nt:o109; 99 pct identical to ygfe_ecoli sw: p45580) (le:6542) (re:6871) (di:direct) AE000374 AE000374 g1789277 Escherichia coli 562 -11535641 5000693244 (de:(ecoli_2833) (pn:hypothetical 12) (gn:ygfe) (gtcfc:13.7:14.1) (ec:) (ygfe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2833 ECOLI_2833 Escherichia coli 562 10054049

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859344	11990	34146	240	79
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859354	11991	34147	471	156
<u>Description</u>				

6500731784 ygfa:b2912 hypothetical 21.1 kd protein in ssr-sera intergenic region:ol82 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2912 b2912 Escherichia coli 562 -11535642 112316 ygfa (de:hypothetical 21.1 kd protein in ssr-sera intergenic region (ol82)) (db:swissprot) YGFA_ECOLI P09160 ESCHERICHIA COLI 562 -11535642 135178 ygfa hypothetical 21.1k protein ssr-sera intergenic region (cl:conserved hypothetical protein hi0858) (db:pir1.dat) QQEC2K A21894 Escherichia coli 562 -11535642 239125 (sr:e.coli (k12 strain fb105) dna, clone plh60-1) (db:genpept-bct1) (de:e.coli ssr gene encoding 6s rna.) (nt:22-kda protein) (le:367) (re:915) (di:direct) ECOSSR M12965 g147874 Escherichia coli 562 -11535642 7500924146 ygfa (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_ol82; two upstream start codons, one within) (le:10632) (re:11180) (di:direct) ECU28377 U28377 g882441 Escherichia coli 562 -11535642 236033 ygfa putative ligase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 264 of 400 of the completegenome.) (nt:ol82; 100 pct identical to ygfa_ecoli sw:) (le:7171) (re:7719) (di:direct) AE000374 AE000374 g1789278 Escherichia coli 562 -11535642 5000693245 (de:(ecoli_2834) (pn:hypothetical 21) (gn:ygfa) (gtcfc:13.7:14.1) (ec:) (ygfa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2834 ECOLI_2834 Escherichia coli 562 10054044

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859355	11992	34148	279	92

Description

6500731785 yqfe:b2915 hypothetical protein:hypothetical 8.4 kd protein in rpia-icia intergenic region:f76 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2915 b2915 Escherichia coli 562 -11535643 115874 yqfe (de:hypothetical 8.4 kd protein in rpia-icia intergenic region (f76)) (db:swissprot) YQFE_ECOLI P52038 ESCHERICHIA COLI 562 -11535643 7000688375 hypothetical protein b2915 (db:pir2.dat) B65076 B65076 Escherichia coli 562 -11535643 7500952421 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f76) (le:13772) (re:14002) (di:complement) ECU28377 U28377 g882444 Escherichia coli 562 -11535643 239128 yqfe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 264 of 400 of the completgenome.) (nt:f76; this 76 aa orf is 30 pct identical (0 gaps)) (le:10311) (re:10541) (di:complement) AE000374 AE000374 g1789281 Escherichia coli 562 -11535643 5000693246 (de:(ecoli_2837) (pn:hypothetical 8) (gtcfc:13.7:14.1) (ec:) (yqfe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2837 ECOLI_2837 Escherichia coli 562 10057600

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859357	11993	34149	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859361	11994	34150	201	66

Description

6500731786 ygfd:b2918 hypothetical protein in sbm-fba intergenic region:hypothetical 36.7 kd protein in sbm-fba intergenic region:orf2:o331 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2918 b2918 Escherichia coli 562 -11535644 112320 argk (ec:2.7.-.-) (de:lao/ao transport system kinase,) (db:swissprot) ARGK_ECOLI P27254 ESCHERICHIA COLI 562 -11535644 7000687811 ygfd hypothetical protein in sbm-fba intergenic region (db:pir2.dat) E65076 E65076 Escherichia coli 562 -11535644 7500924150 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o331; alternate name ygfd; orf2 of x66836) (le:17378) (re:18373) (di:direct) ECU28377 U28377 g882447 Escherichia coli 562 -11535644 239131 ygfd putative nucleotide-binding protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 265 of 400 of the completegenome.) (nt:o331; 100 pct identical to ygfd_ecoli sw:) (le:3335) (re:4330) (di:direct) AE000375 AE000375 g1789285 Escherichia coli 562 -11535644 5000693247 (de:(ecoli_2840) (pn:hypothetical 36) (gn:ygfd) (gtcfc:13.7:14.1) (ec:) (ygfd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2840 ECOLI_2840 Escherichia coli 562 10054048

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859367	11995	34151	339	112

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859389	11996	34152	393	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859406	11997	34153	1269	422

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859414	11998	34154	519	172

Description

5000693248 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2919 b2919 Escherichia coli 562 -11535645
7000691776 hypothetical protein b2919 (cl:enoyl-coa hydratase homology) (db:pir2.dat) F65076 F65076 Escherichia coli 562 -11535645 7500960292 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o275) (le:18342) (re:19169) (di:direct) ECU28377 U28377 g882448 Escherichia coli 562 -11535645 239132 ygfg putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 265 of 400 of the completegenome.) (nt:o275; this 275 aa orf is 30 pct identical (6 gaps)) (le:4299) (re:5126) (di:direct) AE000375 AE000375 g1789286 Escherichia coli 562 -11535645 6500731787 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2919 b2919 Escherichia coli 562 -11535645

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859421	11999	34155	477	158

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859425	12000	34156	1083	360

Description

6500731788 ygfh:b2920 hypothetical protein:hypothetical 53.8 kd protein in sbm-fba intergenic region:o492 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2920 b2920 Escherichia coli 562 -11535646 112325 ygfh (de:hypothetical 53.8 kd protein in sbm-fba intergenic region (o492)) (db:swissprot) YGFH_ECOLI P52043 ESCHERICHIA COLI 562 -11535646 7000687814 hypothetical protein b2920 (cl:acetyl-coa hydrolase) (db:pir2.dat) G65076 G65076 Escherichia coli 562 -11535646 7500924154 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o492) (le:19193) (re:20671) (di:direct) ECU28377 U28377 g882449 Escherichia coli 562 -11535646 239133 ygfh putative coenzyme a transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 265 of 400 of the completegenome.) (nt:o492; this 492 aa orf is 46 pct identical (7 gaps)) (le:5150) (re:6628) (di:direct) AE000375 AE000375 g1789287 Escherichia coli 562 -11535646 5000693249 (de:(ecoli_2842) (pn:hypothetical 53) (gtcfc:13.7:14.1) (ec:.) (ygfh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2842 ECOLI_2842 Escherichia coli 562 10054053

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859435	12001	34157	471	156
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859439	12002	34158	921	307
<u>Description</u>				

6500731789 ygfi:b2921 hypothetical protein:hypothetical transcriptional regulator in sbm-fba intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2921 b2921 Escherichia coli 562 -11535647 112326 ygfi (de:hypothetical transcriptional regulator in sbm-fba intergenic region) (db:swissprot) YGFI_ECOLI P52044 ESCHERICHIA COLI 562 -11535647 7000687815 hypothetical protein b2921 (db:pir2.dat) H65076 H65076 Escherichia coli 562 -11535647 7500924155 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f303) (le:20668) (re:21579) (di:complement) ECU28377 U28377 g882450 Escherichia coli 562 -11535647 239134 ygfi putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 265 of 400 of the completegenome.) (nt:f303; this 303 aa orf is 25 pct identical (11 gaps)) (le:6625) (re:7536) (di:complement) AE000375 AE000375 g1789288 Escherichia coli 562 -11535647 5000693250 (de:(ecoli_2843) (pn:hypothetical transcriptional regulator in sbm-fba intergenic region:f303) (gtcfc:13.7:14.1) (ec:) (ygfi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2843 ECOLI_2843 Escherichia coli 562 10054054

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859469	12003	34159	495	164

Description

6500731790 ygge:b2922 hypothetical 26.6 kd protein in sbm-fba intergenic region:orf 6:f246 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2922 b2922 Escherichia coli 562 -11535648 112340 ygge (de:(f246)) (db:swissprot) YGGE_ECOLI P11668 ESCHERICHIA COLI 562 -11535648 7000687831 ygge hypothetical 26.6k protein sbm-fba intergenic region (db:pir2.dat) (mp:63 min) A65077 A65077 Escherichia coli 562 -11535648 7500924192 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f246; alternate name ygge'; orf6 of x14436) (le:21731) (re:22471) (di:complement) ECU28377 U28377 g882451 Escherichia coli 562 -11535648 239135 ygge putative actin (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 265 of 400 of the completengenome.) (nt:f246; 100 pct identical to ygge_ecoli sw:) (le:7688) (re:8428) (di:complement) AE000375 AE000375 g1789289 Escherichia coli 562 -11535648 5000693251 (de:(ecoli_2844) (pn:hypothetical 26) (gn:ygge) (gtcfc:13.7:14.1) (ec:) (ygge_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2844 ECOLI_2844 Escherichia coli 562 10054068

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859478	12004	34160	765	254

Description

6500731791 ygga:b2923 hypothetical protein in sbm-fba intergenic region:hypothetical 23.2 kd protein in sbm-fba intergenic region:orf 5:f211 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2923 b2923 Escherichia coli 562 -11535649 112336 ygga (de:hypothetical 23.2 kd protein in sbm-fba intergenic region (orf 5)) (db:swissprot) YGGA_ECOLI P11667 ESCHERICHIA COLI 562 -11535649 7000687828 ygga hypothetical 23k protein sbm-fba intergenic region (db:pir1.dat) (mp:63 min) QQEC5A B65077 Escherichia coli 562 -11535649 7500924188 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f211; alternate name ygga; orf5 of x14436) (le:22564) (re:23199) (di:complement) ECU28377 U28377 g882452 Escherichia coli 562 -11535649 239136 ygga orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 265 of 400 of the completengenome.) (nt:f211; 100 pct identical to ygga_ecoli sw: p11667) (le:8521) (re:9156) (di:complement) AE000375 AE000375 g1789290 Escherichia coli 562 -11535649 5000693252 (de:(ecoli_2845) (pn:hypothetical 23) (gn:ygga) (gtcfc:13.7:14.1) (ec:) (ygga_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2845 ECOLI_2845 Escherichia coli 562 10054064

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859479	12005	34161	1422	473

Description

6500731792 yggg:b2924 hypothetical 30.9 kd protein in sbm-fba intergenic region:orf 4:f286 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2924 b2924 Escherichia coli 562 -11535650 239137 yggg (de:(f286)) (db:swissprot) YGGB_ECOLI P11666 ESCHERICHIA COLI 562 -11535650 135195 yggg hypothetical 30.9 kd protein sbm-fba intergenic region (db:pir1.dat) (mp:63 min) QQEC4A S04735 Escherichia coli 562 -11535650 5000693253 (db:genpept-bct1) (de:escherichia coli fda, pgk and gapb genes for fructose1,6-biphosphate aldolase (class ii), phosphoglycerate kinase andglyceraldehyde 3-phosphate dehydrogenase.) (nt:orf4 (aa 1-197)) (le:5838) (re:6698) (di:direct) ECFDAPGK X14436 g41424 Escherichia coli 562 -11535650 7500924189 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f286; alternate name yggg; orf4 of x14436) (le:23338) (re:24198) (di:complement) ECU28377 U28377 g882453 Escherichia coli 562 -11535650 232837 yggg putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 265 of 400 of the completegenome.) (nt:f286; 100 pct identical to yggg_ecoli sw:) (le:9295) (re:10155) (di:complement) AE000375 AE000375 g1789291 Escherichia coli 562 -11535650 112337 yggg (de:(f286)) (db:swissprot) YGGB_ECOLI P11666 ESCHERICHIA COLI 562 -11535650

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859481	12006	34162	354	117

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859498	12007	34163	927	308

Description

6500731793 yggc:b2928 hypothetical 27.1 kd protein in gapb-cmta intergenic region:hypothetical 27.1 kd protein in epd-cmta intergenic region:orf 3:f237 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2928 b2928 Escherichia coli 562 -11535651 112338 yggc (de:(f237)) (db:swissprot) YGGC_ECOLI P11664 ESCHERICHIA COLI 562 -11535651 7000687829 yggc hypothetical 27.1k protein gapb-cmta intergenic region (db:pir1.dat) (mp:63 min) QQEC3B G65077 Escherichia coli 562 -11535651 7500924190 (fn:putative catabolite gene activator protein) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f237; alternate name yggc; orf3 of x14436) (le:28367) (re:29080) (di:complement) ECU28377 U28377 g882457 Escherichia coli 562 -11535651 239141 yggc putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 266 of 400 of the completegenome.) (nt:f237; 100 pct identical to yggc_ecoli sw:) (le:4020) (re:4733) (di:complement) AE000376 AE000376 g1789296 Escherichia coli 562 -11535651 5000693254 (de:(ecoli_2850) (pn:hypothetical 27) (gn:yggc) (gtcfc:13.7:14.1) (ec:) (yggc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2850 ECOLI_2850 Escherichia coli 562 10054066

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859505	12008	34164	531	177

Description

6500731794 yggd:b2929 hypothetical protein in gapb-cmta intergenic region:hypothetical 19.3 kd protein in epd-cmta intergenic region:orf 2:f169 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2929 b2929 Escherichia coli 562 -11535652 112339 yggd (de:(f169)) (db:swissprot) YGGD_ECOLI P11663 ESCHERICHIA COLI 562 -11535652 7000687830 yggd hypothetical protein gapb-cmta intergenic region (db:pir1.dat) (mp:63 min) QQEC2B H65077 Escherichia coli 562 -11535652 7500924191 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f169; alternate name yggd; orf2 of x14436) (le:29077) (re:29586) (di:complement) ECU28377 U28377 g882458 Escherichia coli 562 -11535652 239142 yggd putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 266 of 400 of the completegenome.) (nt:f169; 100 pct identical to yggd_ecoli sw: p11663) (le:4730) (re:5239) (di:complement) AE000376 AE000376 g1789297 Escherichia coli 562 -11535652 5000693255 (de:(ecoli_2851) (pn:hypothetical 19) (gn:yggd) (gtcfc:13.7:14.1) (ec:) (yggd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2851 ECOLI_2851 Escherichia coli 562 10054067

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859519	12009	34165	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859520	12010	34166	861	286

Description

6500731795 yggf:b2930 hypothetical 34.3 kd protein in gapb-cmta intergenic region:hypothetical 34.3 kd protein in epd-cmta intergenic region:orf 1:f321 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2930 b2930 Escherichia coli 562 -11535653 112341 yggf (de:(f321)) (db:swissprot) YGGF_ECOLI P21437 ESCHERICHIA COLI 562 -11535653 7000687832 yggf hypothetical 34k protein gapb-cmta intergenic region (db:pir1.dat) (mp:63 min) QQEC15 A65078 Escherichia coli 562 -11535653 7500924193 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f321; alternate name yggf; orf1 of x14436) (le:29608) (re:30573) (di:complement) ECU28377 U28377 g882459 Escherichia coli 562 -11535653 239143 yggf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 266 of 400 of the completegenome.) (nt:f321; 100 pct identical to yggf_ecoli sw:) (le:5261) (re:6226) (di:complement) AE000376 AE000376 g1789298 Escherichia coli 562 -11535653 5000693256 (de:(ecoli_2852) (pn:hypothetical 34) (gn:yggf) (gtcfc:13.7:14.1) (ec:) (yggf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2852 ECOLI_2852 Escherichia coli 562 10054069

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859534	12011	34167	1158	385

Description

5000693257 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2931 b2931 Escherichia coli 562 -11535654 7000691777 hypothetical protein b2931 (db:pir2.dat) B65078 B65078 Escherichia coli 562 -11535654 7500960293 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f329) (le:30570) (re:31559) (di:complement) ECU28377 U28377 g882460 Escherichia coli 562 -11535654 239144 b2931 putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 266 of 400 of the completegenome.) (nt:f329; this 329 aa orf is 45 pct identical (14 gaps)) (le:6223) (re:7212) (di:complement) AE000376 AE000376 g1789299 Escherichia coli 562 -11535654 6500731796 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2931 b2931 Escherichia coli 562 -11535654

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501859535	12012	34168	456	151

Description

5000693258 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2932 b2932 Escherichia coli 562 -11535655

7000691778 hypothetical protein b2932 (db:pir2.dat) C65078 C65078 Escherichia coli 562 -11535655 7500960294 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f118) (le:31490) (re:31846) (di:complement) ECU28377 U28377 g882461 Escherichia coli 562 -11535655 239145 yggp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 266 of 400 of the completegenome.) (nt:f118; this 118 aa orf is 50 pct identical (1 gap)) (le:7143) (re:7499) (di:complement) AE000376 AE000376 g1789300 Escherichia coli 562 -11535655 6500731797 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2932 b2932 Escherichia coli 562 -11535655

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501859540	12013	34169	498	165

Description

6500731798 yggg:b2936 hypothetical 31.8 kd protein in tkta-speb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2936 b2936 Escherichia coli 562 -11535656 7000690936 yggg transcription regulator yggg (db:pir2.dat) G65078 G65078 Escherichia coli 562 -11535656 239149 (sr:escherichia coli (strain k-12) (clone: plc(2-5,5-8,5-14).) dna) (db:genpept-bct1) (de:e.coli agmatine ureohydrolase (speb) gene, complete cds.) (nt:orf2; putative) (le:1340) (re:2224) (di:complement) ECOSPEAA M32363 g1128974 Escherichia coli 562 -11535656 7500959805 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o294; was o219p before splice; alternate name) (le:36182) (re:37066) (di:direct) ECU28377 U28377 g882465 Escherichia coli 562 -11535656 236021 yggg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 267 of 400 of the completegenome.) (nt:o294; 100 pct identical to yggg_ecoli sw: p25894) (le:105) (re:989) (di:direct) AE000377 AE000377 g1789305 Escherichia coli 562 -11535656 5000693259 (de:(ecoli_2858) (pn:hypothetical 26) (gn:yggg) (gtcfc:13.7:14.1) (ec:) (yggg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2858 ECOLI_2858 Escherichia coli 562 10123910

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859555	12014	34170	564	187

Description

6500731799 yqgb:b2939 hypothetical 5.4 kd protein in spea-metk intergenic region:f48 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2939 b2939 Escherichia coli 562 -11535657 115891 yqgb (de:hypothetical 5.4 kd protein in spea-metk intergenic region (f48)) (db:swissprot) YQGB_ECOLI P46877 ESCHERICHIA COLI 562 -11535657 7000688391 yqgb hypothetical 5.4 kd protein in spea-metk intergenic region (db:pir2.dat) B65079 B65079 Escherichia coli 562 -11535657 7500952437 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f48) (le:40315) (re:40461) (di:complement) ECU28377 U28377 g882468 Escherichia coli 562 -11535657 239152 yqgb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 267 of 400 of the completegenome.) (nt:f48; 100 pct identical to yqgb_ecoli sw: p46877) (le:4238) (re:4384) (di:complement) AE000377 AE000377 g1789308 Escherichia coli 562 -11535657 5000693260 (de:(ecoli_2861) (pn:hypothetical 5) (gn:yqgb) (gtcfc:13.7:14.1) (ec:) (yqgb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2861 ECOLI_2861 Escherichia coli 562 10057617

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859572	12015	34171	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859613	12016	34172	576	191

Description

6500731800 yqgc:b2940 hypothetical 8.1 kd protein in spea-metk intergenic region:o71 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2940 b2940 Escherichia coli 562 -11535658 115893 yqgc (de:hypothetical 8.1 kd protein in spea-metk intergenic region (o71)) (db:swissprot) YQGC_ECOLI P46878 ESCHERICHIA COLI 562 -11535658 7000688393 yqgc hypothetical 8.1 kd protein in spea-metk intergenic region (db:pir2.dat) C65079 C65079 Escherichia coli 562 -11535658 7500952439 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o71) (le:40582) (re:40797) (di:direct) ECU28377 U28377 g882469 Escherichia coli 562 -11535658 239153 yqgc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 267 of 400 of the completgenome.) (nt:o71; 100 pct identical to yqgc_ecoli sw: p46878) (le:4505) (re:4720) (di:direct) AE000377 AE000377 g1789309 Escherichia coli 562 -11535658 5000693261 (de:(ecoli_2862) (pn:hypothetical 8) (gn:yqgc) (gtcfc:13.7:14.1) (ec:) (yqgc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2862 ECOLI_2862 Escherichia coli 562 10057619

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859615	12017	34173	1395	464

Description

6500731801 yqgd:b2941 hypothetical 9.5 kd protein in spea-metk intergenic region:f83 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2941 b2941 Escherichia coli 562 -11535659 115894 yqgd (de:hypothetical 9.5 kd protein in spea-metk intergenic region (f83)) (db:swissprot) YQGD_ECOLI P46879 ESCHERICHIA COLI 562 -11535659 7000688394 yqgd hypothetical 9.5 kd protein in spea-metk intergenic region (db:pir2.dat) D65079 D65079 Escherichia coli 562 -11535659 7500952440 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f83) (le:40794) (re:41045) (di:complement) ECU28377 U28377 g882470 Escherichia coli 562 -11535659 239154 yqgd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 267 of 400 of the completgenome.) (nt:f83; 100 pct identical to yqgd_ecoli sw: p46879) (le:4717) (re:4968) (di:complement) AE000377 AE000377 g1789310 Escherichia coli 562 -11535659 5000693262 (de:(ecoli_2863) (pn:hypothetical 9) (gn:yqgd) (gtcfc:13.7:14.1) (ec:) (yqgd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2863 ECOLI_2863 Escherichia coli 562 10057620

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859618	12018	34174	711	237

Description

6500731802 sprt:b2944 hypothetical 19.3 kd protein in galp-enda intergenic region:sprt protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2944 b2944 Escherichia coli 562 -11535660 99323 sprt (de:sprt protein) (db:swissprot) SPRT_ECOLI P39902 ESCHERICHIA COLI 562 -11535660 7000686659 sprt hypothetical 19.3 kd protein in galp-enda intergenic region (cl:hypothetical protein h1173) (db:pir2.dat) G65079 G65079 Escherichia coli 562 -11535660 239157 sprt sprt (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli dna for sprt involved in bola gene expression at the stationary phase, complete cds.) (le:54) (re:551) (di:direct) ECOSPRT D83644 g1208420 Escherichia coli 562 -11535660 7500891999 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o165; alternate name yggi) (le:44149) (re:44646) (di:direct) ECU28377 U28377 g882473 Escherichia coli 562 -11535660 236028 sprt orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 267 of 400 of the complete genome.) (nt:o165; 100 pct identical to yggi_ecoli sw: p39902) (le:8073) (re:8570) (di:direct) AE000377 AE000377 g1789313 Escherichia coli 562 -11535660 5000693263 (de:(ecoli_2866) (pn:sprt protein) (gn:sprt) (gtcfc:13.7:14.1) (ec:) (sprt_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2866 ECOLI_2866 Escherichia coli 562 10041182

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859635	12019	34175	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859643	12020	34176	1368	455

Description

GTC ORF with score 118 to: (sr:chlamydomonas reinhardtii (strain cc-621) vegetative cDNA to mRNA) (db:genpept-pln1) (de:chlamydomonas reinhardtii structural wall protein (vsp1) mRNA, complete cds.) (le:273) (re:1175) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859647	12021	34177	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859651	12022	34178	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859671	12023	34179	414	137

Description

6500731803 yggj:b2946 hypothetical protein in enda-gshb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2946 b2946 Escherichia coli 562 -11535661 7000691828 yggj hypothetical protein in enda-gshb intergenic region (db:pir2.dat) A65080 A65080 Escherichia coli 562 -11535661 7500960345 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o252) (le:45501) (re:46259) (di:direct) ECU28377 U28377 g882475 Escherichia coli 562 -11535661 239159 yggj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 267 of 400 of the completengenome.) (nt:o252; 98 pct identical to yggj_ecoli sw: p37912 but) (le:9425) (re:10183) (di:direct) AE000377 AE000377 g1789315 Escherichia coli 562 -11535661 5000693264 (de:(ecoli_2868) (pn:hypothetical 26) (gn:yggj) (gtcfc:13.7:14.1) (ec:) (yggj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2868 ECOLI_2868 Escherichia coli 562 10123912

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859672	12024	34180	480	159

Description

5000693265 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2948 b2948 Escherichia coli 562 -11535662 7000691779 hypothetical protein b2948 (cl:hypothetical protein hi0304) (db:pir2.dat) C65080 C65080 Escherichia coli 562 -11535662 7500960295 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o211) (le:47259) (re:47894) (di:direct) ECU28377 U28377 g882477 Escherichia coli 562 -11535662 239161 yqge orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 267 of 400 of the completengenome.) (nt:o211; 45 pct identical (5 gaps) to 175 residues) (le:11183) (re:11818) (di:direct) AE000377 AE000377 g1789317 Escherichia coli 562 -11535662 6500731804 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2948 b2948 Escherichia coli 562 -11535662

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859678	12025	34181	2112	703

Description

6500731805 yqgf:b2949 hypothetical protein:hypothetical 15.2 kd protein in gshb-ansb intergenic region:o180 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2949 b2949 Escherichia coli 562 -11535663 115901 yqgf (de:hypothetical 15.2 kd protein in gshb-ansb intergenic region (o180)) (db:swissprot) YQGF_ECOLI P52050 ESCHERICHIA COLI 562 -11535663 7000688397 hypothetical protein b2949 (cl:haemophilus influenzae conserved hypothetical protein hi0305) (db:pir2.dat) D65080 D65080 Escherichia coli 562 -11535663 7500952444 yqgf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 267 of 400 of the completegenome.) (nt:o138; 70 pct identical to 135 residues) (le:11818) (re:12234) (di:direct) AE000377 AE000377 g1789318 Escherichia coli 562 -11535663 5000693266 (de:(ecoli_2871) (pn:hypothetical 15) (gtcfc:13.7:14.1) (ec:) (yqgf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2871 ECOLI_2871 Escherichia coli 562 10057627

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859679	12026	34182	720	239

Description

5000693267 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2950 b2950 Escherichia coli 562 -11535664 7000691780 hypothetical protein b2950 (cl:pilt protein) (db:pir2.dat) E65080 E65080 Escherichia coli 562 -11535664 7500960296 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f341) (le:48494) (re:49519) (di:complement) ECU28377 U28377 g882479 Escherichia coli 562 -11535664 239163 yggr putative protein transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:f341; this 341 aa orf is 46 pct identical (3 gaps)) (le:122) (re:1147) (di:complement) AE000378 AE000378 g1789320 Escherichia coli 562 -11535664 6500731806 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2950 b2950 Escherichia coli 562 -11535664

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859680	12027	34183	183	60

Description

6500731807 yggs:b2951 hypothetical protein:hypothetical 25.8 kd protein in gshb-ansb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2951 b2951 Escherichia coli 562 -11535665 112353 yggs (de:hypothetical 25.8 kd protein in gshb-ansb intergenic region) (db:swissprot) YGGS_ECOLI P52054 ESCHERICHIA COLI 562 -11535665 7000687836 hypothetical protein b2951 (cl:conserved hypothetical protein hi0090) (db:pir2.dat) F65080 F65080 Escherichia coli 562 -11535665 7500924200 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o234) (le:49492) (re:50196) (di:direct) ECU28377 U28377 g882480 Escherichia coli 562 -11535665 239164 yggs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:o234; this 234 aa orf is 55 pct identical (6 gaps)) (le:1120) (re:1824) (di:direct) AE000378 AE000378 g1789321 Escherichia coli 562 -11535665 5000693268 (de:(ecoli_2873) (pn:hypothetical 25) (gtcfc:13.7:14.1) (ec:) (yggs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2873 ECOLI_2873 Escherichia coli 562 10054081

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859686	12028	34184	246	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859701	12029	34185	828	275

Description

6500731808 ygg:b2952 hypothetical protein:hypothetical 21.2 kd protein in gshb-ansb intergenic region:o188 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2952 b2952 Escherichia coli 562 -11535666 112355 ygg (de:hypothetical 21.2 kd protein in gshb-ansb intergenic region (o188)) (db:swissprot) YGGT_ECOLI P52058 ESCHERICHIA COLI 562 -11535666 7000687837 hypothetical protein b2952 (cl:hypothetical protein hi1036) (db:pir2.dat) G65080 G65080 Escherichia coli 562 -11535666 7500924202 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o188) (le:50214) (re:50780) (di:direct) ECU28377 U28377 g882481 Escherichia coli 562 -11535666 239165 ygg putative resistance protein (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:o188; this 188 aa orf is 40 pct identical (2 gaps)) (le:1842) (re:2408) (di:direct) AE000378 AE000378 g1789322 Escherichia coli 562 -11535666 5000693269 (de:(ecoli_2874) (pn:hypothetical 21) (gtcfc:13.7:14.1) (ec:) (ygg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2874 ECOLI_2874 Escherichia coli 562 10054083

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859708	12030	34186	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859718	12031	34187	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859726	12032	34188	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859733	12033	34189	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859741	12034	34190	333	110

Description

6500731809 yggu:b2953 hypothetical protein:hypothetical 10.9 kd protein in gshb-ansb intergenic region:o100 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2953 b2953 Escherichia coli 562 -11535667 112357 yggu (de:hypothetical 10.9 kd protein in gshb-ansb intergenic region (o100)) (db:swissprot) YGGU_ECOLI P52060 ESCHERICHIA COLI 562 -11535667 7000687838 hypothetical protein b2953 (db:pir2.dat) H65080 H65080 Escherichia coli 562 -11535667 7500924203 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o100) (le:50765) (re:51067) (di:direct) ECU28377 U28377 g882482 Escherichia coli 562 -11535667 239166 yggu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:o100; this 100 aa orf is 23 pct identical (3 gaps)) (le:2393) (re:2695) (di:direct) AE000378 AE000378 g1789323 Escherichia coli 562 -11535667 5000693270 (de:(ecoli_2875) (pn:hypothetical 10) (gtcfc:13.7:14.1) (ec:) (yggu_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2875 ECOLI_2875 Escherichia coli 562 10054085

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859762	12035	34191	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859763	12036	34192	537	178

Description

6500731810 yggv:b2954 hypothetical protein:hypothetical 21.0 kd protein in gshb-ansb intergenic region:o197 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2954 b2954 Escherichia coli 562 -11535668 112358 yggv (de:hypothetical 21.0 kd protein in gshb-ansb intergenic region (o197)) (db:swissprot) YGGV_ECOLI P52061 ESCHERICHIA COLI 562 -11535668 7000687839 hypothetical protein b2954 (cl:methanococcus jannaschii conserved hypothetical protein mj0226) (db:pir2.dat) A65081 A65081 Escherichia coli 562 -11535668 7500924204 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o197) (le:51075) (re:51668) (di:direct) ECU28377 U28377 g882483 Escherichia coli 562 -11535668 239167 yggv putative ribosomal protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:o197; residues 2-187 are 57 pct identical) (le:2703) (re:3296) (di:direct) AE000378 AE000378 g1789324 Escherichia coli 562 -11535668 5000693271 (de:(ecoli_2876) (pn:hypothetical 21) (gtcfc:13.7:14.1) (ec:) (yggv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2876 ECOLI_2876 Escherichia coli 562 10054086

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859781	12037	34193	639	212

Description

GTC ORF with score 142 to: (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #263(30.5-30.9 min.).) (nt:orf_id:o263#22; similar to (swissprot accession) (le:14961) (re:18323) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859787	12038	34194	1014	337

Description

6500731811 yggw:b2955 hypothetical protein:hypothetical 42.6 kd protein in gshb-ansb intergenic region:o378 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2955 b2955 Escherichia coli 562 -11535669 112360 yggw (de:hypothetical 42.6 kd protein in gshb-ansb intergenic region (o378)) (db:swissprot) YGGW_ECOLI P52062 ESCHERICHIA COLI 562 -11535669 7000687840 hypothetical protein b2955 (cl:oxygen-independent coproporphyrinogen oxidase) (db:pir2.dat) B65081 B65081 Escherichia coli 562 -11535669 7500924206 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o378) (le:51661) (re:52797) (di:direct) ECU28377 U28377 g882484 Escherichia coli 562 -11535669 239168 yggw putative oxidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:o378; this 378 aa orf is 67 pct identical (4 gaps)) (le:3289) (re:4425) (di:direct) AE000378 AE000378 g1789325 Escherichia coli 562 -11535669 5000693272 (de:(ecoli_2877) (pn:hypothetical 42) (gtcfc:13.7:14.1) (ec:) (yggw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2877 ECOLI_2877 Escherichia coli 562 10054088

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859801	12039	34195	1038	345

Description

6500731812 yggm:b2956 hypothetical protein in ansb 3 region:hypothetical 38.5 kd protein in gshb-ansb intergenic region:f335 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2956 b2956 Escherichia coli 562 -11535670 112349 yggm (de:hypothetical 38.5 kd protein in gshb-ansb intergenic region (f335)) (db:swissprot) YGGM_ECOLI P46142 ESCHERICHIA COLI 562 -11535670 7000687834 yggm hypothetical protein in ansb 3 region (db:pir2.dat) C65081 C65081 Escherichia coli 562 -11535670 7500924198 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f335) (le:52952) (re:53959) (di:complement) ECU28377 U28377 g882485 Escherichia coli 562 -11535670 239169 yggm putative alpha helix chain (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:f335; 97 pct identical to 45 aa fragment) (le:4580) (re:5587) (di:complement) AE000378 AE000378 g1789326 Escherichia coli 562 -11535670 5000693273 (de:(ecoli_2878) (pn:hypothetical 38) (gn:yggm) (gtcfc:13.7:14.1) (ec:) (yggm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2878 ECOLI_2878 Escherichia coli 562 10054077

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859806	12040	34196	903	300

Description

6500731813 yggg:b2958 hypothetical protein in ansb 5region:hypothetical 26.4 kd protein in gshb-ansb intergenic region:f239 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2958 b2958 Escherichia coli 562 -11535671 112350 yggg (de:hypothetical 26.4 kd protein in gshb-ansb intergenic region (f239)) (db:swissprot) YGGG_ECOLI P46143 ESCHERICHIA COLI 562 -11535671 7000687835 yggg hypothetical protein in ansb 5region (db:pir2.dat) E65081 E65081 Escherichia coli 562 -11535671 7500924199 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f239; was orf_f191 and orf_f194 before splice) (le:55298) (re:56017) (di:complement) ECU28377 U28377 g882487 Escherichia coli 562 -11535671 239171 yggg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:f239; 100 pct identical to fragment yggg_ecoli) (le:6926) (re:7645) (di:complement) AE000378 AE000378 g1789328 Escherichia coli 562 -11535671 5000693274 (de:(ecoli_2880) (pn:hypothetical 26) (gn:yggg) (gtcfc:13.7:14.1) (ec:) (yggg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2880 ECOLI_2880 Escherichia coli 562 10054078

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859815	12041	34197	666	221

Description

6500731814 yggl:b2959 hypothetical protein in muty 5 region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2959 b2959 Escherichia coli 562 -11535672 7000691837 yggl hypothetical protein in muty 5 region (db:pir2.dat) F65081 F65081 Escherichia coli 562 -11535672 7500960351 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f118) (le:56200) (re:56556) (di:complement) ECU28377 U28377 g882488 Escherichia coli 562 -11535672 239172 yggl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:f118; 100 pct identical to 72 aa of yggl_ecoli) (le:7828) (re:8184) (di:complement) AE000378 AE000378 g1789329 Escherichia coli 562 -11535672 5000693275 (de:(ecoli_2881) (pn:hypothetical 12) (gn:yggl) (gtcfc:13.7:14.1) (ec:) (yggl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2881 ECOLI_2881 Escherichia coli 562 10123915

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859818	12042	34198	345	114

Description

6500731815 yggh:b2960 hypothetical 27.3 kd protein in muty 5 region:hypothetical 27.3 kd protein in ansb-muty intergenic region:f239 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2960 b2960 Escherichia coli 562 -11535673 112343 yggh (de:hypothetical 27.3 kd protein in ansb-muty intergenic region (f239)) (db:swissprot) YGGH_ECOLI P32049 ESCHERICHIA COLI 562 -11535673 7000687833 yggh hypothetical 27.3 kd protein in muty 5 region:hypothetical protein mica region (cl:hypothetical protein hi0340) (db:pir2.dat) G65081 G65081 Escherichia coli 562 -11535673 7500924194 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f239; alternate name yggh; orf of m59471) (le:56526) (re:57245) (di:complement) ECU28377 U28377 g882489 Escherichia coli 562 -11535673 239173 yggh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:f239; 99 pct identical to yggh_ecoli sw: p32049;) (le:8154) (re:8873) (di:complement) AE000378 AE000378 g1789330 Escherichia coli 562 -11535673 5000693276 (de:(ecoli_2882) (pn:hypothetical 27) (gn:yggh) (gtcfc:13.7:14.1) (ec:) (yggh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2882 ECOLI_2882 Escherichia coli 562 10054071

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859819	12043	34199	258	85

Description

6500731816 yggx:b2962 hypothetical protein:hypothetical 11.0 kd protein in muty-nupg intergenic region:o91 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2962 b2962 Escherichia coli 562 -11535674 7000687841 hypothetical protein b2962 (db:pir2.dat) A65082 A65082 Escherichia coli 562 -11535674 7500924208 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o91) (le:58486) (re:58761) (di:direct) ECU28377 U28377 g882491 Escherichia coli 562 -11535674 239175 yggx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 268 of 400 of the completegenome.) (nt:o91; this 91 aa orf is 78 pct identical (0 gaps)) (le:10114) (re:10389) (di:direct) AE000378 AE000378 g1789332 Escherichia coli 562 -11535674 112362 yggx (de:hypothetical 11.0 kd protein in muty-nupg intergenic region (o91)) (db:swissprot) YGGX_ECOLI P52065 ESCHERICHIA COLI 562 -11535674 5000693277 (de:(ecoli_2884) (pn:hypothetical 11) (gtcfc:13.7:14.1) (ec:) (yggx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2884 ECOLI_2884 Escherichia coli 562 10054090

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859820	12044	34200	390	129

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859832	12045	34201	666	221

Description

GTC ORF with score 106 to: (sr:house mouse) (db:genpept-rod) (de:mus musculus thrombospondin 3 (thbs3) gene, partial cds and mucin 1(muc1) gene, complete cds.) (nt:episialin, polymorphic epithelial mucin) (le:3983:4774:6176:6364) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859842	12046	34202	714	237

Description

6500731817 yqga:b2966 hypothetical protein: hypothetical 24.6 kd protein in spec-glcb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2966 b2966 Escherichia coli 562 -11535675
 1500686280 yqga (de: hypothetical 24.6 kd protein in spec-glcb intergenic region) (db:swissprot) YQGA_ECOLI Q46831 ESCHERICHIA COLI 562 -11535675
 7000688389 hypothetical protein b2966 (cl: conserved hypothetical protein b2966) (db:pir2.dat) E65082 E65082 Escherichia coli 562 -11535675
 7500952435 (db:genpept-bct1) (de: escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o235) (le:63946) (re:64653) (di:direct) ECU28377 U28377 g882496 Escherichia coli 562 -11535675 239180 yqga putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de: escherichia coli k-12 mg1655 section 269 of 400 of the complete genome.) (nt:o235; this 235 aa orf is 23 pct identical (10 gaps)) (le:5183) (re:5890) (di:direct) AE000379 AE000379 g1789338 Escherichia coli 562 -11535675 5000693280 (de: (ecoli_2889) (pn: function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2889 ECOLI_2889 Escherichia coli 562 10061038

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859846	12047	34203	972	323

Description

6500731818 yghd:b2968 hypothetical protein:putative general secretion pathway protein m-type yghd (gtcfc:12.10) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2968 b2968 Escherichia coli 562 -11535676 1500686161 yghd (de:putative general secretion pathway protein m-type yghd) (db:swissprot) YGHD_ECOLI Q46832 ESCHERICHIA COLI 562 -11535676 7000687844 hypothetical protein b2968 (cl:epsm protein) (db:pir2.dat) F65082 F65082 Escherichia coli 562 -11535676 7500924220 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f178) (le:64983) (re:65519) (di:complement) ECU28377 U28377 g882497 Escherichia coli 562 -11535676 239181 yghd putative secretion pathway protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 269 of 400 of the completegenome.) (nt:f178; this 178 aa orf is 32 pct identical (5 gaps)) (le:6220) (re:6756) (di:complement) AE000379 AE000379 g1789339 Escherichia coli 562 -11535676 5000693281 (de:(ecoli_2890) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2890 ECOLI_2890 Escherichia coli 562 10060717

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859873	12048	34204	1368	456

Description

5000693282 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2969 b2969 Escherichia coli 562 -11535677 7500924221 yghe (de:putative general secretion pathway protein l-type yghe) (db:swissprot) YGHE_ECOLI Q46833 ESCHERICHIA COLI 562 -11535677 7000691781 hypothetical protein b2969 (db:pir2.dat) G65082 G65082 Escherichia coli 562 -11535677 239182 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f286) (le:65521) (re:66381) (di:complement) ECU28377 U28377 g882498 Escherichia coli 562 -11535677 7500924223 yghe putative general secretion pathway for protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 269 of 400 of the completegenome.) (nt:f286; this 286 aa orf is 29 pct identical (18 gaps)) (le:6758) (re:7618) (di:complement) AE000379 AE000379 g1789340 Escherichia coli 562 -11535677 6500731819 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2969 b2969 Escherichia coli 562 -11535677

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859874	12049	34205	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859877	12050	34206	747	248

Description

5000693283 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2970 b2970 Escherichia coli 562 -11535678
 7502852276 yghf (de:putative general secretion pathway protein c-type yghf precursor) (db:swissprot) YGHF_ECOLI Q46834 ESCHERICHIA COLI 562 -11535678
 7000691782 hypothetical protein b2970 (db:pir2.dat) H65082 H65082 Escherichia coli 562 -11535678 7500960297 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f288) (le:66447) (re:67313) (di:complement) ECU28377 U28377 g882499 Escherichia coli 562 -11535678 239183 b2970 putative general secretion pathway for protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 269 of 400 of the completegenome.) (nt:f288; residues 208-276 are 46 pct identical) (le:7684) (re:8550) (di:complement) AE000379 AE000379 g1789341 Escherichia coli 562 -11535678 6500731820 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2970 b2970 Escherichia coli 562 -11535678

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859881	12051	34207	441	146

Description

5000693284 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2971 b2971 Escherichia coli 562 -11535679
 7000691783 hypothetical protein b2971 (db:pir2.dat) A65083 A65083 Escherichia coli 562 -11535679 7500960298 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f136) (le:67460) (re:67870) (di:complement) ECU28377 U28377 g882500 Escherichia coli 562 -11535679 239184 b2971 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 269 of 400 of the completegenome.) (nt:f136; this 136 aa orf is 26 pct identical (8 gaps)) (le:8697) (re:9107) (di:complement) AE000379 AE000379 g1789342 Escherichia coli 562 -11535679 6500731821 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2971 b2971 Escherichia coli 562 -11535679

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859884	12052	34208	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859891	12053	34209	393	130

Description

5000693285 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2972 b2972 Escherichia coli 562 -11535680
7000689497 hypothetical protein b2972 (cl:hypothetical protein b2972) (db:pir2.dat) B65083 B65083 Escherichia coli 562 -11535680 7500955797 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f310) (le:67936) (re:68868) (di:complement) ECU28377 U28377 g882501 Escherichia coli 562 -11535680 239185 b2972 putative peptidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 269 of 400 of the completegenome.) (nt:f310; this 310 aa orf is 43 pct identical (13 gaps)) (le:9173) (re:10105) (di:complement) AE000379 AE000379 g1789343 Escherichia coli 562 -11535680 6500731822 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2972 b2972 Escherichia coli 562 -11535680

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859894	12054	34210	1494	497

Description

5000693286 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2973 b2973 Escherichia coli 562 -11535681
7000691784 hypothetical protein b2973 (db:pir2.dat) C65083 C65083 Escherichia coli 562 -11535681 7500960299 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f848) (le:68943) (re:71489) (di:complement) ECU28377 U28377 g882502 Escherichia coli 562 -11535681 239186 b2973 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 270 of 400 of the completegenome.) (nt:f848; this 848 aa orf is 24 pct identical (7 gaps)) (le:68) (re:2614) (di:complement) AE000380 AE000380 g1789345 Escherichia coli 562 -11535681 6500731823 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2973 b2973 Escherichia coli 562 -11535681

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859897	12055	34211	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859898	12056	34212	261	86

Description

5000693287 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2974 b2974 Escherichia coli 562 -11535682
7000691785 hypothetical protein b2974 (cl:murein-lipoprotein) (db:pir2.dat) D65083 D65083 Escherichia coli 562 -11535682 7500960300 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f675) (le:71477) (re:73504) (di:complement) ECU28377 U28377 g882503 Escherichia coli 562 -11535682 239187 b2974 putative endoglucanase (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 270 of 400 of the completegenome.) (nt:f675; this 675 aa orf is 53 pct identical (3 gaps)) (le:2602) (re:4629) (di:complement) AE000380 AE000380 g1789346 Escherichia coli 562 -11535682 6500731824 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2974 b2974 Escherichia coli 562 -11535682

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859912	12057	34213	255	84

Description

6500731825 yghk:b2975 hypothetical protein:putative l-lactate permease (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2975 b2975 Escherichia coli 562 -11535683 1500686281 yghk (de:putative l-lactate permease) (db:swissprot) YGHK_ECOLI Q46839 ESCHERICHIA COLI 562 -11535683
7000687845 hypothetical protein b2975 (cl:l-lactate permease) (db:pir2.dat) E65083 E65083 Escherichia coli 562 -11535683 7500924225 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f560) (le:73989) (re:75671) (di:complement) ECU28377 U28377 g882504 Escherichia coli 562 -11535683 239188 yghk putative permease (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 270 of 400 of the completegenome.) (nt:f560; this 560 aa orf is 63 pct identical (8 gaps)) (le:5114) (re:6796) (di:complement) AE000380 AE000380 g1789347 Escherichia coli 562 -11535683 5000693288 (de:(ecoli_2897) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2897 ECOLI_2897 Escherichia coli 562 10061039

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859913	12058	34214	1032	343

Description

5000693289 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2981 b2981 Escherichia coli 562 -11535684
7000691786 hypothetical protein b2981 (db:pir2.dat) C65084 C65084
Escherichia coli 562 -11535684 7500960301 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f390) (le:83434) (re:84606) (di:complement) ECU28377 U28377 g882510 Escherichia coli 562 -11535684 239194 b2981 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 271 of 400 of the completegenome.) (nt:f390; this 390 aa orf is 24 pct identical (13 gaps)) (le:927) (re:2099) (di:complement) AE000381 AE000381 g1789354 Escherichia coli 562 -11535684 6500731826 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2981 b2981 Escherichia coli 562 -11535684

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859914	12059	34215	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859917	12060	34216	399	132

Description

5000693290 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2983 b2983 Escherichia coli 562 -11535685
7000687846 yghq (de:hypothetical 35.2 kd protein in glcc-pitb intergenic region) (db:swissprot) YGHQ_ECOLI Q46841 ESCHERICHIA COLI 562 -11535685
7000687847 hypothetical protein b2983 (db:pir2.dat) E65084 E65084
Escherichia coli 562 -11535685 7500924226 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f325) (le:85732) (re:86709) (di:complement) ECU28377 U28377 g882512 Escherichia coli 562 -11535685 239196 yghq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 271 of 400 of the completegenome.) (nt:f325; this 325 aa orf is 17 pct identical (23 gaps)) (le:3225) (re:4202) (di:complement) AE000381 AE000381 g1789356 Escherichia coli 562 -11535685 6500731827 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2983 b2983 Escherichia coli 562 -11535685

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859918	12061	34217	639	212

Description

5000693291 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2984 b2984 Escherichia coli 562 -11535686
 7000687848 yghr (de:region) (db:swissprot) YGHR_ECOLI Q46842 ESCHERICHIA COLI 562 -11535686 7000687849 hypothetical protein b2984 (cl:conserved hypothetical protein b2986) (db:pir2.dat) F65084 F65084 Escherichia coli 562 -11535686 7500924227 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f252; was orf_f87p and orf_f234p before splice) (le:86845) (re:87603) (di:complement) ECU28377 U28377 g882513 Escherichia coli 562 -11535686 239197 yghr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 271 of 400 of the completegenome.) (nt:f252; this 252 aa orf is 34 pct identical (2 gaps)) (le:4338) (re:5096) (di:complement) AE000381 AE000381 g1789357 Escherichia coli 562 -11535686 6500731828 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2984 b2984 Escherichia coli 562 -11535686

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859926	12062	34218	381	126

Description

5000693292 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2985 b2985 Escherichia coli 562 -11535687
 7000687850 yghs (de:region) (db:swissprot) YGHS_ECOLI Q46843 ESCHERICHIA COLI 562 -11535687 7000687851 hypothetical protein b2985 (cl:conserved hypothetical protein b2986) (db:pir2.dat) G65084 G65084 Escherichia coli 562 -11535687 7500924228 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f237; gtg start) (le:87635) (re:88348) (di:complement) ECU28377 U28377 g882514 Escherichia coli 562 -11535687 239198 yghs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 271 of 400 of the completegenome.) (nt:f237; this 237 aa orf is 35 pct identical (1 gap)) (le:5128) (re:5841) (di:complement) AE000381 AE000381 g1789358 Escherichia coli 562 -11535687 6500731829 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2985 b2985 Escherichia coli 562 -11535687

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859934	12063	34219	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859937	12064	34220	471	156

Description

5000693293 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2986 b2986 Escherichia coli 562 -11535688
7000687852 yght (de:region) (db:swissprot) YGHT_ECOLI Q46844 ESCHERICHIA COLI 562 -11535688 7000687853 hypothetical protein b2986 (cl:conserved hypothetical protein b2986) (db:pir2.dat) H65084 H65084 Escherichia coli 562 -11535688 7500924229 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o230) (le:88522) (re:89214) (di:direct) ECU28377 U28377 g882515 Escherichia coli 562 -11535688 239199 yght orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 271 of 400 of the completegenome.) (nt:o230; this 230 aa orf is 39 pct identical (9 gaps)) (le:6015) (re:6707) (di:direct) AE000381 AE000381 g1789359 Escherichia coli 562 -11535688 6500731830 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2986 b2986 Escherichia coli 562 -11535688

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859943	12065	34221	528	175

Description

5000693295 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2989 b2989 Escherichia coli 562 -11535689
7500924230 yghu (de:hypothetical 34.2 kd protein in gsp-hybg intergenic region) (db:swissprot) YGHU_ECOLI Q46845 ESCHERICHIA COLI 562 -11535689
7000691787 hypothetical protein b2989 (db:pir2.dat) C65085 C65085 Escherichia coli 562 -11535689 239202 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o304; gtg start) (le:93070) (re:93984) (di:direct) ECU28377 U28377 g882518 Escherichia coli 562 -11535689 7500924232 b2989 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:o304; this 304 aa orf is 37 pct identical (19 gaps)) (le:109) (re:1023) (di:direct) AE000382 AE000382 g1789363 Escherichia coli 562 -11535689 6500731831 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2989 b2989 Escherichia coli 562 -11535689

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859948	12066	34222	459	152

Description

5000693296 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2997 b2997 Escherichia coli 562 -11535690
 7502852277 hyb0 (ec:1.18.99.1) (de:(membrane-bound hydrogenase 2 small subunit) (hyd2)) (db:swissprot) MBHT_ECOLI Q46847 ESCHERICHIA COLI 562 -11535690 7000691788 hypothetical protein b2997 (cl:hydrogenase (nife) small chain) (db:pir2.dat) C65086 C65086 Escherichia coli 562 -11535690
 7500960302 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f372) (le:99531) (re:100649) (di:complement) ECU28377 U28377 g882526 Escherichia coli 562 -11535690
 239210 b2997 putative hydrogenase subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f372; this 372 aa orf is 40 pct identical (12 gaps)) (le:6573) (re:7691) (di:complement) AE000382 AE000382 g1789371 Escherichia coli 562 -11535690 6500731832 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2997 b2997 Escherichia coli 562 -11535690

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501859951	12067	34223	633	210

Description

GTC ORF with score 394 to: (db:genpept-pln1) (de:cochliobolus heterostrophus gtpase activating protein homolog(gap1), hmg dna binding protein (mat-2), and beta glucosidasehomolog (bgl1) genes, complete cds.) (nt:orf1; similar to unknown saccharomyces ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859957	12068	34224	1149	382

Description

5000693297 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2998 b2998 Escherichia coli 562 -11535691
 7500924234 yghw (de:hypothetical 10.9 kd protein in hyba-exbd intergenic region) (db:swissprot) YGHW_ECOLI Q46848 ESCHERICHIA COLI 562 -11535691
 7000691789 hypothetical protein b2998 (db:pir2.dat) D65086 D65086 Escherichia coli 562 -11535691 239211 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f95) (le:100838) (re:101125) (di:complement) ECU28377 U28377 g882527 Escherichia coli 562 -11535691 7500924236 b2998 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 272 of 400 of the completegenome.) (nt:f95; this 95 aa orf is 27 pct identical (8 gaps)) (le:7880) (re:8167) (di:complement) AE000382 AE000382 g1789372 Escherichia coli 562 -11535691 6500731833 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2998 b2998 Escherichia coli 562 -11535691

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859968	12069	34225	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859974	12070	34226	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859982	12071	34227	1953	650

Description

5000693298 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2999 b2999 Escherichia coli 562 -11535692
 7000691790 hypothetical protein b2999 (db:pir2.dat) E65086 E65086
 Escherichia coli 562 -11535692 7500960303 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f136) (le:101244) (re:101654) (di:complement) ECU28377 U28377 g882528 Escherichia coli 562 -11535692 239212 b2999 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f136) (le:8286) (re:8696) (di:complement) AE000382 AE000382 g1789373 Escherichia coli 562 -11535692 6500731834 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b2999 b2999 Escherichia coli 562 -11535692

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501859983	12072	34228	195	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860001	12073	34229	948	315

Description

GTC ORF with score 123 to: (sr:pisum sativum (strain alaska) (clone: na481-5) (clone library) (db:genpept-pln1) (de:pisum sativum l. (clone na-481-5) mrna, complete cds.) (nt:protein localized in the nucleoli of pea nuclei;) (le:75) (re:1910) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860011	12074	34230	822	273

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860015	12075	34231	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860022	12076	34232	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860044	12077	34233	597	198

Description

5000693299 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3000 b3000 Escherichia coli 562 -11535693
7000691791 hypothetical protein b3000 (db:pir2.dat) F65086 F65086
Escherichia coli 562 -11535693 7500960304 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f141) (le:101654) (re:102079) (di:complement) ECU28377 U28377 g882529 Escherichia coli 562 -11535693 239213 b3000 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f141; this 141 aa orf is 43 pct identical (9 gaps)) (le:8696) (re:9121) (di:complement) AE000382 AE000382 g1789374 Escherichia coli 562 -11535693 6500731835 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3000 b3000
Escherichia coli 562 -11535693

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860048	12078	34234	348	115

Description

5000693300 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3001 b3001 Escherichia coli 562 -11535694
7000691792 hypothetical protein b3001 (cl:conserved hypothetical protein ypl088w) (db:pir2.dat) G65086 G65086 Escherichia coli 562 -11535694
7500960305 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o346) (le:102285) (re:103325) (di:direct) ECU28377 U28377 g882530 Escherichia coli 562 -11535694 239214 b3001 putative reductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:o346; this 346 aa orf is 31 pct identical (23 gaps)) (le:9327) (re:10367) (di:direct) AE000382 AE000382 g1789375 Escherichia coli 562 -11535694 6500731836 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3001 b3001 Escherichia coli 562 -11535694

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860053	12079	34235	864	287

Description

6500731837 ygha:b3002 hypothetical protein:hypothetical 18.6 kd protein in hyba-exbd intergenic region:f164 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3002 b3002 Escherichia coli 562 -11535695 115925 ygha (de:hypothetical 18.6 kd protein in hyba-exbd intergenic region (f164)) (db:swissprot) YQHA_ECOLI P52082 ESCHERICHIA COLI 562 -11535695 7000688419 hypothetical protein b3002 (cl:conserved hypothetical protein hi0507) (db:pir2.dat) H65086 H65086 Escherichia coli 562 -11535695 7500952466 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f164) (le:103365) (re:103859) (di:complement) ECU28377 U28377 g882531 Escherichia coli 562 -11535695 239215 ygha orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 272 of 400 of the completegenome.) (nt:f164; residues 32-151 are 67 pct identical to) (le:10407) (re:10901) (di:complement) AE000382 AE000382 g1789376 Escherichia coli 562 -11535695 5000693301 (de:(ecoli_2924) (pn:hypothetical 18) (gtcfc:13.7:14.1) (ec:) (ygha_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2924 ECOLI_2924 Escherichia coli 562 10057651

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860057	12080	34236	441	146

Description

6500731838 ygha:b3003 hypothetical protein:hypothetical oxidoreductase in hyba-exbd intergenic region (gtcfc:14.1) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3003 b3003 Escherichia coli 562 -11535696 112370 ygha (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YGHA_ECOLI P25887 ESCHERICHIA COLI 562 -11535696 7000687842 hypothetical protein b3003 (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) A65087 A65087 Escherichia coli 562 -11535696 7500924218 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o294) (le:104050) (re:104934) (di:direct) ECU28377 U28377 g882532 Escherichia coli 562 -11535696 239216 ygha putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:o294; this 294 aa orf is 65 pct identical (3 gaps)) (le:126) (re:1010) (di:direct) AE000383 AE000383 g1789378 Escherichia coli 562 -11535696 5000693302 (de:(ecoli_2925) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2925 ECOLI_2925 Escherichia coli 562 10123939

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860075	12081	34237	621	207

Description

5000693303 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3004 b3004 Escherichia coli 562 -11535697
 7000691793 hypothetical protein b3004 (db:pir2.dat) B65087 B65087
 Escherichia coli 562 -11535697 7500960306 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o81; alternate name ygga) (le:105110) (re:105355) (di:direct) ECU28377 U28377 g882533
 Escherichia coli 562 -11535697 239217 b3004 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:o81; alternate name ygga; this 81 aa orf is 28 pct) (le:1186) (re:1431) (di:direct) AE000383 AE000383 g1789379
 Escherichia coli 562 -11535697 6500731839 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3004 b3004
 Escherichia coli 562 -11535697

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860079	12082	34238	372	123

Description

GTC ORF with score 96 to: (or:Anolis pulchellus) (fn:precursor of yolk proteins, serum transport) (db:genpept-vrt) (de:anolis pulchellus vitellogenin mrna, partial cds.) (nt:apvtg5; similar to chicken and xenopus phosvitin) (le:<1) (re:546) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860080	12083	34239	276	91

Description

GTC ORF with score 116 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome xii cosmid 8083.) (nt:similar to kluyveromyces lactis deoxyribonucleic) (le:23775) (re:26219) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860104	12084	34240	417	138

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860106	12085	34241	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860109	12086	34242	195	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860127	12087	34243	786	261

Description

5000693304 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3007 b3007 Escherichia coli 562 -11535698
7000691794 hypothetical protein b3007 (db:pir2.dat) E65087 E65087
Escherichia coli 562 -11535698 7500960307 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f51) (le:106365) (re:106520) (di:complement) ECU28377 U28377 g882536 Escherichia coli 562 -11535698 239220 b3007 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:f51; this 51 aa orf is 34 pct identical (6 gaps)) (le:2441) (re:2596) (di:complement) AE000383 AE000383 g1789382 Escherichia coli 562 -11535698 6500731840 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3007 b3007 Escherichia coli 562 -11535698

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860129	12088	34244	372	123

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860140	12089	34245	846	281

Description

6500731841 yghb:b3009 hypothetical 24.1 kd protein in metc-sufi intergenic region:o219 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3009 b3009 Escherichia coli 562 -11535699 112371 yghb (de:hypothetical 24.1 kd protein in metc-sufi intergenic region) (db:swissprot) YGHB_ECOLI P33196 ESCHERICHIA COLI 562 -11535699 7000687843 yghb hypothetical 24.1 kd protein in metc-sufi intergenic region (cl:deda protein) (db:pir2.dat) G65087 G65087 Escherichia coli 562 -11535699 7500924219 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o219; alternate name yghb) (le:107951) (re:108610) (di:direct) ECU28377 U28377 g882538 Escherichia coli 562 -11535699 239222 yghb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:o219; 100 pct identical to yghb_ecoli sw: p33196) (le:4027) (re:4686) (di:direct) AE000383 AE000383 g1789384 Escherichia coli 562 -11535699 5000693305 (de:(ecoli_2931) (pn:hypothetical 24) (gn:yghb) (gtcfc:13.7:14.1) (ec:) (yghb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2931 ECOLI_2931 Escherichia coli 562 10054099

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860141	12090	34246	498	166

Description

5000693306 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3010 b3010 Escherichia coli 562 -11535700 7500952469 yqhc (de:hypothetical transcriptional regulator in metc-sufi intergenic region) (db:swissprot) YQHC_ECOLI Q46855 ESCHERICHIA COLI 562 -11535700 7000691795 hypothetical protein b3010 (db:pir2.dat) H65087 H65087 Escherichia coli 562 -11535700 239223 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f375) (le:108649) (re:109776) (di:complement) ECU28377 U28377 g882539 Escherichia coli 562 -11535700 7500952471 yqhc putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:f375; this 375 aa orf is 24 pct identical (10 gaps)) (le:4725) (re:5852) (di:complement) AE000383 AE000383 g1789385 Escherichia coli 562 -11535700 6500731842 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3010 b3010 Escherichia coli 562 -11535700

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860142	12091	34247	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860147	12092	34248	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860162	12093	34249	450	150

Description

5000693307 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3011 b3011 Escherichia coli 562 -11535701
 7500952473 yqhd (de:hypothetical oxidoreductase in metc-sufi intergenic region) (db:swissprot) YQHD_ECOLI Q46856 ESCHERICHIA COLI 562 -11535701
 7000691796 hypothetical protein b3011 (cl:lactaldehyde reductase:lactaldehyde reductase homology) (db:pir2.dat) A65088 A65088 Escherichia coli 562 -11535701 239224 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o387) (le:109742) (re:110905) (di:direct) ECU28377 U28377 g882540 Escherichia coli 562 -11535701 7500952475 yqhd putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:o387; this 387 aa orf is 40 pct identical (11 gaps)) (le:5818) (re:6981) (di:direct) AE000383 AE000383 g1789386 Escherichia coli 562 -11535701 6500731843 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3011 b3011 Escherichia coli 562 -11535701

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860164	12094	34250	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860167	12095	34251	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860186	12096	34252	1209	402

Description

5000693308 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3012 b3012 Escherichia coli 562 -11535702
7000691797 hypothetical protein b3012 (cl:aldehyde reductase) (db:pir2.dat) B65088 B65088 Escherichia coli 562 -11535702 7500953795 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o236) (le:111126) (re:111836) (di:direct) ECU28377 U28377 g882541 Escherichia coli 562 -11535702 239225 yqhe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:o236; this 236 aa orf is 45 pct identical (3 gaps)) (le:7203) (re:7913) (di:direct) AE000383 AE000383 g1789387 Escherichia coli 562 -11535702 6500731844 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3012 b3012 Escherichia coli 562 -11535702

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860190	12097	34253	645	214

Description

6500731845 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b3013 b3013 Escherichia coli 562 -11535703 7500952479 yqhg (de:hypothetical 35.1 kd protein in metc-sufi intergenic region precursor) (db:swissprot) YQHG_ECOLI Q46858 ESCHERICHIA COLI 562 -11535703 7000691798 hypothetical protein b3013 (db:pir2.dat) C65088 C65088 Escherichia coli 562 -11535703 7500952481 yqhg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:o309; joins 2 orfs from earlier version; gtg start) (le:8113) (re:9042) (di:direct) AE000383 AE000383 g2367185 Escherichia coli 562 -11535703

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860200	12098	34254	981	326

Description

5000693311 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3014 b3014 Escherichia coli 562 -11535704
7500952483 yqhh (de:precursor) (db:swissprot) YQHH_ECOLI Q46860 ESCHERICHIA COLI 562 -11535704 7000689396 murein-lipoprotein homolog:hypothetical protein b3014 (cl:murein-lipoprotein) (db:pir2.dat) D65088 D65088 Escherichia coli 562 -11535704 239228 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o85) (le:113015) (re:113272) (di:direct) ECU28377 U28377 g882544 Escherichia coli 562 -11535704 7500952485 yqhh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:o85; this 85 aa orf is 48 pct identical (0 gaps)) (le:9093) (re:9350) (di:direct) AE000383 AE000383 g1789390 Escherichia coli 562 -11535704 6500731846 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3014 b3014 Escherichia coli 562 -11535704

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860208	12099	34255	1311	436

Description

5000693312 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3015 b3015 Escherichia coli 562 -11535705
7500924264 ygiq (de:hypothetical 46.9 kd protein in metc-sufi intergenic region) (db:swissprot) YGIQ_ECOLI Q46861 ESCHERICHIA COLI 562 -11535705
7000691799 hypothetical protein b3015 (db:pir2.dat) E65088 E65088 Escherichia coli 562 -11535705 239229 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f413) (le:113315) (re:114556) (di:complement) ECU28377 U28377 g882545 Escherichia coli 562 -11535705 7500924266 b3015 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:f413) (le:9393) (re:10634) (di:complement) AE000383 AE000383 g1789391 Escherichia coli 562 -11535705 6500731847 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3015 b3015 Escherichia coli 562 -11535705

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860214	12100	34256	387	128

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860215	12101	34257	357	118

Description

5000693313 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3016 b3016 Escherichia coli 562 -11535706
7000687861 ygir (de:hypothetical 36.5 kd protein in metc-sufi intergenic region) (db:swissprot) YGIR_ECOLI Q46862 ESCHERICHIA COLI 562 -11535706
7000687862 hypothetical protein b3016 (db:pir2.dat) F65088 F65088 Escherichia coli 562 -11535706 7500924268 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f325) (le:114556) (re:115533) (di:complement) ECU28377 U28377 g882546 Escherichia coli 562 -11535706 239230 ygir orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 273 of 400 of the completegenome.) (nt:f325; this 325 aa orf is 33 pct identical (1 gap)) (le:10634) (re:11611) (di:complement) AE000383 AE000383 g1789392 Escherichia coli 562 -11535706 6500731848 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3016 b3016 Escherichia coli 562 -11535706

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860216	12102	34258	396	131

Description

5000693315 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3020 b3020 Escherichia coli 562 -11535707
7000691800 hypothetical protein b3020 (cl:dipeptide transport protein) (db:pir2.dat) B65089 B65089 Escherichia coli 562 -11535707 7500960308 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f535) (le:120498) (re:122105) (di:complement) ECU28377 U28377 g882550 Escherichia coli 562 -11535707 239234 b3020 putative transport periplasmic protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:f535; this 535 aa orf is 45 pct identical (5 gaps)) (le:4940) (re:6547) (di:complement) AE000384 AE000384 g1789397 Escherichia coli 562 -11535707 6500731849 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3020 b3020 Escherichia coli 562 -11535707

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860217	12103	34259	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860222	12104	34260	489	162

Description

GTC ORF with score 210 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1522.) (nt:similar to saccharomyces cerevisiae porphobilinogen) (le:345) (re:1352) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860225	12105	34261	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860233	12106	34262	348	115

Description

5000693316 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3021 b3021 Escherichia coli 562 -11535708
7000691801 hypothetical protein b3021 (db:pir2.dat) C65089 C65089
Escherichia coli 562 -11535708 7500960309 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f131) (le:122238) (re:122633) (di:complement) ECU28377 U28377 g882551 Escherichia coli 562 -11535708 239235 b3021 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:f131; this 131 aa orf is 37 pct identical (0 gaps)) (le:6680) (re:7075) (di:complement) AE000384 AE000384 g1789398 Escherichia coli 562 -11535708 6500731850 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3021 b3021 Escherichia coli 562 -11535708

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860241	12107	34263	645	214

Description

5000693317 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3022 b3022 Escherichia coli 562 -11535709
7500924269 ygiu (de:hypothetical 11.2 kd protein in parc-mdab intergenic region) (db:swissprot) YGIU_ECOLI Q46865 ESCHERICHIA COLI 562 -11535709
7000691802 hypothetical protein b3022 (db:pir2.dat) D65089 D65089 Escherichia coli 562 -11535709 239236 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f98) (le:122635) (re:122931) (di:complement) ECU28377 U28377 g882552 Escherichia coli 562 -11535709 7500924271 b3022 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:f98; this 98 aa orf is 25 pct identical (0 gaps)) (le:7077) (re:7373) (di:complement) AE000384 AE000384 g1789399 Escherichia coli 562 -11535709 6500731851 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3022 b3022 Escherichia coli 562 -11535709

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860242	12108	34264	756	251

Description

5000693318 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3023 b3023 Escherichia coli 562 -11535710
7000691803 hypothetical protein b3023 (db:pir2.dat) E65089 E65089 Escherichia coli 562 -11535710 7500960310 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f160) (le:123136) (re:123618) (di:complement) ECU28377 U28377 g882553 Escherichia coli 562 -11535710 239237 b3023 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:f160; this 160 aa orf is 27 pct identical (7 gaps)) (le:7578) (re:8060) (di:complement) AE000384 AE000384 g1789400 Escherichia coli 562 -11535710 6500731852 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3023 b3023 Escherichia coli 562 -11535710

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860259	12109	34265	1653	550

Description

6500731853 ygiw:b3024 hypothetical protein:11.9 kd protein in parc-mdab intergenic region precursor:f130 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3024 b3024 Escherichia coli 562 -11535711 112403 ygiw (de:11.9 kd protein in parc-mdab intergenic region precursor (f130)) (db:swissprot) YGIW_ECOLI P52083 ESCHERICHIA COLI 562 -11535711 7000687863 ygiw ygiw protein precursor (cl:hypothetical protein b3024) (db:pir2.dat) F65089 F65089 Escherichia coli 562 -11535711 7500924273 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f130) (le:123671) (re:124063) (di:complement) ECU28377 U28377 g882554 Escherichia coli 562 -11535711 239238 ygiw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:f130; this 130 aa orf is 38 pct identical (10 gaps)) (le:8113) (re:8505) (di:complement) AE000384 AE000384 g1789401 Escherichia coli 562 -11535711 5000693319 (de:(ecoli_2947) (pn:hypothetical 14) (gtcfc:13.7:14.1) (ec:) (ygiw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2947 ECOLI_2947 Escherichia coli 562 10054131

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860277	12110	34266	1344	447

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860299	12111	34267	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860300	12112	34268	273	90

Description

5000693322 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3027 b3027 Escherichia coli 562 -11535712
 7500924279 ygiz (de:hypothetical 13.2 kd protein in parc-madb intergenic region) (db:swissprot) YGIZ_ECOLI Q46867 ESCHERICHIA COLI 562 -11535712
 7000691804 hypothetical protein b3027 (db:pir2.dat) A65090 A65090 Escherichia coli 562 -11535712 239241 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f110) (le:126266) (re:126598) (di:complement) ECU28377 U28377 g882557 Escherichia coli 562 -11535712 7500924281 b3027 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:f110; this 110 aa orf is 19 pct identical (4 gaps)) (le:10708) (re:11040) (di:complement) AE000384 AE000384 g1789404 Escherichia coli 562 -11535712 6500731854 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3027 b3027 Escherichia coli 562 -11535712

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860301	12113	34269	420	139

Description

6500731855 ygin:b3029 hypothetical 11.5 kd protein in mdab 3region:11.5 kd protein in parc-pare intergenic region:o104 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3029 b3029 Escherichia coli 562 -11535713 112401 ygin (de:11.5 kd protein in parc-pare intergenic region) (db:swissprot) YGIN_ECOLI P40718 ESCHERICHIA COLI 562 -11535713 7000687859 ygin hypothetical 11.5 kd protein in mdab 3region (db:pir2.dat) C65090 C65090 Escherichia coli 562 -11535713 7500924262 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o104) (le:127530) (re:127844) (di:direct) ECU28377 U28377 g882559 Escherichia coli 562 -11535713 239243 ygin orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 275 of 400 of the completegenome.) (nt:o104; 100 pct identical to ygin_ecoli sw: p40718) (le:802) (re:1116) (di:direct) AE000385 AE000385 g1789407 Escherichia coli 562 -11535713 5000693324 (de:(ecoli_2952) (pn:hypothetical 11) (gn:ygin) (gtcfc:13.7:14.1) (ec:) (ygin_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2952 ECOLI_2952 Escherichia coli 562 10054129

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860304	12114	34270	693	230

Description

6500731856 yqia:b3031 hypothetical 15.2 kd protein in icc
3region:hypothetical 21.6 kd protein in pare-icc intergenic region:f193
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3031
b3031 Escherichia coli 562 -11535714 115951 yqia (de:hypothetical 21.6 kd
protein in pare-icc intergenic region (f193)) (db:swissprot) YQIA_ECOLI
P36653 ESCHERICHIA COLI 562 -11535714 7000688434 yqia hypothetical 15.2 kd
protein in icc 3region (db:pir2.dat) E65090 E65090 Escherichia coli 562
-11535714 7500952496 (db:genpept-bct1) (de:escherichia coli k-12 genome;
approximately 65 to 68 minutes.) (nt:orf_f193) (le:129813) (re:130394)
(di:complement) ECU28377 U28377 g882561 Escherichia coli 562 -11535714
239245 yqia orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 275 of 400 of the completegenome.)
(nt:f193; 100 pct identical to 134 residues of) (le:3085) (re:3666)
(di:complement) AE000385 AE000385 g1789409 Escherichia coli 562 -11535714
5000693325 (de:(ecoli_2954) (pn:hypothetical 21) (gn:yqia)
(gtcfc:13.7:14.1) (ec:) (yqia_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2954 ECOLI_2954 Escherichia coli 562
10057677

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860322	12115	34271	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860328	12116	34272	783	260

Description

6500731857 yqib:b3033 hypothetical 16.5 kd protein in icc-tolc intergenic region:orf2:f140 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3033 b3033 Escherichia coli 562 -11535715 115953 yqib (de:(f140)) (db:swissprot) YQIB_ECOLI P36652 ESCHERICHIA COLI 562 -11535715 7000688435 yqib hypothetical 16.5 kd protein in icc-tolc intergenic region:hypothetical protein 2:cpda 5 region (db:pir2.dat) (mp:68.4 min) G65090 G65090 Escherichia coli 562 -11535715 239247 orf2 (sr:escherichia coli (strain k12, isolate w3110) dna) (db:genpept-bct1) (de:e. coli dna for icc protein, complete cds.) (nt:product was detected by maxicell method) (le:538) (re:960) (di:direct) ECOICC D16557 g453395 Escherichia coli 562 -11535715 7500952497 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f140; orf2 of d16557) (le:131246) (re:131668) (di:complement) ECU28377 U28377 g882563 Escherichia coli 562 -11535715 234832 yqib putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 275 of 400 of the completegenome.) (nt:f140; 100 pct identical to yzzh_ecoli sw: p36652) (le:4518) (re:4940) (di:complement) AE000385 AE000385 g1789411 Escherichia coli 562 -11535715 5000693327 (de:(ecoli_2956) (pn:hypothetical 16) (gn:yqib) (gtcfc:13.7:14.1) (ec:) (yqib_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2956 ECOLI_2956 Escherichia coli 562 10057679

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860334	12117	34273	813	270

Description

GTC ORF with score 260 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana dna chromosome 4, essa i ap2 contig fragmentno. 2.) (nt:strong similarity to beta vulgaris putative sugar) (le:79935:80357) (re:80034:81738) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860341	12118	34274	252	83

Description

6500731858 ygie:b3034 hypothetical protein:hypothetical 23.7 kd protein in
icc-tolc intergenic region:f209 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3034 b3034 Escherichia coli 562 -11535716 115956
ygie (de:hypothetical 23.7 kd protein in icc-tolc intergenic region (f209))
(db:swissprot) YQIE_ECOLI P36651 ESCHERICHIA COLI 562 -11535716 7000688437
hypothetical protein b3034 (db:pir2.dat) H65090 H65090 Escherichia coli 562
-11535716 7500952502 (db:genpept-bct1) (de:escherichia coli k-12 genome;
approximately 65 to 68 minutes.) (nt:orf_f209) (le:131669) (re:132298)
(di:complement) ECU28377 U28377 g882564 Escherichia coli 562 -11535716
239248 ygie orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 275 of 400 of the completegenome.)
(nt:f209; this 209 aa orf is 54 pct identical (3 gaps)) (le:4941) (re:5570)
(di:complement) AE000385 AE000385 g1789412 Escherichia coli 562 -11535716
5000693328 (de:(ecoli_2957) (pn:hypothetical 23) (gtcfc:13.7:14.1) (ec:)
(ygie_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_2957 ECOLI_2957 Escherichia coli 562 10057682

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860346	12119	34275	651	216

Description

6500731859 ygia:b3036 hypothetical 9.9 kd protein in tolcr-ribb/htrp
intergenic region:hypothetical 9.9 kd protein in tolcr-ribb intergenic
region:o87 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia
coli) b3036 b3036 Escherichia coli 562 -11535717 163351 ygia hypothetical
9.9k protein tolcr-ribb/htrp intergenic region (db:pir2.dat) S11458 S11458
Escherichia coli 562 -11535717 238375 (db:genpept-bct1) (de:e.coli tolcr
gene for outer membrane protein.) (nt:unidentified reading frame) (le:1783)
(re:2043) (di:direct) ECTOLCMP X54049 g43108 Escherichia coli 562 -11535717
239250 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65
to 68 minutes.) (nt:orf_o87; alternate name ygia; urf of x00016) (le:133984)
(re:134244) (di:direct) ECU28377 U28377 g882566 Escherichia coli 562
-11535717 7500959840 ygia orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 275 of 400 of the
completegenome.) (nt:o86; 100 pct identical to ygia_ecoli sw: p21862)
(le:7256) (re:7516) (di:direct) AE000385 AE000385 g1789414 Escherichia coli
562 -11535717 112385 ygia_ecoli (de:hypothetical 9.9 kd protein in
tolcr-ribb intergenic region (o87).) P21862 P21862 Escherichia coli 562
-11535717 5000693329 (de:(ecoli_2959) (pn:hypothetical 9) (gn:ygia)
(gtcfc:13.7:14.1) (ec:)) (ygia_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2959 ECOLI_2959 Escherichia coli 562
10054113

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860367	12120	34276	516	171

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860373	12121	34277	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860382	12122	34278	1290	429

Description

6500731860 ygib:b3037 hypothetical 24.9 kd protein in tolC-ribB/htrp intergenic region:hypothetical 24.9 kd protein in tolC-ribB intergenic region:orfD:o234 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3037 b3037 Escherichia coli 562 -11535718 112386 ygib (de:o234) (db:swissprot) YGIB_ECOLI P24195 ESCHERICHIA COLI 562 -11535718 163539 ygib hypothetical protein d (db:pir2.dat) S22360 S22360 Escherichia coli 562 -11535718 239251 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli luxh gene, complete cds; orfA-orfD, complete cds.) (nt:orfD) (le:118) (re:822) (di:direct) ECOLUXH M77129 g146677 Escherichia coli 562 -11535718 7500924251 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o234; alternate name ygib; orfD of m77129) (le:134099) (re:134803) (di:direct) ECU28377 U28377 g882567 Escherichia coli 562 -11535718 235025 ygib orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 275 of 400 of the complete genome.) (nt:o234; 100 pct identical to ygib_ecoli sw: p24195) (le:7371) (re:8075) (di:direct) AE000385 AE000385 g1789415 Escherichia coli 562 -11535718 5000693330 (de:(ecoli_2960) (pn:hypothetical 24) (gn:ygib) (gtcfc:13.7:14.1) (ec:) (ygib_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2960 ECOLI_2960 Escherichia coli 562 10054114

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501860386	12123	34279	375	124

Description

6500731861 ygic:b3038 hypothetical 45.0 kd protein in tolC-ribB/htrP intergenic region:hypothetical 45.0 kd protein in tolC-ribB intergenic region:orfa:o386 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3038 b3038 Escherichia coli 562 -11535719 112387 ygic (de:(o386)) (db:swissprot) YGIC_ECOLI P24196 ESCHERICHIA COLI 562 -11535719 163526 ygic hypothetical protein a (cl:conserved hypothetical protein hi0929) (db:pir2.dat) S22361 S22361 Escherichia coli 562 -11535719 239252 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli luxH gene, complete cds; orfa-orfd, complete cds.) (nt:orfa) (le:828) (re:1988) (di:direct) ECOLUXH M77129 g146678 Escherichia coli 562 -11535719 7500924252 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o386; alternate name ygic; orfa of m77129) (le:134809) (re:135969) (di:direct) ECU28377 U28377 g882568 Escherichia coli 562 -11535719 235026 ygic putative synthetase/amidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 275 of 400 of the completegenome.) (nt:o386; 100 pct identical to ygic_ecoli sw: p24196) (le:8081) (re:9241) (di:direct) AE000385 AE000385 g1789416 Escherichia coli 562 -11535719 5000693331 (de:(ecoli_2961) (pn:hypothetical 45) (gn:ygic) (gtcfc:13.7:14.1) (ec:) (ygic_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2961 ECOLI_2961 Escherichia coli 562 10054115

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501860389	12124	34280	360	119

Description

6500731862 ygie:b3040 hypothetical 26.5 kd protein in tolC-ribB/htrP intergenic region:hypothetical 26.5 kd protein in tolC-ribB intergenic region:orfb:o265 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3040 b3040 Escherichia coli 562 -11535720 112390 ygie (de:(o265)) (db:swissprot) YGIE_ECOLI P24198 ESCHERICHIA COLI 562 -11535720 163532 ygie gufa protein homolog (cl:gufa protein) (db:pir2.dat) S22363 S22363 Escherichia coli 562 -11535720 7500924255 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli luxH gene, complete cds; orfa-orfd, complete cds.) (nt:orfb) (le:2958) (re:3731) (di:direct) ECOLUXH M77129 g146680 Escherichia coli 562 -11535720 235028 ygie orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 276 of 400 of the completegenome.) (nt:o257; 100 pct identical to ygie_ecoli sw: p24198) (le:88) (re:861) (di:direct) AE000386 AE000386 g1789419 Escherichia coli 562 -11535720 5000693333 (de:(ecoli_2963) (pn:hypothetical 26) (gn:ygie) (gtcfc:13.7:14.1) (ec:) (ygie_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2963 ECOLI_2963 Escherichia coli 562 10054118

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860400	12125	34281	636	211

Description

5000693334 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3042 b3042 Escherichia coli 562 -11535721
7500952498 yqic (de:hypothetical 13.8 kd protein in ribb-glgs intergenic region) (db:swissprot) YQIC_ECOLI Q46868 ESCHERICHIA COLI 562 -11535721
7000691805 hypothetical protein b3042 (db:pir2.dat) H65091 H65091 Escherichia coli 562 -11535721 239256 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o116) (le:139168) (re:139518) (di:direct) ECU28377 U28377 g882572 Escherichia coli 562 -11535721 7500952500 b3042 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 276 of 400 of the completegenome.) (nt:o116; this 116 aa orf is 25 pct identical (2 gaps)) (le:2318) (re:2668) (di:direct) AE000386 AE000386 g1789421 Escherichia coli 562 -11535721 6500731863 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3042 b3042 Escherichia coli 562 -11535721

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860406	12126	34282	513	170

Description

6500731864 ygil:b3043 hypothetical fimbrial-like protein in ribb 5region:hypothetical fimbrial-like protein in ribb-glgs intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3043 b3043 Escherichia coli 562 -11535722 112398 ygil (de:fimbrial-like protein in ribb-glgs intergenic region precursor) (db:swissprot) YGIL_ECOLI P39834 ESCHERICHIA COLI 562 -11535722 7000687857 ygil hypothetical fimbrial-like protein in ribb 5region (cl:f7-2 fimbrial protein) (db:pir2.dat) A65092 A65092 Escherichia coli 562 -11535722 7500924259 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o183) (le:139802) (re:140353) (di:direct) ECU28377 U28377 g882573 Escherichia coli 562 -11535722 239257 ygil putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 276 of 400 of the completegenome.) (nt:o183; 97 pct identical to fragment ygil_ecoli) (le:2952) (re:3503) (di:direct) AE000386 AE000386 g1789422 Escherichia coli 562 -11535722 5000693335 (de:(ecoli_2966) (pn:hypothetical fimbrial-like protein in ribb 5"region:fragment) (gn:ygil) (gtcfc:13.7:14.1) (ec:) (ygil_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2966 ECOLI_2966 Escherichia coli 562 10123957

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860415	12127	34283	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860420	12128	34284	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860422	12129	34285	1188	395

Description

6500731865 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3046 b3046 Escherichia coli 562 -11535723
 7500952505 yqig (de:region precursor) (db:swissprot) YQIG_ECOLI P76655
 ESCHERICHIA COLI 562 -11535723 7000689492 outer membrane usher protein pmfc precursor (cl:outer membrane usher protein fimd) (db:pir2.dat) D65092 D65092
 Escherichia coli 562 -11535723 7500952507 yqig putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 276 of 400 of the completegenome.) (nt:o821; phage ecoli) (le:4938) (re:7403) (di:direct) AE000386 AE000386 g2367188
 Escherichia coli 562 -11535723

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860441	12130	34286	2223	740

Description

5000693337 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3047 b3047 Escherichia coli 562 -11535724
 7000688441 yqih (de:precursor) (db:swissprot) YQIH_ECOLI P77616 ESCHERICHIA COLI 562 -11535724 7000688442 hypothetical protein b3047 (cl:chaperone protein papd) (db:pir2.dat) E65092 E65092 Escherichia coli 562 -11535724
 225267 pmfd chaperone protein pmfd precursor. (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:e.coli genomic dna, 68.6-68.8 min.) (nt:similar to (swissprot accession number p53520)) (le:2517) (re:3275) (di:direct) D90897 D90897 g1805588 Escherichia coli 562 -11535724
 7500952509 yqih putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 276 of 400 of the completegenome.) (nt:o252; phage ecoli) (le:7410) (re:8168) (di:direct) AE000386 AE000386 g1789426 Escherichia coli 562 -11535724
 6500731866 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3047 b3047 Escherichia coli 562 -11535724

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860442	12131	34287	195	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860453	12132	34288	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860454	12133	34289	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860467	12134	34290	918	305

Description

5000693338 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3048 b3048 Escherichia coli 562 -11535725
7000688443 yqii (de:hypothetical 38.6 kd protein in ribb-glgs intergenic region precursor) (db:swissprot) YQII_ECOLI P76656 ESCHERICHIA COLI 562 -11535725 7000688444 hypothetical protein b3048 (cl:ybgo protein) (db:pir2.dat) F65092 F65092 Escherichia coli 562 -11535725 7500952510 yqii orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 276 of 400 of the completegenome.) (nt:o354; phage ecoli) (le:8170) (re:9234) (di:direct) AE000386 AE000386 g1789427 Escherichia coli 562 -11535725 6500731867 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3048 b3048 Escherichia coli 562 -11535725

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860476	12135	34291	528	176

Description

5000693339 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3050 b3050 Escherichia coli 562 -11535726
 7000691806 hypothetical protein b3050 (db:pir2.dat) H65092 H65092 Escherichia coli 562 -11535726 7500960311 b3050 putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 276 of 400 of the completegenome.) (nt:o209; phage ecoli) (le:9746) (re:10375) (di:direct) AE000386 AE000386 g1789429 Escherichia coli 562 -11535726 6500731868 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3050 b3050 Escherichia coli 562 -11535726

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860478	12136	34292	1170	389

Description

5000693340 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3051 b3051 Escherichia coli 562 -11535727
 7502852278 yqik (de:hypothetical 60.7 kd protein in glgs-waae intergenic region) (db:swissprot) YQIK_ECOLI P77306 ESCHERICHIA COLI 562 -11535727
 7000691807 hypothetical protein b3051 (db:pir2.dat) A65093 A65093 Escherichia coli 562 -11535727 225269 caldesmon:smooth muscle cad . (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:e.coli genomic dna, 68.6-68.8 min.) (nt:similar to (swissprot accession number p12957)) (le:5510) (re:7171) (di:direct) D90897 D90897 g1805590 Escherichia coli 562 -11535727 7500960312 b3051 putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 276 of 400 of the completegenome.) (nt:o553; phage ecoli) (le:10402) (re:12063) (di:direct) AE000386 AE000386 g1789430 Escherichia coli 562 -11535727 6500731869 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3051 b3051 Escherichia coli 562 -11535727

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860484	12137	34293	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860485	12138	34294	465	154

Description

5000693341 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3052 b3052 Escherichia coli 562 -11535728
7000689488 adp-heptose synthase homolog:hypothetical protein b3052 (cl:hypothetical protein b3052) (db:pir2.dat) B65093 B65093 Escherichia coli 562 -11535728 7500955789 b3052 putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 277 of 400 of the completegenome.) (nt:f477) (le:240) (re:1673) (di:complement) AE000387 AE000387 g1789432 Escherichia coli 562 -11535728 6500731870 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3052 b3052 Escherichia coli 562 -11535728

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860493	12139	34295	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860494	12140	34296	447	148

Description

6500731871 ygim:b3055 hypothetical protein in glne-cca intergenic region:fragment:hypothetical 23.1 kd protein in glne-cca intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3055 b3055 Escherichia coli 562 -11535729 112399 ygim (de:hypothetical 23.1 kd protein in glne-cca intergenic region precursor) (db:swissprot) YGIM_ECOLI P39202 ESCHERICHIA COLI 562 -11535729 7000687858 ygim hypothetical protein in glne-cca intergenic region (cl:hypothetical protein hi1605) (db:pir2.dat) E65093 E65093 Escherichia coli 562 -11535729 7500924260 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:alternate name ygim; orf_o206) (le:6002) (re:6622) (di:direct) ECU28379 U28379 g1203798 Escherichia coli 562 -11535729 239260 ygim orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 277 of 400 of the completegenome.) (nt:o206; 100 pct identical to 127 amino acids of) (le:6127) (re:6747) (di:direct) AE000387 AE000387 g1789435 Escherichia coli 562 -11535729 5000693343 (de:(ecoli_2978) (pn:hypothetical 23) (gn:ygim) (gtcfc:13.7:14.1) (ec:) (ygim_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2978 ECOLI_2978 Escherichia coli 562 10054127

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860495	12141	34297	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860520	12142	34298	807	269

Description

GTC ORF with score 254 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f53f10.) (nt:similar to nucleoporins; coded for by c. elegans) (le:2756:2915:3079:4609) (re:2867:3007:4558:5079) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860539	12143	34299	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860542	12144	34300	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860545	12145	34301	762	253

Description

6500731872 ygip:b3060 hypothetical protein:hypothetical transcriptional regulator in baca-ttda intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3060 b3060 Escherichia coli 562 -11535730 112402 ygip (de:hypothetical transcriptional regulator in baca-ttda intergenic region) (db:swissprot) YGIP_ECOLI P45463 ESCHERICHIA COLI 562 -11535730 7000687860 hypothetical protein b3060 (cl:conserved hypothetical protein h11364) (db:pir2.dat) B65094 B65094 Escherichia coli 562 -11535730 7500924263 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:alternate name ygip; orf_310) (le:10119) (re:11051) (di:complement) ECU28379 U28379 g1203799 Escherichia coli 562 -11535730 239265 ygip putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 277 of 400 of the completegenome.) (nt:f310; this 310 aa orf is 28 pct identical (4 gaps)) (le:10244) (re:11176) (di:complement) AE000387 AE000387 g1789440 Escherichia coli 562 -11535730 5000693346 (de:(ecoli_2983) (pn:hypothetical transcriptional regulator in baca-ttda intergenic region:f161) (gtcfc:13.7:14.1) (ec:) (ygip_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2983 ECOLI_2983 Escherichia coli 562 10054130

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860563	12146	34302	306	101

Description

6500731873 ygjd:b3064 hypothetical 36.0 kd protein in ttdd-rpsu intergenic region:orf-x:f337 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3064 b3064 Escherichia coli 562 -11535731 7000688995 ygjd o-sialoglycoprotein endopeptidase (cl:o-sialoglycoprotein endopeptidase) (ec:3.4.24.57) (db:pir1.dat) (mp:67 min) QQECR6 F65094 Escherichia coli 562 -11535731 7500953699 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:orf_f337) (le:14325) (re:15338) (di:complement) ECU28379 U28379 g882587 Escherichia coli 562 -11535731 239269 ygjd putative o-sialoglycoprotein endopeptidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 278 of 400 of the completegenome.) (nt:f337; 99 pct identical amino acid sequence and) (le:3201) (re:4214) (di:complement) AE000388 AE000388 g1789445 Escherichia coli 562 -11535731 5000693348 (de:(ecoli_2987) (pn:hypothetical 36) (gn:ygjd) (gtcfc:13.7:14.1) (ec:) (ygjd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2987 ECOLI_2987 Escherichia coli 562 10123967

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860566	12147	34303	804	267

Description

6500731874 ygjf:b3068 hypothetical protein:hypothetical 18.7 kd protein in rpod-ilex intergenic region:f168 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3068 b3068 Escherichia coli 562 -11535732 112418 mug (ec:3.2.2.-) (de:uracil dna-glycosylase) (udg)) (db:swissprot) MUG_ECOLI P43342 ESCHERICHIA COLI 562 -11535732 7000687867 hypothetical protein b3068 (db:pir2.dat) B65095 B65095 Escherichia coli 562 -11535732 7500924294 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:orf_f168) (le:19762) (re:20268) (di:complement) ECU28379 U28379 g882591 Escherichia coli 562 -11535732 239273 ygjf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 278 of 400 of the completegenome.) (nt:f168; this 168 aa orf is 63 pct identical (0 gaps)) (le:8638) (re:9144) (di:complement) AE000388 AE000388 g1789449 Escherichia coli 562 -11535732 5000693349 (de:(ecoli_2991) (pn:hypothetical 18) (gtcfc:13.7:14.1) (ec:)) (ygjf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2991 ECOLI_2991 Escherichia coli 562 10054146

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860576	12148	34304	528	175

Description

5000693350 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3070 b3070 Escherichia coli 562 -11535733 7000688465 yqjh (de:hypothetical 28.9 kd protein in rpod-aer intergenic region) (db:swissprot) YQJH_ECOLI Q46871 ESCHERICHIA COLI 562 -11535733 7000688466 hypothetical protein b3070 (db:pir2.dat) C65095 C65095 Escherichia coli 562 -11535733 7500952534 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:orf_f254) (le:20522) (re:21286) (di:complement) ECU28379 U28379 g882592 Escherichia coli 562 -11535733 239274 yqjh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 278 of 400 of the completegenome.) (nt:f254; this 254 aa orf is 24 pct identical (5 gaps)) (le:9398) (re:10162) (di:complement) AE000388 AE000388 g1789450 Escherichia coli 562 -11535733 6500731875 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3070 b3070 Escherichia coli 562 -11535733

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860585	12149	34305	294	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860587	12150	34306	561	186

Description

5000693351 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3071 b3071 Escherichia coli 562 -11535734
7000688468 yqji (de:hypothetical 23.4 kd protein in rpod-aer intergenic region) (db:swissprot) YQJI_ECOLI Q46872 ESCHERICHIA COLI 562 -11535734
7000688469 hypothetical protein b3071 (db:pir2.dat) D65095 D65095 Escherichia coli 562 -11535734 7500952536 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:orf_o207) (le:21574) (re:22197) (di:direct) ECU28379 U28379 g882593 Escherichia coli 562 -11535734 239275 yqji orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 279 of 400 of the complete genome.) (nt:o207; this 207 aa orf is 42 pct identical (7 gaps)) (le:174) (re:797) (di:direct) AE000389 AE000389 g1789452 Escherichia coli 562 -11535734 6500731876 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3071 b3071 Escherichia coli 562 -11535734

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860593	12151	34307	351	116

Description

GTC ORF with score 195 to: (sr:yeast (s.cerevisiae; strain ab320) germline dna) (db:genpept-pln1) (de:yeast (s.cerevisiae) sec18 gene encoding the process of secretory protein transport between endoplasmic reticulum and the golgi complex, complete cds.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860594	12152	34308	1092	363

Description

6500731877 ygji:b3078 hypothetical 52.1 kd protein in ebgc-exut intergenic region:hypothetical 52.1 kd protein in ebgc-uxaa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3078 b3078 Escherichia coli 562 -11535735 112421 ygji (de:hypothetical 52.1 kd protein in ebgc-uxaa intergenic region) (db:swissprot) YGJI_ECOLI P42590 ESCHERICHIA COLI 562 -11535735 7000687869 ygji hypothetical 52.1 kd protein in ebgc-exut intergenic region (db:pir2.dat) C65096 C65096 Escherichia coli 562 -11535735 7500924296 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o477) (le:6987) (re:8420) (di:direct) ECOUW67 U18997 g606016 Escherichia coli 562 -11535735 236315 ygji putative oxidoreductase (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 279 of 400 of the completegenome.) (nt:100 pct identical amino acid sequence and equal) (le:9629) (re:11062) (di:direct) AE000389 AE000389 g1789459 Escherichia coli 562 -11535735 5000693353 (de:(ecoli_3000) (pn:hypothetical 52) (gn:ygji) (gtcfc:13.7:14.1) (ec:) (ygji_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3000 ECOLI_3000 Escherichia coli 562 10054149

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860598	12153	34309	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860599	12154	34310	618	205

Description

GTC ORF with score 450 to: (sr:yeast (s.cerevisiae; strain ab320) germline dna) (db:genpept-pln1) (de:yeast (s.cerevisiae) sec18 gene encoding the process of secretoryprotein transport between endoplasmic reticulum and the golgicomplex, complete cds.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860615	12155	34311	324	107

Description

6500731878 ygjj:b3079 hypothetical 40.1 kd protein in ebgc-exut intergenic region:hypothetical 40.1 kd protein in ebgc-uxaa intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3079 b3079 Escherichia coli 562 -11535736 112422 ygjj (de:hypothetical 40.1 kd protein in ebgc-uxaa intergenic region precursor) (db:swissprot) YGJJ_ECOLI P42591 ESCHERICHIA COLI 562 -11535736 7000687870 ygjj hypothetical 40.1 kd protein in ebgc-exut intergenic region (db:pir2.dat) D65096 D65096 Escherichia coli 562 -11535736 7500924297 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o356) (le:8554) (re:9624) (di:direct) ECOUW67 U18997 g606017 Escherichia coli 562 -11535736 236316 ygjj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 280 of 400 of the completegenome.) (nt:o356; 100 pct identical amino acid sequence and) (le:97) (re:1167) (di:direct) AE000390 AE000390 g1789461 Escherichia coli 562 -11535736 5000693354 (de:(ecoli_3001) (pn:hypothetical 40) (gn:ygjj) (gtcfc:13.7:14.1) (ec:) (ygjj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3001 ECOLI_3001 Escherichia coli 562 10054150

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860616	12156	34312	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860617	12157	34313	198	65

Description

6500731879 ygjk:b3080 hypothetical 88.3 kd protein in ebgc-exut intergenic region:hypothetical 88.3 kd protein in ebgc-uxaa intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3080 b3080 Escherichia coli 562 -11535737 112423 ygjk (de:hypothetical 88.3 kd protein in ebgc-uxaa intergenic region precursor) (db:swissprot) YGJK_ECOLI P42592 ESCHERICHIA COLI 562 -11535737 7000687871 ygjk hypothetical 88.3 kd protein in ebgc-exut intergenic region (db:pir2.dat) E65096 E65096 Escherichia coli 562 -11535737 7500924298 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o783) (le:9641) (re:11992) (di:direct) ECOUW67 U18997 g606018 Escherichia coli 562 -11535737 236317 ygjk putative isomerase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 280 of 400 of the completegenome.) (nt:o783; 100 pct identical amino acid sequence and) (le:1184) (re:3535) (di:direct) AE000390 AE000390 g1789462 Escherichia coli 562 -11535737 5000693355 (de:(ecoli_3002) (pn:hypothetical 88) (gn:ygjk) (gtcfc:13.7:14.1) (ec:) (ygjk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3002 ECOLI_3002 Escherichia coli 562 10054151

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860619	12158	34314	588	196

Description

6500731880 ygjm:b3082 hypothetical 15.0 kd protein in ebgc-exut intergenic region:hypothetical 15.0 kd protein in ebgc-uxaa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3082 b3082 Escherichia coli 562 -11535738 112425 ygjm (de:hypothetical 15.0 kd protein in ebgc-uxaa intergenic region) (db:swissprot) YGJM_ECOLI P42594 ESCHERICHIA COLI 562 -11535738 7000687873 ygjm hypothetical 15.0 kd protein in ebgc-exut intergenic region (db:pir2.dat) G65096 G65096 Escherichia coli 562 -11535738 7500924299 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f138) (le:14479) (re:14895) (di:complement) ECOUW67 U18997 g606020 Escherichia coli 562 -11535738 236319 ygjm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 280 of the completegenome.) (nt:f138; 100 pct identical amino acid sequence and) (le:6024) (re:6440) (di:complement) AE000390 AE000390 g1789464 Escherichia coli 562 -11535738 5000693357 (de:(ecoli_3004) (pn:hypothetical 15) (gn:ygjm) (gtcfc:13.7:14.1) (ec:) (ygjm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3004 ECOLI_3004 Escherichia coli 562 10054153

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860620	12159	34315	423	140

Description

6500731881 ygjn:b3083 hypothetical 12.1 kd protein in ebgc-exut intergenic region:hypothetical 12.1 kd protein in ebgc-uxaa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3083 b3083 Escherichia coli 562 -11535739 112426 ygjn (de:hypothetical 12.1 kd protein in ebgc-uxaa intergenic region) (db:swissprot) YGJN_ECOLI P42595 ESCHERICHIA COLI 562 -11535739 7000687874 ygjn hypothetical 12.1 kd protein in ebgc-exut intergenic region (db:pir2.dat) H65096 H65096 Escherichia coli 562 -11535739 7500924300 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f104) (le:14892) (re:15206) (di:complement) ECOUW67 U18997 g606021 Escherichia coli 562 -11535739 236320 ygjn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 280 of 400 of the completegenome.) (nt:f104; 100 pct identical amino acid sequence and) (le:6437) (re:6751) (di:complement) AE000390 AE000390 g1789465 Escherichia coli 562 -11535739 5000693358 (de:(ecoli_3005) (pn:hypothetical 12) (gn:ygjn) (gtcfc:13.7:14.1) (ec:) (ygjn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3005 ECOLI_3005 Escherichia coli 562 10054154

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860622	12160	34316	474	157

Description

6500731882 ygjo:b3084 hypothetical 43.4 kd protein in ebgc-exut intergenic region:hypothetical 43.4 kd protein in ebgc-uxaa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3084 b3084 Escherichia coli 562 -11535740 112427 ygjo (de:hypothetical 43.4 kd protein in ebgc-uxaa intergenic region) (db:swissprot) YGJO_ECOLI P42596 ESCHERICHIA COLI 562 -11535740 7000687875 ygjo hypothetical 43.4 kd protein in ebgc-exut intergenic region (db:pir2.dat) A65097 A65097 Escherichia coli 562 -11535740 7500924301 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f388) (le:15490) (re:16656) (di:complement) ECOUW67 U18997 g606022 Escherichia coli 562 -11535740 236321 ygjo putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 280 of 400 of the completegenome.) (nt:f388; 100 pct identical amino acid sequence and) (le:7035) (re:8201) (di:complement) AE000390 AE000390 g1789466 Escherichia coli 562 -11535740 5000693359 (de:(ecoli_3006) (pn:hypothetical 43) (gn:ygjo) (gtcfc:13.7:14.1) (ec:) (ygjo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3006 ECOLI_3006 Escherichia coli 562 10054155

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860624	12161	34317	276	91
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860636	12162	34318	510	169
<u>Description</u>				

6500731883 ygjp:b3085 hypothetical 20.9 kd protein in ebgc-exut intergenic region:hypothetical 20.9 kd protein in ebgc-uxaa intergenic region:o179 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3085 b3085 Escherichia coli 562 -11535741 112428 ygjp (de:hypothetical 20.9 kd protein in ebgc-uxaa intergenic region (o179)) (db:swissprot) YGJP_ECOLI P42597 ESCHERICHIA COLI 562 -11535741 7000687876 ygjp hypothetical 20.9 kd protein in ebgc-exut intergenic region (db:pir2.dat) B65097 B65097 Escherichia coli 562 -11535741 7500924302 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o179) (le:16675) (re:17214) (di:direct) ECOUW67 U18997 g606023 Escherichia coli 562 -11535741 236322 ygjp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 280 of 400 of the completegenome.) (nt:o179; 100 pct identical amino acid sequence and) (le:8220) (re:8759) (di:direct) AE000390 AE000390 g1789467 Escherichia coli 562 -11535741 5000693360 (de:(ecoli_3007) (pn:hypothetical 20) (gn:ygjp) (gtcfc:13.7:14.1) (ec:) (ygjp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3007 ECOLI_3007 Escherichia coli 562 10054156

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860646	12163	34319	945	314

Description

6500731884 ygjq:b3086 hypothetical 25.5 kd protein in ebgc-exut intergenic region:hypothetical 25.5 kd protein in ebgc-uxaa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3086 b3086 Escherichia coli 562 -11535742 112429 ygjq (de:hypothetical 25.5 kd protein in ebgc-uxaa intergenic region) (db:swissprot) YGJQ_ECOLI P42598 ESCHERICHIA COLI 562 -11535742 7000687877 ygjq hypothetical 25.5 kd protein in ebgc-exut intergenic region (cl:conserved hypothetical protein h1262) (db:pir2.dat) C65097 C65097 Escherichia coli 562 -11535742 7500924303 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o230) (le:17291) (re:17983) (di:direct) ECOUW67 U18997 g606024 Escherichia coli 562 -11535742 236323 ygjq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 280 of 400 of the completegenome.) (nt:o230; 100 pct identical amino acid sequence and) (le:8836) (re:9528) (di:direct) AE000390 AE000390 g1789468 Escherichia coli 562 -11535742 5000693361 (de:(ecoli_3008) (pn:hypothetical 25) (gn:ygjq) (gtcfc:13.7:14.1) (ec:) (ygjq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3008 ECOLI_3008 Escherichia coli 562 10054157

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860649	12164	34320	501	166

Description

6500731885 ygjt:b3088 hypothetical 35.8 kd protein in ebgc-exut intergenic region:hypothetical 35.8 kd protein in ebgc-uxaa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3088 b3088 Escherichia coli 562 -11535743 112432 ygjt (de:hypothetical 35.8 kd protein in ebgc-uxaa intergenic region) (db:swissprot) YGJT_ECOLI P42601 ESCHERICHIA COLI 562 -11535743 7000687878 ygjt hypothetical 35.8 kd protein in ebgc-exut intergenic region (db:pir2.dat) E65097 E65097 Escherichia coli 562 -11535743 7500924307 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o321) (le:19331) (re:20296) (di:direct) ECOUW67 U18997 g606027 Escherichia coli 562 -11535743 236326 ygjt putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 281 of 400 of the completegenome.) (nt:o321; 100 pct identical amino acid sequence and) (le:172) (re:1137) (di:direct) AE000391 AE000391 g1789472 Escherichia coli 562 -11535743 5000693364 (de:(ecoli_3011) (pn:hypothetical 35) (gn:ygjt) (gtcfc:13.7:14.1) (ec:) (ygjt_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3011 ECOLI_3011 Escherichia coli 562 10054160

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860656	12165	34321	315	104

Description

6500731886 ygju:b3089 hypothetical 43.5 kd protein in ebgc-exut intergenic region:hypothetical 43.5 kd protein in ebgc-uxaa intergenic region:o414 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3089 b3089 Escherichia coli 562 -11535744 112433 ygju (de:hypothetical 43.5 kd protein in ebgc-uxaa intergenic region (o414)) (db:swissprot) YGJU_ECOLI P42602 ESCHERICHIA COLI 562 -11535744 7000687879 ygju hypothetical 43.5 kd protein in ebgc-exut intergenic region (db:pir2.dat) F65097 F65097 Escherichia coli 562 -11535744 7500924308 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o414; geneplot suggests frameshift near start) (le:20693) (re:21937) (di:direct) ECOUW67 U18997 g606028 Escherichia coli 562 -11535744 236327 ygju putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 281 of 400 of the completegenome.) (nt:o414; o414; geneplot suggests frameshift near start) (le:1534) (re:2778) (di:direct) AE000391 AE000391 g1789473 Escherichia coli 562 -11535744 5000693365 (de:(ecoli_3012) (pn:hypothetical 43) (gn:ygju) (gtcfc:13.7:14.1) (ec:) (ygju_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3012 ECOLI_3012 Escherichia coli 562 10054161

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860668	12166	34322	1548	515

Description

6500731887 ygjv:b3090 hypothetical 20.5 kd protein in ebgc-exut intergenic region:hypothetical 20.5 kd protein in ebgc-uxaa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3090 b3090 Escherichia coli 562 -11535745 112435 ygjv (de:hypothetical 20.5 kd protein in ebgc-uxaa intergenic region) (db:swissprot) YGJV_ECOLI P42603 ESCHERICHIA COLI 562 -11535745 7000687880 ygjv hypothetical 20.5 kd protein in ebgc-exut intergenic region (db:pir2.dat) G65097 G65097 Escherichia coli 562 -11535745 7500924310 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f183) (le:21942) (re:22493) (di:complement) ECOUW67 U18997 g606029 Escherichia coli 562 -11535745 236328 ygjv orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 281 of 400 of the completegenome.) (nt:f183; 100 pct identical amino acid sequence and) (le:2783) (re:3334) (di:complement) AE000391 AE000391 g1789474 Escherichia coli 562 -11535745 5000693366 (de:(ecoli_3013) (pn:hypothetical 20) (gn:ygjv) (gtcfc:13.7:14.1) (ec:) (ygjv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3013 ECOLI_3013 Escherichia coli 562 10054163

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860675	12167	34323	363	120

Description

6500731888 yqja:b3095 hypothetical protein:hypothetical 24.6 kd protein in exur-tdcc intergenic region:o220 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3095 b3095 Escherichia coli 562 -11535746 115970 yqja (de:hypothetical 24.6 kd protein in exur-tdcc intergenic region) (db:swissprot) YQJA_ECOLI P42614 ESCHERICHIA COLI 562 -11535746 7000688453 hypothetical protein b3095 (cl:deda protein) (db:pir2.dat) D65098 D65098 Escherichia coli 562 -11535746 7500952519 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o220) (le:28525) (re:29187) (di:direct) ECOUW67 U18997 g606036 Escherichia coli 562 -11535746 236335 yqja orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 281 of 400 of the completegenome.) (nt:o220) (le:9363) (re:10025) (di:direct) AE000391 AE000391 g1789481 Escherichia coli 562 -11535746 5000693369 (de:(ecoli_3020) (pn:hypothetical 24) (gtcfc:13.7:14.1) (ec:)) (yqja_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3020 ECOLI_3020 Escherichia coli 562 10057696

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860694	12168	34324	1428	475

Description

6500731889 yqjb:b3096 hypothetical 14.2 kd protein in exur-tdcc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3096 b3096 Escherichia coli 562 -11535747 115972 yqjb (de:hypothetical 14.2 kd protein in exur-tdcc intergenic region) (db:swissprot) YQJB_ECOLI P42615 ESCHERICHIA COLI 562 -11535747 7000688455 yqjb hypothetical 14.2 kd protein in exur-tdcc intergenic region (db:pir2.dat) E65098 E65098 Escherichia coli 562 -11535747 7500952521 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o127a) (le:29191) (re:29574) (di:direct) ECOUW67 U18997 g606037 Escherichia coli 562 -11535747 236336 yqjb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 281 of 400 of the completegenome.) (nt:o127; 100 pct identical amino acid sequence and) (le:10029) (re:10412) (di:direct) AE000391 AE000391 g1789482 Escherichia coli 562 -11535747 5000693370 (de:(ecoli_3021) (pn:hypothetical 14) (gn:yqjb) (gtcfc:13.7:14.1) (ec:)) (yqjb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3021 ECOLI_3021 Escherichia coli 562 10057698

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860701	12169	34325	528	176

Description

6500731890 yqjc:b3097 hypothetical 14.5 kd protein in exur-tdcc intergenic region:hypothetical 14.5 kd protein in exur-tdcc intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3097 b3097 Escherichia coli 562 -11535748 7500952523 yqjc (de:hypothetical 14.5 kd protein in exur-tdcc intergenic region precursor) (db:swissprot) YQJC_ECOLI P42616 ESCHERICHIA COLI 562 -11535748 7000690917 yqjc hypothetical 14.5 kd protein in exur-tdcc intergenic region (db:pir2.dat) F65098 F65098 Escherichia coli 562 -11535748 7500952525 yqjc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:o127; 99 pct identical amino acid sequence and) (le:96) (re:479) (di:direct) AE000392 AE000392 g2367195 Escherichia coli 562 -11535748

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860714	12170	34326	1032	343

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860740	12171	34327	804	267

Description

6500731891 yqjd:b3098 hypothetical 11.1 kd protein in exur-tdcc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3098 b3098 Escherichia coli 562 -11535749 115975 yqjd (de:hypothetical 11.1 kd protein in exur-tdcc intergenic region) (db:swissprot) YQJD_ECOLI P42617 ESCHERICHIA COLI 562 -11535749 7000688457 yqjd hypothetical 11.1 kd protein in exur-tdcc intergenic region (cl:conserved hypothetical protein b2672) (db:pir2.dat) G65098 G65098 Escherichia coli 562 -11535749 7500952526 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o101) (le:30127) (re:30432) (di:direct) ECOUW67 U18997 g606039 Escherichia coli 562 -11535749 236338 yqjd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:o101; 100 pct identical to yqjd_ecoli sw: p42617) (le:517) (re:822) (di:direct) AE000392 AE000392 g1789485 Escherichia coli 562 -11535749 5000693372 (de:(ecoli_3023) (pn:hypothetical 11) (gn:yqjd) (gtcfc:13.7:14.1) (ec:)) (yqjd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3023 ECOLI_3023 Escherichia coli 562 10057701

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860743	12172	34328	738	245

Description

6500731892 yqje:b3099 hypothetical 15.1 kd protein in exur-tdcc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3099 b3099 Escherichia coli 562 -11535750 115977 yqje (de:hypothetical 15.1 kd protein in exur-tdcc intergenic region) (db:swissprot) YQJE_ECOLI P42618 ESCHERICHIA COLI 562 -11535750 7000688459 yqje hypothetical 15.1 kd protein in exur-tdcc intergenic region (db:pir2.dat) H65098 H65098 Escherichia coli 562 -11535750 7500952528 yqje orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:o134; 100 pct identical to yqje_ecoli sw: p42618) (le:825) (re:1229) (di:direct) AE000392 AE000392 g1789486 Escherichia coli 562 -11535750 5000693373 (de:(ecoli_3024) (pn:hypothetical 15) (gn:yqje) (gtcfc:13.7:14.1) (ec:) (yqje_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3024 ECOLI_3024 Escherichia coli 562 10057703

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860754	12173	34329	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860756	12174	34330	306	101

Description

5000693374 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3100 b3100 Escherichia coli 562 -11535751 7500952538 yqjk (de:hypothetical 11.8 kd protein in exur-tdce intergenic region) (db:swissprot) YQJK_ECOLI Q47710 ESCHERICHIA COLI 562 -11535751 7000691808 hypothetical protein b3100 (db:pir2.dat) A65099 A65099 Escherichia coli 562 -11535751 236340 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o99; 8 base overlap with o157) (le:30829) (re:31128) (di:direct) ECUW67 U18997 g606041 Escherichia coli 562 -11535751 7500952540 b3100 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:o99; 32 pct identical to 46 residues from) (le:1219) (re:1518) (di:direct) AE000392 AE000392 g1789487 Escherichia coli 562 -11535751 6500731893 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3100 b3100 Escherichia coli 562 -11535751

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860765	12175	34331	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860768	12176	34332	723	240

Description

6500731894 yqjf:b3101 hypothetical 17.2 kd protein in exur-tdcc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3101 b3101 Escherichia coli 562 -11535752 115979 yqjf (de:hypothetical 17.2 kd protein in exur-tdcc intergenic region) (db:swissprot) YQJF_ECOLI P42619 ESCHERICHIA COLI 562 -11535752 7000688461 yqjf hypothetical 17.2 kd protein in exur-tdcc intergenic region (db:pir2.dat) B65099 B65099 Escherichia coli 562 -11535752 7500952530 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o160) (le:31224) (re:31706) (di:direct) ECOUW67 U18997 g606042 Escherichia coli 562 -11535752 236341 yqjf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:o160; 100 pct identical amino acid sequence and) (le:1614) (re:2096) (di:direct) AE000392 AE000392 g1789488 Escherichia coli 562 -11535752 5000693375 (de:(ecoli_3026) (pn:hypothetical 17) (gn:yqjf) (gtcfc:13.7:14.1) (ec:) (yqjf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3026 ECOLI_3026 Escherichia coli 562 10057705

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860772	12177	34333	666	222

Description

6500731895 yqjg:b3102 hypothetical 37.4 kd protein in exur-tdcc intergenic region:o328 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3102 b3102 Escherichia coli 562 -11535753 115981 yqjg (de:hypothetical 37.4 kd protein in exur-tdcc intergenic region (o328)) (db:swissprot) YQJG_ECOLI P42620 ESCHERICHIA COLI 562 -11535753 7000688463 yqjg hypothetical 37.4 kd protein in exur-tdcc intergenic region (db:pir2.dat) C65099 C65099 Escherichia coli 562 -11535753 7500952532 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o328) (le:31776) (re:32762) (di:direct) ECOUW67 U18997 g606043 Escherichia coli 562 -11535753 236342 yqjg putative transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:o328; 100 pct identical amino acid sequence and) (le:2166) (re:3152) (di:direct) AE000392 AE000392 g1789489 Escherichia coli 562 -11535753 5000693376 (de:(ecoli_3027) (pn:hypothetical 37) (gn:yqjg) (gtcfc:13.7:14.1) (ec:) (yqjg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3027 ECOLI_3027 Escherichia coli 562 10057707

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860779	12178	34334	411	136

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860783	12179	34335	666	221

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860787	12180	34336	726	241

Description

GTC ORF with score 164 to: (sr:pyrococcus horikoshii (strain:ot3) dna, clone:pyrococcus horikoshi) (db:genpept-bct2) (de:pyrococcus horikoshii ot3 genomic dna, 1166001-1485000 nt. position(6/7).) (nt:similar to pir:d64479 percent identity: 46.396 in) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860798	12181	34337	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860802	12182	34338	693	230

Description

6500731896 yah:b3103 hypothetical 14.3 kd protein in exur-tdcc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3103 b3103 Escherichia coli 562 -11535754 112611 yah (de:hypothetical 14.3 kd protein in exur-tdcc intergenic region) (db:swissprot) YHAH_ECOLI P42621 ESCHERICHIA COLI 562 -11535754 7000687886 yah hypothetical 14.3 kd protein in exur-tdcc intergenic region (db:pir2.dat) D65099 D65099 Escherichia coli 562 -11535754 7500936745 yah putative cytochrome (fn:putative carrier; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:o121; c-terminal differs from earlier version) (le:3446) (re:3811) (di:direct) AE000392 AE000392 g2367196 Escherichia coli 562 -11535754

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860810	12183	34339	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860814	12184	34340	666	221

Description

GTC ORF with score 437 to: (gtcfc:12.5:11.1) (keggfc:14.2) (sgdfc:1.2.3:7.2.2:8.7.0:9.1.0:17.0.0) (db:gtc-saccharomyces cerevisiae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_):cell envelope-membrane proteins--porins--and lipoproteins)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860816	12185	34341	408	135

Description

6500731897 yhai:b3104 hypothetical 13.5 kd protein in exur-tdcc intergenic region:o118 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3104 b3104 Escherichia coli 562 -11535755 112612 yhai (de:hypothetical 13.5 kd protein in exur-tdcc intergenic region) (db:swissprot) YHAI_ECOLI P42622 ESCHERICHIA COLI 562 -11535755 7000687887 yhai hypothetical 13.5 kd protein in exur-tdcc intergenic region (db:pir2.dat) E65099 E65099 Escherichia coli 562 -11535755 7500936746 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o118) (le:33664) (re:34020) (di:direct) ECOUW67 U18997 g606045 Escherichia coli 562 -11535755 236344 yhai putative cytochrome (fn:putative carrier; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:o118; 100 pct identical amino acid sequence and) (le:4053) (re:4409) (di:direct) AE000392 AE000392 g1789491 Escherichia coli 562 -11535755 5000693378 (de:(ecoli_3029) (pn:hypothetical 13) (gn:yhai) (gtcfc:13.7:14.1) (ec:) (yhai_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3029 ECOLI_3029 Escherichia coli 562 10054340

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860817	12186	34342	648	215

Description

GTC ORF with score 628 to: (gtcfc:12.5:11.1) (keggfc:14.2) (sgdgc:1.2.3:7.2.2:8.7.0:9.1.0:17.0.0) (db:gtc-saccharomyces cerevisiae) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_):cell envelope-membrane proteins--porins--and lipoproteins)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860819	12187	34343	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860820	12188	34344	501	166

Description

GTC ORF with score 319 to: (sr:sphingomonas paucimobilis tmy1009) (db:genpept-bct2) (de:lignostilbene-alpha,beta-dioxygenase (pseudomonas paucimobilis,tmy1009, genomic, 1914 nt).) (nt:method: conceptual translation with partial peptide) (le:251) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860827	12189	34345	675	224

Description

6500731898 yhaj:b3105 hypothetical transcriptional regulator in exur-tdcc intergenic region:hypothetical transcriptional regulator in exur-tdcc intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3105 b3105 Escherichia coli 562 -11535756 112613 yhaj (de:hypothetical transcriptional regulator in exur-tdcc intergenic region) (db:swissprot) YHAJ_ECOLI P42623 ESCHERICHIA COLI 562 -11535756 7000687888 yhaj hypothetical transcription regulator exur-tdcc intergenic region (cl:hypothetical protein b2015) (db:pir2.dat) F65099 F65099 Escherichia coli 562 -11535756 7500936747 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f298) (le:34071) (re:34967) (di:complement) ECOUW67 U18997 g606046 Escherichia coli 562 -11535756 236345 yhaj putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:f298; 100 pct identical amino acid sequence and) (le:4460) (re:5356) (di:complement) AE000392 AE000392 g1789492 Escherichia coli 562 -11535756 5000693379 (de:(ecoli_3030) (pn:hypothetical transcriptional regulator in exur-tdcc intergenic region:f298) (gn:yhaj) (gtcfc:13.7:14.1) (ec:) (yhaj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3030 ECOLI_3030 Escherichia coli 562 10054341

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860836	12190	34346	1245	414

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860841	12191	34347	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860855	12192	34348	1284	427

Description

GTC ORF with score 235 to: (fn:implicated involvement in chromatin regulated) (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c3g9.) (nt:spac3g9.08; len:283aa, similarity: to yhr090c,) (le:14516) (re:15367) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860866	12193	34349	537	178
<u>Description</u>				
6500731899 yhak:b3106 hypothetical 25.9 kd protein in exur-tdcc intergenic region:o233 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3106 b3106 Escherichia coli 562 -11535757 112614 yhak (de:hypothetical 25.9 kd protein in exur-tdcc intergenic region (o233)) (db:swissprot) YHAK_ECOLI P42624 ESCHERICHIA COLI 562 -11535757 7000687889 yhak hypothetical 25.9 kd protein in exur-tdcc intergenic region (cl:conserved hypothetical protein sll1773) (db:pir2.dat) G65099 G65099 Escherichia coli 562 -11535757 7500936748 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o233) (le:35072) (re:35773) (di:direct) ECOUW67 U18997 g606047 Escherichia coli 562 -11535757 236346 yhak orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:o233; 100 pct identical amino acid sequence and) (le:5461) (re:6162) (di:direct) AE000392 AE000392 g1789493 Escherichia coli 562 -11535757 5000693380 (de:(ecoli_3031) (pn:hypothetical 25) (gn:yhak) (gtcfc:13.7:14.1) (ec:) (yhak_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3031 ECOLI_3031 Escherichia coli 562 10054342				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860878	12194	34350	1065	354
<u>Description</u>				
6500731900 yhal:b3107 hypothetical 6.2 kd protein in exur-tdcc intergenic region:o56 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3107 b3107 Escherichia coli 562 -11535758 112615 yhal (de:hypothetical 6.2 kd protein in exur-tdcc intergenic region (o56)) (db:swissprot) YHAL_ECOLI P42625 ESCHERICHIA COLI 562 -11535758 7000687890 yhal hypothetical 6.2 kd protein in exur-tdcc intergenic region (db:pir2.dat) H65099 H65099 Escherichia coli 562 -11535758 7500936749 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o56) (le:35790) (re:35960) (di:direct) ECOUW67 U18997 g606048 Escherichia coli 562 -11535758 236347 yhal orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:o56; 100 pct identical amino acid sequence and) (le:6179) (re:6349) (di:direct) AE000392 AE000392 g1789494 Escherichia coli 562 -11535758 5000693381 (de:(ecoli_3032) (pn:hypothetical 6) (gn:yhal) (gtcfc:13.7:14.1) (ec:) (yhal_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3032 ECOLI_3032 Escherichia coli 562 10054343				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860889	12195	34351	228	75

Description

6500731901 yham:b3108 hypothetical 19.4 kd protein in exur-tdcc intergenic region:f188 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3108 b3108 Escherichia coli 562 -11535759 112616 yham (de:hypothetical 19.4 kd protein in exur-tdcc intergenic region (f188)) (db:swissprot) YHAM_ECOLI P42626 ESCHERICHIA COLI 562 -11535759 7000687891 yham hypothetical 19.4 kd protein in exur-tdcc intergenic region (db:pir2.dat) A65100 A65100 Escherichia coli 562 -11535759 7500936750 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f188) (le:36094) (re:36660) (di:complement) ECOUW67 U18997 g606049 Escherichia coli 562 -11535759 236348 yham orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:f188; 100 pct identical amino acid sequence and) (le:6483) (re:7049) (di:complement) AE000392 AE000392 g1789495 Escherichia coli 562 -11535759 5000693382 (de:(ecoli_3033) (pn:hypothetical 19) (gn:yham) (gtcfc:13.7:14.1) (ec:) (yham_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3033 ECOLI_3033 Escherichia coli 562 10054344

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860891	12196	34352	477	158

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860894	12197	34353	978	325

Description

6500731902 yhan:b3109 hypothetical 19.4 kd protein in exur-tdcc intergenic region:f187 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3109 b3109 Escherichia coli 562 -11535760 112617 yhan (de:hypothetical 19.4 kd protein in exur-tdcc intergenic region (f187)) (db:swissprot) YHAN_ECOLI P42627 ESCHERICHIA COLI 562 -11535760 7000687892 yhan hypothetical 19.4 kd protein in exur-tdcc intergenic region (db:pir2.dat) B65100 B65100 Escherichia coli 562 -11535760 7500936751 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f187) (le:36842) (re:37405) (di:complement) ECOUW67 U18997 g606050 Escherichia coli 562 -11535760 236349 yhan orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:f187; 100 pct identical amino acid sequence and) (le:7231) (re:7794) (di:complement) AE000392 AE000392 g1789496 Escherichia coli 562 -11535760 5000693383 (de:(ecoli_3034) (pn:hypothetical 19) (gn:yhan) (gtcfc:13.7:14.1) (ec:) (yhan_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3034 ECOLI_3034 Escherichia coli 562 10054345

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860900	12198	34354	327	108

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860901	12199	34355	417	138

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501860938	12200	34356	2580	859

Description

GTC ORF with score 2316 to: (sr:homo sapiens male myeloblast cell_line kg-1 cdna to mrna) (db:genpept-pri2) (de:human mrna for kiaa0031 gene, complete cds.) (nt:similar to human elongation factor 2 mrna (hsef2).) (le:61) (re:2979) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860942	12201	34357	288	95

Description

6500731903 yhao:b3110 hypothetical 46.6 kd protein in exur-tdcc intergenic region:f425 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3110 b3110 Escherichia coli 562 -11535761 112619 yhao (de:hypothetical 46.6 kd protein in exur-tdcc intergenic region (f425)) (db:swissprot) YHAO_ECOLI P42628 ESCHERICHIA COLI 562 -11535761 7000687893 yhao hypothetical 46.6 kd protein in exur-tdcc intergenic region (db:pir2.dat) C65100 C65100 Escherichia coli 562 -11535761 7500936753 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f425) (le:37433) (re:38710) (di:complement) ECOUW67 U18997 g606051 Escherichia coli 562 -11535761 236350 yhao putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 282 of 400 of the completegenome.) (nt:f425; 100 pct identical amino acid sequence and) (le:7822) (re:9099) (di:complement) AE000392 AE000392 g1789497 Escherichia coli 562 -11535761 5000693384 (de:(ecoli_3035) (pn:hypothetical 46) (gn:yhao) (gtcfc:13.7:14.1) (ec:) (yhao_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3035 ECOLI_3035 Escherichia coli 562 10054347

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860948	12202	34358	198	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860954	12203	34359	243	80

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501860960	12204	34360	543	180

Description

6500731904 yhar:b3113 hypothetical 16.3 kd protein in exur-tdcc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3113 b3113 Escherichia coli 562 -11535762 112620 yhar (de:hypothetical 16.3 kd protein in exur-tdcc intergenic region) (db:swissprot) YHAR_ECOLI P42631 ESCHERICHIA COLI 562 -11535762 7000687894 yhar hypothetical 16.3 kd protein in exur-tdcc intergenic region (cl:hypothetical protein hi0719) (db:pir2.dat) F65100 F65100 Escherichia coli 562 -11535762 7500936758 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f150) (le:40476) (re:40928) (di:complement) ECOUW67 U18997 g606054 Escherichia coli 562 -11535762 236353 yhar orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 283 of 400 of the completegenome.) (nt:f150; 100 pct identical amino acid sequence and) (le:578) (re:1030) (di:complement) AE000393 AE000393 g1789501 Escherichia coli 562 -11535762 5000693385 (de:(ecoli_3038) (pn:hypothetical 16) (gn:yhar) (gtcfc:13.7:14.1) (ec:) (yhar_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3038 ECOLI_3038 Escherichia coli 562 10054348

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501860965	12205	34361	585	194

Description

6500731905 yhaa:b3115 hypothetical protein in exur-tdcc intergenic region:orf x (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3115 b3115 Escherichia coli 562 -11535763 7000688996 yhaa exur-tdcc intergenic region acetate kinase homolog (cl:acetate kinase) (db:pir1.dat) (mp:67 min) Q3ECTD H65100 Escherichia coli 562 -11535763 7500953262 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f406; differences from database entries) (le:43206) (re:44426) (di:complement) ECOUW67 U18997 g606056 Escherichia coli 562 -11535763 236355 tdcd putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 283 of 400 of the completegenome.) (nt:f406; formerly designated yhaa) (le:3308) (re:4528) (di:complement) AE000393 AE000393 g1789503 Escherichia coli 562 -11535763 5000693386 (de:(ecoli_3040) (pn:hypothetical protein in exur-tdcc intergenic region:orf x) (gn:yhaa) (gtcfc:13.7:14.1) (ec:) (yhaa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3040 ECOLI_3040 Escherichia coli 562 10123978

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860966	12206	34362	543	180

Description

6500731906 yhab:b3120 hypothetical 20.6 kd protein in tdc-rnpb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3120 b3120 Escherichia coli 562 -11535764 7000689000 yhab hypothetical 20.6k protein tdc-rnpb intergenic region (db:pir1.dat) (mp:67 min) Q3ECTR E65101 Escherichia coli 562 -11535764 7500953704 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o186) (le:48587) (re:49147) (di:direct) ECOUW67 U18997 g606061 Escherichia coli 562 -11535764 236360 yhab orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 283 of 400 of the completegenome.) (nt:o186; 100 pct identical to 179 amino acids of) (le:8689) (re:9249) (di:direct) AE000393 AE000393 g1789508 Escherichia coli 562 -11535764 5000693387 (de:(ecoli_3045) (pn:hypothetical 20) (gn:yhab) (gtcfc:13.7:14.1) (ec:) (yhab_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3045 ECOLI_3045 Escherichia coli 562 10123980

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860971	12207	34363	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860974	12208	34364	990	329

Description

6500731907 yha:b3121 hypothetical 45.2 kd protein in tdc-rnpb intergenic region:orf b:orfx:o395 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3121 b3121 Escherichia coli 562 -11535765 112605 yha (de:(orfx) (o395)) (db:swissprot) YHAC_ECOLI P11864 ESCHERICHIA COLI 562 -11535765 163350 yha hypothetical 45.2k protein tdc-rnpb intergenic region (db:pir2.dat) (mp:68 min) Q0ECTR JU0026 Escherichia coli 562 -11535765 7500936739 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o395) (le:49169) (re:50356) (di:direct) ECOUW67 U18997 g606062 Escherichia coli 562 -11535765 236361 yha orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 283 of 400 of the completegenome.) (nt:o395; 100 pct identical amino acid sequence and) (le:9271) (re:10458) (di:direct) AE000393 AE000393 g1789509 Escherichia coli 562 -11535765 5000693388 (de:(ecoli_3046) (pn:hypothetical 45) (gn:yha) (gtcfc:13.7:14.1) (ec:) (yha_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3046 ECOLI_3046 Escherichia coli 562 10054333

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860979	12209	34365	261	86
<u>Description</u>				
5000693389 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3122 b3122 Escherichia coli 562 -11535766				
7000691809 hypothetical protein b3122 (db:pir2.dat) G65101 G65101 Escherichia coli 562 -11535766 7500960313 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o54) (le:50417) (re:50581) (di:direct) ECOUW67 U18997 g606063 Escherichia coli 562 -11535766 236362 b3122 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:o54; this 54 aa orf is 32 pct identical (2 gaps)) (le:61) (re:225) (di:direct) AE000394 AE000394 g1789511 Escherichia coli 562 -11535766 6500731908 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3122 b3122 Escherichia coli 562 -11535766				
<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860983	12210	34366	327	108
<u>Description</u>				
6500731909 yhad:b3124 hypothetical 42.1 kd protein in rnpb-soha intergenic region:orf 3:f408 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3124 b3124 Escherichia coli 562 -11535767 163280 yhad yhad protein:hypothetical protein 3 (cl:yhad protein) (db:pir2.dat) (mp:68 min) JQ0614 JQ0614 Escherichia coli 562 -11535767 236363 (sr:e.coli (strain k12; isolate w3110)genomic dna, clone 6b5(#515) fro) (db:genpept-bct1) (de:e.coli rnpb gene and orfs.) (nt:orf3) (le:1443) (re:2669) (di:direct) ECORNPBW D90212 g216633 Escherichia coli 562 -11535767 7500936740 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f408) (le:51378) (re:52604) (di:complement) ECOUW67 U18997 g606064 Escherichia coli 562 -11535767 235856 yhad orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:f408; 100 pct identical amino acid sequence and) (le:1023) (re:2249) (di:complement) AE000394 AE000394 g1789512 Escherichia coli 562 -11535767 112606 yhad (de:(f408)) (db:swissprot) YHAD_ECOLI P23524 ESCHERICHIA COLI 562 -11535767 5000693390 (de:(ecoli_3048) (pn:hypothetical 42) (gn:yhad) (gtcfc:13.7:14.1) (ec:) (yhad_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3048 ECOLI_3048 Escherichia coli 562 10054334				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501860984	12211	34367	1089	362
<u>Description</u>				
6500731910 yhae:b3125 hypothetical 31.0 kd protein in rnpb-soha intergenic region:orf 2:f299 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3125 b3125 Escherichia coli 562 -11535768 112608 yhae (de:hypothetical 31.0 kd protein in rnpb-soha intergenic region (orf 2)) (db:swissprot) YHAE_ECOLI P23523 ESCHERICHIA COLI 562 -11535768 136240 yhae 3-hydroxyisobutyrate dehydrogenase:homolog:hypothetical 31k protein rnpb-soha intergenic region (cl:3-hydroxyisobutyrate dehydrogenase:3-hydroxyisobutyrate dehydrogenase homology) (ec:1.1.1.31) (db:pir2.dat) (mp:68 min) JQ0613 JQ0613 Escherichia coli 562 -11535768 236364 (sr:e.coli (strain k12; isolate w3110)genomic dna, clone 6b5(#515) fro) (db:genpept-bct1) (de:e.coli rnpb gene and orfs.) (nt:orf2) (le:528) (re:1427) (di:direct) ECORNPBW D90212 g216632 Escherichia coli 562 -11535768 7500936742 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f299) (le:52620) (re:53519) (di:complement) ECOUW67 U18997 g606065 Escherichia coli 562 -11535768 235855 yhae putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:f299; 100 pct identical amino acid sequence and) (le:2265) (re:3164) (di:complement) AE000394 AE000394 g1789513 Escherichia coli 562 -11535768 5000693391 (de:(ecoli_3049) (pn:hypothetical 31) (gn:yhae) (gtcfc:13.7:14.1) (ec:) (yhae_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3049 ECOLI_3049 Escherichia coli 562 10054336				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501860992	12212	34368	567	188

Description

6500731911 yhaf:b3126 hypothetical 27.4 kd protein in rnpb-soha intergenic region:orf 1 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3126 b3126 Escherichia coli 562 -11535769 112609 yhaf (de:hypothetical 27.4 kd protein in rnpb-soha intergenic region (orf 1)) (db:swissprot) YHAF_ECOLI P23522 ESCHERICHIA COLI 562 -11535769 7000687884 yhaf hypothetical 27.4k protein rnpb-soha intergenic region (cl:2,4-dihydroxyhept-2-ene-1,7) (db:pir2.dat) (mp:68 min) B65102 B65102 Escherichia coli 562 -11535769 7500936743 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f256) (le:53540) (re:54310) (di:complement) ECOUW67 U18997 g606066 Escherichia coli 562 -11535769 236365 yhaf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:f256; 100 pct identical amino acid sequence and) (le:3185) (re:3955) (di:complement) AE000394 AE000394 g1789514 Escherichia coli 562 -11535769 5000693392 (de:(ecoli_3050) (pn:hypothetical 27) (gn:yhaf) (gtcfc:13.7:14.1) (ec:) (yhaf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3050 ECOLI_3050 Escherichia coli 562 10054337

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501861006	12213	34369	384	128

Description

6500731912 yhau:b3127 hypothetical 49.0 kd protein in rnpb-soha intergenic region:f444 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3127 b3127 Escherichia coli 562 -11535770 112621 yhau (de:hypothetical 49.0 kd protein in rnpb-soha intergenic region) (db:swissprot) YHAU_ECOLI P42613 ESCHERICHIA COLI 562 -11535770 7000687895 yhau hypothetical 49.0 kd protein in rnpb-soha intergenic region (cl:hexuronate transporter) (db:pir2.dat) C65102 C65102 Escherichia coli 562 -11535770 7500936759 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f444) (le:54326) (re:55660) (di:complement) ECOUW67 U18997 g606067 Escherichia coli 562 -11535770 236366 yhau putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:f444; 100 pct identical amino acid sequence and) (le:3971) (re:5305) (di:complement) AE000394 AE000394 g1789515 Escherichia coli 562 -11535770 5000693393 (de:(ecoli_3051) (pn:hypothetical 49) (gn:yhau) (gtcfc:13.7:14.1) (ec:) (yhau_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3051 ECOLI_3051 Escherichia coli 562 10054349

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861007	12214	34370	1074	357

Description

6500731913 yhag:b3128 hypothetical 56.4 kd protein in rnpb-soha intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3128 b3128 Escherichia coli 562 -11535771 112610 yhag (de:hypothetical 56.4 kd protein in rnpb-soha intergenic region) (db:swissprot) YHAG_ECOLI P39829 ESCHERICHIA COLI 562 -11535771 7000687885 yhag hypothetical 56.4 kd protein in rnpb-soha intergenic region (db:pir2.dat) D65102 D65102 Escherichia coli 562 -11535771 7500936744 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o523) (le:56035) (re:57606) (di:direct) ECOUW67 U18997 g606068 Escherichia coli 562 -11535771 236367 yhag putative hydrolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:o523; 100 pct identical amino acid sequence and) (le:5680) (re:7251) (di:direct) AE000394 AE000394 g1789516 Escherichia coli 562 -11535771 5000693394 (de:(ecoli_3052) (pn:hypothetical 56) (gn:yhag) (gtcfc:13.7:14.1) (ec:) (yhag_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3052 ECOLI_3052 Escherichia coli 562 10054338

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861036	12215	34371	2091	696

Description

6500731914 yhav:b3130 hypothetical 17.8 kd protein in soha-agar intergenic region:o154 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3130 b3130 Escherichia coli 562 -11535772 112622 yhav (de:hypothetical 17.8 kd protein in soha-agar intergenic region (o154)) (db:swissprot) YHAV_ECOLI P42901 ESCHERICHIA COLI 562 -11535772 7000687896 yhav hypothetical 17.8 kd protein in soha-agar intergenic region (cl:hypothetical protein slr0725) (db:pir2.dat) F65102 F65102 Escherichia coli 562 -11535772 7500936760 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o154) (le:58090) (re:58554) (di:direct) ECOUW67 U18997 g606070 Escherichia coli 562 -11535772 236369 yhav orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:o154; 100 pct identical amino acid sequence and) (le:7735) (re:8199) (di:direct) AE000394 AE000394 g1789518 Escherichia coli 562 -11535772 5000693395 (de:(ecoli_3054) (pn:hypothetical 17) (gn:yhav) (gtcfc:13.7:14.1) (ec:) (yhav_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3054 ECOLI_3054 Escherichia coli 562 10054350

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861039	12216	34372	336	111

Description

6500731915 yrah:b3142 hypothetical fimbrial-like protein in agai-mtr intergenic reg:hypothetical fimbrial-like protein in agai-mtr intergenic region precursor:o194 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3142 b3142 Escherichia coli 562 -11535773 116073 yrah (de:precursor) (db:swissprot) YRAH_ECOLI P42913 ESCHERICHIA COLI 562 -11535773 7000688516 yrah hypothetical fimbrial-like protein in agai-mtr intergenic reg (db:pir2.dat) B65104 B65104 Escherichia coli 562 -11535773 7500952593 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o194) (le:68178) (re:68762) (di:direct) ECOUW67 U18997 g606082 Escherichia coli 562 -11535773 236381 yrah putative fimbrial-like protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 285 of 400 of the completegenome.) (nt:o194; 100 pct identical amino acid sequence and) (le:5661) (re:6245) (di:direct) AE000395 AE000395 g1789531 Escherichia coli 562 -11535773 5000693401 (de:(ecoli_3066) (pn:hypothetical fimbrial-like protein in agai-mtr intergenic region precursor:o194) (gn:yrah) (gtcfc:13.7:14.1) (ec:) (yrah_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3066 ECOLI_3066 Escherichia coli 562 10057799

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861040	12217	34373	420	140

Description

6500731916 yrai:b3143 hypothetical 25.7 kd fimbrial chaperone in agai-mtr intergeni:hypothetical 25.7 kd fimbrial chaperone in agai-mtr intergenic region precursor:o231 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3143 b3143 Escherichia coli 562 -11535774 116074 yrai (de:precursor) (db:swissprot) YRAI_ECOLI P42914 ESCHERICHIA COLI 562 -11535774 7000688517 yrai hypothetical 25.7 kd fimbrial chaperone in agai-mtr intergeni (cl:chaperone protein papd) (db:pir2.dat) C65104 C65104 Escherichia coli 562 -11535774 7500952594 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o231) (le:68842) (re:69537) (di:direct) ECOUW67 U18997 g606083 Escherichia coli 562 -11535774 236382 yrai putative chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 285 of 400 of the completegenome.) (nt:o231; 100 pct identical amino acid sequence and) (le:6325) (re:7020) (di:direct) AE000395 AE000395 g1789532 Escherichia coli 562 -11535774 5000693402 (de:(ecoli_3067) (pn:hypothetical 25) (gn:yrai) (gtcfc:13.7:14.1) (ec:) (yrai_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3067 ECOLI_3067 Escherichia coli 562 10057800

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861043	12218	34374	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861046	12219	34375	222	73

Description

6500731917 yraj:b3144 hypothetical outer membrane usher protein in agai-mtr intergenic region:hypothetical outer membrane usher protein in agai-mtr intergenic region precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3144 b3144 Escherichia coli 562 -11535775 116075 yraj (de:region precursor) (db:swissprot) YRAJ_ECOLI P42915 ESCHERICHIA COLI 562 -11535775 7000688518 yraj probable outer membrane usher protein precursor agai-mtr intergenic region (cl:outer membrane usher protein fimd) (db:pir2.dat) D65104 D65104 Escherichia coli 562 -11535775 7500952595 yraj putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 285 of 400 of the completegenome.) (nt:o838; 100 pct identical to yraj_ecoli sw: p42915) (le:7049) (re:9565) (di:direct) AE000395 AE000395 g1789533 Escherichia coli 562 -11535775 5000693403 (de:(ecoli_3068) (pn:hypothetical outer membrane usher protein in agai-mtr intergenic region precursor) (gn:yraj) (gtcfc:13.7:14.1) (ec:) (yraj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3068 ECOLI_3068 Escherichia coli 562 10057801

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861051	12220	34376	789	262

Description

6500731918 yrak:b3145 hypothetical 38.5 kd protein in agai-mtr intergenic region:hypothetical 38.5 kd protein in agai-mtr intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3145 b3145 Escherichia coli 562 -11535776 116076 yrak (de:hypothetical 38.5 kd protein in agai-mtr intergenic region precursor) (db:swissprot) YRAK_ECOLI P43319 ESCHERICHIA COLI 562 -11535776 7000688519 yrak hypothetical 38.5 kd protein in agai-mtr intergenic region (db:pir2.dat) E65104 E65104 Escherichia coli 562 -11535776 7500952596 yrak putative fimbrial protein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 285 of 400 of the completegenome.) (nt:o363; 100 pct identical to yrak_ecoli sw: p43319) (le:9576) (re:10667) (di:direct) AE000395 AE000395 g1789534 Escherichia coli 562 -11535776 5000693404 (de:(ecoli_3069) (pn:hypothetical 38) (gn:yrak) (gtcfc:13.7:14.1) (ec:) (yrak_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3069 ECOLI_3069 Escherichia coli 562 10057802

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861076	12221	34377	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861078	12222	34378	1134	377

Description

6500731919 yral:b3146 hypothetical 31.3 kd protein in agai-mtr intergenic region:f286 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3146 b3146 Escherichia coli 562 -11535777 116077 yral (de:hypothetical 31.3 kd protein in agai-mtr intergenic region (f286)) (db:swissprot) YRAL_ECOLI P45528 ESCHERICHIA COLI 562 -11535777 7000688520 yral hypothetical 31.3 kd protein in agai-mtr intergenic region (cl:conserved hypothetical protein mg056) (db:pir2.dat) F65104 F65104 Escherichia coli 562 -11535777 7500952597 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f286) (le:73227) (re:74087) (di:complement) ECOUW67 U18997 g606086 Escherichia coli 562 -11535777 236385 yral orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 285 of 400 of the completegenome.) (nt:f286; 100 pct identical amino acid sequence and) (le:10710) (re:11570) (di:complement) AE000395 AE000395 g1789535 Escherichia coli 562 -11535777 5000693405 (de:(ecoli_3070) (pn:hypothetical 31) (gn:yral) (gtcfc:13.7:14.1) (ec:) (yral_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3070 ECOLI_3070 Escherichia coli 562 10057803

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861082	12223	34379	726	241

Description

GTC ORF with score 124 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome ii bac t28m21 genomic sequence,complete sequence.) (nt:unknown protein) (le:97328:98826:99416) (re:98518:98940:99530) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861087	12224	34380	477	158

Description

6500731920 yram:b3147 hypothetical 72.8 kd protein in agai-mtr intergenic region:o678 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3147 b3147 Escherichia coli 562 -11535778 116079 yram (de:hypothetical 72.8 kd protein in agai-mtr intergenic region (o678)) (db:swissprot) YRAM_ECOLI P45464 ESCHERICHIA COLI 562 -11535778 7000688523 yram hypothetical 72.8 kd protein in agai-mtr intergenic region (db:pir2.dat) G65104 G65104 Escherichia coli 562 -11535778 7500952600 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o678) (le:74152) (re:76188) (di:direct) ECOUW67 U18997 g606087 Escherichia coli 562 -11535778 236386 yram putative glycosylase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 286 of 400 of the completegenome.) (nt:o678; 100 pct identical amino acid sequence and) (le:63) (re:2099) (di:direct) AE000396 AE000396 g1789537 Escherichia coli 562 -11535778 5000693406 (de:(ecoli_3071) (pn:hypothetical 72) (gn:yram) (gtcfc:13.7:14.1) (ec:) (yram_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3071 ECOLI_3071 Escherichia coli 562 10057805

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861090	12225	34381	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861093	12226	34382	1068	355

Description

6500731921 yran:b3148 hypothetical 14.8 kd protein in agai-mtr intergenic region:o131 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3148 b3148 Escherichia coli 562 -11535779 116081 yran (de:hypothetical 14.8 kd protein in agai-mtr intergenic region (o131)) (db:swissprot) YRAN_ECOLI P45465 ESCHERICHIA COLI 562 -11535779 7000688524 yran hypothetical 14.8 kd protein in agai-mtr intergenic region (cl:hypothetical protein h1656) (db:pir2.dat) H65104 H65104 Escherichia coli 562 -11535779 7500952602 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o131; overlaps o678, other starts possible) (le:76146) (re:76541) (di:direct) ECOUW67 U18997 g606088 Escherichia coli 562 -11535779 236387 yran orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 286 of 400 of the completgenome.) (nt:o131; o131; overlaps o678, other starts) (le:2057) (re:2452) (di:direct) AE000396 AE000396 g1789538 Escherichia coli 562 -11535779 5000693407 (de:(ecoli_3072) (pn:hypothetical 14) (gn:yran) (gtcfc:13.7:14.1) (ec:) (yran_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3072 ECOLI_3072 Escherichia coli 562 10057807

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861095	12227	34383	417	138

Description

6500731922 yrao:b3149 hypothetical 21.1 kd protein in agai-mtr intergenic region:o196 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3149 b3149 Escherichia coli 562 -11535780 116083 yrao (de:hypothetical 21.1 kd protein in agai-mtr intergenic region (o196)) (db:swissprot) YRAO_ECOLI P45466 ESCHERICHIA COLI 562 -11535780 7000688525 yrao phosphoheptose isomerase homolog:hypothetical 21.1 kd protein in agai-mtr intergenic region (cl:phosphoheptose isomerase) (db:pir2.dat) A65105 A65105 Escherichia coli 562 -11535780 7500952604 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o196) (le:76561) (re:77151) (di:direct) ECOUW67 U18997 g606089 Escherichia coli 562 -11535780 236388 yrao orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 286 of 400 of the completgenome.) (nt:o196; 100 pct identical amino acid sequence and) (le:2472) (re:3062) (di:direct) AE000396 AE000396 g1789539 Escherichia coli 562 -11535780 5000693408 (de:(ecoli_3073) (pn:hypothetical 21) (gn:yrao) (gtcfc:13.7:14.1) (ec:) (yrao_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3073 ECOLI_3073 Escherichia coli 562 10057809

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861104	12228	34384	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861106	12229	34385	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861111	12230	34386	462	153

Description

6500731923 yrap:b3150 hypothetical 20.0 kd protein in agai-mtr intergenic region:hypothetical 20.0 kd protein in agai-mtr intergenic region
precursor:o191 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3150 b3150 Escherichia coli 562 -11535781 116085
yrap (de:(o191)) (db:swissprot) YRAP_ECOLI P45467 ESCHERICHIA COLI 562
-11535781 7000688526 yrap hypothetical 20.0 kd protein in agai-mtr
intergenic region (db:pir2.dat) B65105 B65105 Escherichia coli 562 -11535781
7500952606 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region
from 67.4 to 76.0 minutes.) (nt:orf_o191) (le:77161) (re:77736) (di:direct)
ECOUW67 U18997 g606090 Escherichia coli 562 -11535781 236389 yrap putative
periplasmic protein (fn:putative transport; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 286 of 400 of the
completegenome.) (nt:o191; 100 pct identical amino acid sequence and)
(le:3072) (re:3647) (di:direct) AE000396 AE000396 gl789540 Escherichia coli
562 -11535781 5000693409 (de:(ecoli_3074) (pn:hypothetical 20) (gn:yrap)
(gtcfc:13.7:14.1) (ec:) (yrap_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) ECOLI_3074 ECOLI_3074 Escherichia coli 562
10057811

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861112	12231	34387	804	267

Description

6500731924 yraq:b3151 hypothetical 37.3 kd protein in agai-mtr intergenic region:f346 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3151 b3151 Escherichia coli 562 -11535782 116087 yraq (de:hypothetical 37.3 kd protein in agai-mtr intergenic region (f346)) (db:swissprot) YRAQ_ECOLI P45468 ESCHERICHIA COLI 562 -11535782 7000688527 yraq hypothetical 37.3 kd protein in agai-mtr intergenic region (db:pir2.dat) C65105 C65105 Escherichia coli 562 -11535782 7500952608 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f346) (le:77850) (re:78890) (di:complement) ECOUW67 U18997 g606091 Escherichia coli 562 -11535782 236390 yraq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 286 of 400 of the completegenome.) (nt:f346; 100 pct identical amino acid sequence and) (le:3761) (re:4801) (di:complement) AE000396 AE000396 g1789541 Escherichia coli 562 -11535782 5000693410 (de:(ecoli_3075) (pn:hypothetical 37) (gn:yraq) (gtcfc:13.7:14.1) (ec:) (yraq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3075 ECOLI_3075 Escherichia coli 562 10057813

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861127	12232	34388	654	217

Description

GTC ORF with score 537 to: (de:(yel042w) (pn:guanosine-diphosphatase:gdpase:guanosine diphosphatase) (gn:sygp-orf16:gda1) (gtcfc:10.7:12.13:12.16) (ec:3.6.1.42) (gda1_yeast) (keggfc:11.1) (sgdfc:6.3.0:9.4.0:16.0.0) (db:gtc-saccharomyces cerevisiae))

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861129	12233	34389	1038	345

Description

6500731925 yrar:b3152 hypothetical 24.8 kd protein in agai-mtr intergenic region:f226 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3152 b3152 Escherichia coli 562 -11535783 116088 yrar (de:hypothetical 24.8 kd protein in agai-mtr intergenic region (f226)) (db:swissprot) YRAR_ECOLI P45469 ESCHERICHIA COLI 562 -11535783 7000688528 yrar hypothetical 24.8 kd protein in agai-mtr intergenic region (db:pir2.dat) D65105 D65105 Escherichia coli 562 -11535783 7500952609 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f226) (le:78963) (re:79643) (di:complement) ECOUW67 U18997 g606092 Escherichia coli 562 -11535783 236391 yrar orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 286 of 400 of the completegenome.) (nt:f226; 100 pct identical amino acid sequence and) (le:4874) (re:5554) (di:complement) AE000396 AE000396 g1789542 Escherichia coli 562 -11535783 5000693411 (de:(ecoli_3076) (pn:hypothetical 24) (gn:yrar) (gtcfc:13.7:14.1) (ec:) (yrar_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3076 ECOLI_3076 Escherichia coli 562 10057814

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861148	12234	34390	522	173

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861156	12235	34391	216	71

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501861159	12236	34392	2220	740

Description

6500731926 yhbo:b3153 hypothetical 20.3 kd protein in soha-mtr intergenic region:o186 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3153 b3153 Escherichia coli 562 -11535784 112644 yhbo (de:hypothetical 20.3 kd protein in soha-mtr intergenic region) (db:swissprot) YHBO_ECOLI P45470 ESCHERICHIA COLI 562 -11535784 7000687903 yhbo hypothetical 20.3 kd protein in soha-mtr intergenic region (cl:archaeoglobus intracellular proteinase i) (db:pir2.dat) E65105 E65105 Escherichia coli 562 -11535784 7500936776 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o186) (le:79684) (re:80244) (di:direct) ECOUW67 U18997 g606093 Escherichia coli 562 -11535784 236392 yhbo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 286 of 400 of the completegenome.) (nt:o186; 100 pct identical amino acid sequence and) (le:5595) (re:6155) (di:direct) AE000396 AE000396 g1789543 Escherichia coli 562 -11535784 5000693412 (de:(ecoli_3077) (pn:hypothetical 20) (gn:yhbo) (gtcfc:13.7:14.1) (ec:) (yhbo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3077 ECOLI_3077 Escherichia coli 562 10054372

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501861180	12237	34393	1194	397

Description

6500731927 yhbp:b3154 hypothetical 16.8 kd protein in soha-mtr intergenic region:f147 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3154 b3154 Escherichia coli 562 -11535785 112645 yhbp (de:hypothetical 16.8 kd protein in soha-mtr intergenic region (f147)) (db:swissprot) YHBP_ECOLI P45471 ESCHERICHIA COLI 562 -11535785 7000687904 yhbp hypothetical 16.8 kd protein in soha-mtr intergenic region (db:pir2.dat) F65105 F65105 Escherichia coli 562 -11535785 7500936777 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f147; end overlaps end of o186 by 20 bases) (le:80224) (re:80667) (di:complement) ECOUW67 U18997 g606094 Escherichia coli 562 -11535785 236393 yhbp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 286 of 400 of the completegenome.) (nt:f147; f147; end overlaps end of o186 by 20) (le:6135) (re:6578) (di:complement) AE000396 AE000396 g1789544 Escherichia coli 562 -11535785 5000693413 (de:(ecoli_3078) (pn:hypothetical 16) (gn:yhbp) (gtcfc:13.7:14.1) (ec:) (yhbp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3078 ECOLI_3078 Escherichia coli 562 10054373

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861205	12238	34394	423	140

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861209	12239	34395	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861214	12240	34396	441	146

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861216	12241	34397	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861232	12242	34398	693	231

Description

6500731928 yhbq:b3155 hypothetical 11.3 kd protein in soha-mtr intergenic region:o100 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3155 b3155 Escherichia coli 562 -11535786 112646 yhbq (de:hypothetical 11.3 kd protein in soha-mtr intergenic region (o100)) (db:swissprot) YHBQ_ECOLI P45472 ESCHERICHIA COLI 562 -11535786 7000687905 yhbq hypothetical 11.3 kd protein in soha-mtr intergenic region (cl:hypothetical protein 312) (db:pir2.dat) G65105 G65105 Escherichia coli 562 -11535786 7500936778 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o100) (le:80718) (re:81020) (di:direct) ECOUW67 U18997 g606095 Escherichia coli 562 -11535786 236394 yhbq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 286 of 400 of the completegenome.) (nt:o100; 100 pct identical amino acid sequence and) (le:6629) (re:6931) (di:direct) AE000396 AE000396 gl789545 Escherichia coli 562 -11535786 5000693414 (de:(ecoli_3079) (pn:hypothetical 11) (gn:yhbq) (gtcfc:13.7:14.1) (ec:) (yhbq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3079 ECOLI_3079 Escherichia coli 562 10054374

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861234	12243	34399	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861235	12244	34400	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861241	12245	34401	255	84

Description

6500731929 yhbs:b3156 hypothetical protein: hypothetical 18.5 kd protein in soha-mtr intergenic region: f167 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3156 b3156 Escherichia coli 562 -11535787 112647 yhbs (de: hypothetical 18.5 kd protein in soha-mtr intergenic region (f167)) (db:swissprot) YHBS_ECOLI P45473 ESCHERICHIA COLI 562 -11535787 7000687906 hypothetical protein b3156 (db:pir2.dat) H65105 H65105 Escherichia coli 562 -11535787 7500936779 (db:genpept-bct1) (de: escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f167; end overlaps end of o100 by 14 bases;) (le:81007) (re:81510) (di:complement) ECOUW67 U18997 g606096 Escherichia coli 562 -11535787 236395 yhbs orf: hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de: escherichia coli k-12 mg1655 section 286 of 400 of the complete genome.) (nt:f167; f167; end overlaps end of o100 by 14) (le:6918) (re:7421) (di:complement) AE000396 AE000396 g1789546 Escherichia coli 562 -11535787 5000693415 (de: (ecoli_3080) (pn: hypothetical 18) (gtcfc:13.7:14.1) (ec:) (yhbs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3080 ECOLI_3080 Escherichia coli 562 10054375

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861242	12246	34402	330	110

Description

6500731930 yhbt:b3157 hypothetical 19.7 kd protein in soha-mtr intergenic region:f174 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3157 b3157 Escherichia coli 562 -11535788 112648 yhbt (de:hypothetical 19.7 kd protein in soha-mtr intergenic region (f174)) (db:swissprot) YHBT_ECOLI P45474 ESCHERICHIA COLI 562 -11535788 7000687907 yhbt hypothetical 19.7 kd protein in soha-mtr intergenic region (db:pir2.dat) A65106 A65106 Escherichia coli 562 -11535788 7500936780 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f174) (le:81504) (re:82028) (di:complement) ECOUW67 U18997 g606097 Escherichia coli 562 -11535788 236396 yhbt orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 286 of 400 of the completegenome.) (nt:f174; 100 pct identical amino acid sequence and) (le:7415) (re:7939) (di:complement) AE000396 AE000396 g1789547 Escherichia coli 562 -11535788 5000693416 (de:(ecoli_3081) (pn:hypothetical 19) (gn:yhbt) (gtcfc:13.7:14.1) (ec:) (yhbt_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3081 ECOLI_3081 Escherichia coli 562 10054376

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861245	12247	34403	285	94

Description

6500731931 yhbv:b3159 hypothetical 33.2 kd protein in soha-mtr intergenic region:o298 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3159 b3159 Escherichia coli 562 -11535789 112651 yhbv (de:hypothetical 33.2 kd protein in soha-mtr intergenic region (o298)) (db:swissprot) YHBV_ECOLI P45475 ESCHERICHIA COLI 562 -11535789 7000687909 yhbv hypothetical 33.2 kd protein in soha-mtr intergenic region (db:pir2.dat) C65106 C65106 Escherichia coli 562 -11535789 7500936782 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o298; overlaps o298, other starts possible) (le:83223) (re:84119) (di:direct) ECOUW67 U18997 g606099 Escherichia coli 562 -11535789 236398 yhbv orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 286 of 400 of the completegenome.) (nt:o298; o298; overlaps o298, other starts) (le:9134) (re:10030) (di:direct) AE000396 AE000396 g1789549 Escherichia coli 562 -11535789 5000693417 (de:(ecoli_3083) (pn:hypothetical 33) (gn:yhbv) (gtcfc:13.7:14.1) (ec:) (yhbv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3083 ECOLI_3083 Escherichia coli 562 10054379

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861269	12248	34404	1224	407

Description

6500731932 yhbw:b3160 hypothetical 37.1 kd protein in soha-mtr intergenic region:o335 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3160 b3160 Escherichia coli 562 -11535790 112652 yhbw (de:hypothetical 37.1 kd protein in soha-mtr intergenic region (o335)) (db:swissprot) YHBW_ECOLI P45529 ESCHERICHIA COLI 562 -11535790 7000687910 yhbw hypothetical 37.1 kd protein in soha-mtr intergenic region (cl:ynbw protein) (db:pir2.dat) D65106 D65106 Escherichia coli 562 -11535790 7500936783 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o335) (le:84200) (re:85207) (di:direct) ECOUW67 U18997 g606100 Escherichia coli 562 -11535790 236399 yhbw putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 287 of 400 of the completegenome.) (nt:o335; 100 pct identical amino acid sequence and) (le:71) (re:1078) (di:direct) AE000397 AE000397 g1789551 Escherichia coli 562 -11535790 5000693418 (de:(ecoli_3084) (pn:hypothetical 37) (gn:yhbw) (gtcfc:13.7:14.1) (ec:) (yhbw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3084 ECOLI_3084 Escherichia coli 562 10054380

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861276	12249	34405	429	142

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861293	12250	34406	765	254

Description

6500731933 yhbm:b3163 hypothetical 33.6 kd protein in dead-pnp intergenic region:f294 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3163 Escherichia coli 562 -11535791 112640 yhbm (de:hypothetical 33.6 kd protein in dead-pnp intergenic region (f294)) (db:swissprot) YHBM_ECOLI P39833 ESCHERICHIA COLI 562 -11535791 7000687901 yhbm hypothetical 33.6 kd protein in dead-pnp intergenic region (cl:hypothetical protein hi0230:tetratricopeptide repeat homology) (db:pir2.dat) G65106 Escherichia coli 562 -11535791 7500936773 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f294) (le:88792) (re:89676) (di:complement) ECOUW67 U18997 g606103 Escherichia coli 562 -11535791 236402 yhbm putative control proteins (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 287 of 400 of the completegenome.) (nt:f294; 100 pct identical amino acid sequence and) (le:4663) (re:5547) (di:complement) AE000397 AE000397 g1789554 Escherichia coli 562 -11535791 5000693419 (de:(ecoli_3087) (pn:hypothetical 33) (gn:yhbm) (gtcfc:13.7:14.1) (ec:) (yhbm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3087 ECOLI_3087 Escherichia coli 562 10054368

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861308	12251	34407	1353	450

Description

6500731934 yhbc:b3170 hypothetical 16.8 kd protein in nusa-mety intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3170 Escherichia coli 562 -11535792 112627 yhbc (de:hypothetical 16.8 kd protein in nusa-mety intergenic region) (db:swissprot) YHBC_ECOLI P03843 ESCHERICHIA COLI 562 -11535792 7000687897 yhbc nus operon 15k protein (cl:nus operon 15k protein) (db:pir1.dat) (mp:69 min) WMECN5 F65107 Escherichia coli 562 -11535792 7500936767 yhbc (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:gtg start; differences from database entry) (le:98306) (re:98764) (di:complement) ECOUW67 U18997 g606110 Escherichia coli 562 -11535792 236409 yhbc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 287 of 400 of the completegenome.) (nt:f152; 100 pct identical to yhbc_ecoli sw: p03843) (le:14177) (re:14635) (di:complement) AE000397 AE000397 g1789561 Escherichia coli 562 -11535792 5000693422 (de:(ecoli_3094) (pn:hypothetical 16) (gn:yhbc) (gtcfc:13.7:14.1) (ec:) (yhbc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3094 ECOLI_3094 Escherichia coli 562 10054355

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861313	12252	34408	627	208

Description

6500731935 yhbz:b3173 hypothetical 61.6 kd protein in argg-leuu intergenic region:f547 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3173 b3173 Escherichia coli 562 -11535793 112653 yhbz (de:hypothetical 61.6 kd protein in argg-leuu intergenic region (f547)) (db:swissprot) YHBX_ECOLI P42640 ESCHERICHIA COLI 562 -11535793 7000687911 yhbz hypothetical 61.6 kd protein in argg-leuu intergenic region (db:pir2.dat) H65107 H65107 Escherichia coli 562 -11535793 7500936784 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f547; gtg start) (le:100740) (re:102383) (di:complement) ECOUW67 U18997 g606112 Escherichia coli 562 -11535793 236411 yhbz putative alkaline phosphatase i (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 288 of 400 of the completengenome.) (nt:f547; 100 pct identical to yhbz_ecoli sw: p42640) (le:1849) (re:3492) (di:complement) AE000398 AE000398 g1789564 Escherichia coli 562 -11535793 5000693423 (de:(ecoli_3096) (pn:hypothetical 61) (gn:yhbz) (gtcfc:13.7:14.1) (ec:) (yhbz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3096 ECOLI_3096 Escherichia coli 562 10054381

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861315	12253	34409	1734	577

Description

6500731936 yhbz:b3180 hypothetical 10.8 kd protein in ftsj-grea intergenic region:o97 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3180 b3180 Escherichia coli 562 -11535794 112654 yhbz (de:hypothetical 10.8 kd protein in ftsj-grea intergenic region (o97)) (db:swissprot) YHBY_ECOLI P42550 ESCHERICHIA COLI 562 -11535794 7000687912 yhbz hypothetical 10.8 kd protein in ftsj-grea intergenic region (cl:methanococcus jannaschii conserved hypothetical protein mj0652) (db:pir2.dat) F65108 F65108 Escherichia coli 562 -11535794 7500936785 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o97) (le:108542) (re:108835) (di:direct) ECOUW67 U18997 g606118 Escherichia coli 562 -11535794 236417 yhbz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 288 of 400 of the completengenome.) (nt:o97; 100 pct identical amino acid sequence and) (le:9651) (re:9944) (di:direct) AE000398 AE000398 g1789570 Escherichia coli 562 -11535794 5000693426 (de:(ecoli_3102) (pn:hypothetical 10) (gn:yhbz) (gtcfc:13.7:14.1) (ec:) (yhbz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3102 ECOLI_3102 Escherichia coli 562 10054382

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861337	12254	34410	762	253

Description

6500731937 yhbz:b3183 hypothetical 43.3 kd gtp-binding protein in dacb-rpma intergenic region:f390 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3183 b3183 Escherichia coli 562 -11535795 112655 yhbz (de:region) (db:swissprot) YHBZ_ECOLI P42641 ESCHERICHIA COLI 562 -11535795 7000687913 yhbz gtp-binding protein obg (cl:gtp-binding protein obg:translation elongation factor tu homology) (db:pir1.dat) A65109 A65109 Escherichia coli 562 -11535795 7500936790 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f390) (le:111334) (re:112506) (di:complement) ECOUW67 U18997 g606121 Escherichia coli 562 -11535795 236420 yhbz putative gtp-binding factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:f390; 100 pct identical amino acid sequence and) (le:1855) (re:3027) (di:complement) AE000399 AE000399 g1789574 Escherichia coli 562 -11535795 5000693427 (de:(ecoli_3105) (pn:hypothetical 43) (gn:yhbz) (gtcfc:13.7:14.1) (ec:) (yhbz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3105 ECOLI_3105 Escherichia coli 562 10054383

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861386	12255	34411	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861408	12256	34412	444	147

Description

6500731938 yhbe:b3184 hypothetical 35.0 kd protein in dacb-rpma intergenic region:f321 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3184 b3184 Escherichia coli 562 -11535796 112629 yhbe (de:hypothetical 35.0 kd protein in dacb-rpma intergenic region (f321)) (db:swissprot) YHBE_ECOLI P28636 ESCHERICHIA COLI 562 -11535796 7000687899 yhbe hypothetical 35.0k protein dacb-rpma intergenic region (db:pir2.dat) B65109 B65109 Escherichia coli 562 -11535796 7500936770 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f321) (le:112522) (re:113487) (di:complement) ECOUW67 U18997 g606122 Escherichia coli 562 -11535796 236421 yhbe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completgenome.) (nt:f321; 100 pct identical amino acid sequence and) (le:3043) (re:4008) (di:complement) AE000399 AE000399 g1789575 Escherichia coli 562 -11535796 5000693428 (de:(ecoli_3106) (pn:hypothetical 35) (gn:yhbe) (gtcfc:13.7:14.1) (ec:) (yhbe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3106 ECOLI_3106 Escherichia coli 562 10054357

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861410	12257	34413	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861420	12258	34414	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861426	12259	34415	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861429	12260	34416	1686	561

Description

6500731939 yrba:b3190 hypothetical 9.5 kd protein in murz-rpon intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3190 b3190 Escherichia coli 562 -11535797 7000690977 yrba hypothetical 9.5 kd protein in murz-rpon intergenic region (cl:bola protein) (db:pir2.dat) H65109 H65109 Escherichia coli 562 -11535797 7500959836 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f89) (le:117301) (re:117570) (di:complement) ECOUW67 U18997 g606128 Escherichia coli 562 -11535797 236427 yrba orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:f89; 100 pct identical to 84 amino acids of) (le:7822) (re:8091) (di:complement) AE000399 AE000399 g1789581 Escherichia coli 562 -11535797 5000693429 (de:(ecoli_3112) (pn:hypothetical 9) (gn:yrba) (gtcfc:13.7:14.1) (ec:) (yrba_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3112 ECOLI_3112 Escherichia coli 562 10123990

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861444	12261	34417	582	193

Description

6500731940 yrbb:b3191 hypothetical 14.4 kd protein in murz-rpon intergenic region:hypothetical 14.4 kd protein in mura-rpon intergenic region:f129 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3191 b3191 Escherichia coli 562 -11535798 116099 yrbb (de:hypothetical 14.4 kd protein in mura-rpon intergenic region (f129)) (db:swissprot) YRBB_ECOLI P45389 ESCHERICHIA COLI 562 -11535798 7000688529 yrbb hypothetical 14.4 kd protein in murz-rpon intergenic region (db:pir2.dat) A65110 A65110 Escherichia coli 562 -11535798 7500952611 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f129) (le:117715) (re:118104) (di:complement) ECOUW67 U18997 g606129 Escherichia coli 562 -11535798 236428 yrbb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:f129; 100 pct identical amino acid sequence and) (le:8236) (re:8625) (di:complement) AE000399 AE000399 g1789582 Escherichia coli 562 -11535798 5000693430 (de:(ecoli_3113) (pn:hypothetical 14) (gn:yrbb) (gtcfc:13.7:14.1) (ec:) (yrbb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3113 ECOLI_3113 Escherichia coli 562 10057825

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861449	12262	34418	270	90

Description

6500731941 yrbc:b3192 hypothetical 24.0 kd protein in murz-rpon intergenic region:hypothetical 24.0 kd protein in mura-rpon intergenic region precursor:f211 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3192 b3192 Escherichia coli 562 -11535799 116100 yrbc (de:(f211)) (db:swissprot) YRBC_ECOLI P45390 ESCHERICHIA COLI 562 -11535799 7000688530 yrbc hypothetical 24.0 kd protein in murz-rpon intergenic region (cl:hypothetical protein hil084) (db:pir2.dat) B65110 B65110 Escherichia coli 562 -11535799 7500952612 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f211) (le:118008) (re:118643) (di:complement) ECOUW67 U18997 g606130 Escherichia coli 562 -11535799 236429 yrbc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:f211; 100 pct identical amino acid sequence and) (le:8529) (re:9164) (di:complement) AE000399 AE000399 g1789583 Escherichia coli 562 -11535799 5000693431 (de:(ecoli_3114) (pn:hypothetical 24) (gn:yrbc) (gtcfc:13.7:14.1) (ec:) (yrbc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3114 ECOLI_3114 Escherichia coli 562 10057826

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861454	12263	34419	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861479	12264	34420	330	109

Description

6500731942 yrbd:b3193 hypothetical protein:hypothetical 19.6 kd protein in mura-rpon intergenic region precursor:f183 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3193 b3193 Escherichia coli 562 -11535800 116102 yrbd (de:(f183)) (db:swissprot) YRBD_ECOLI P45391 ESCHERICHIA COLI 562 -11535800 7000688531 hypothetical protein b3193 (db:pir2.dat) C65110 C65110 Escherichia coli 562 -11535800 7500952614 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f183) (le:118662) (re:119213) (di:complement) ECOUW67 U18997 g606131 Escherichia coli 562 -11535800 236430 yrbd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:f183) (le:9183) (re:9734) (di:complement) AE000399 AE000399 g1789584 Escherichia coli 562 -11535800 5000693432 (de:(ecoli_3115) (pn:hypothetical 19) (gtcfc:13.7:14.1) (ec:) (yrbd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3115 ECOLI_3115 Escherichia coli 562 10057828

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861480	12265	34421	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861483	12266	34422	276	91

Description

6500731943 yrbe:b3194 hypothetical 27.9 kd protein in murz-rpon intergenic region:hypothetical 27.9 kd protein in mura-rpon intergenic region:f260 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3194 b3194 Escherichia coli 562 -11535801 116104 yrbe (de:hypothetical 27.9 kd protein in mura-rpon intergenic region (f260)) (db:swissprot) YRBE_ECOLI P45392 ESCHERICHIA COLI 562 -11535801 7000688532 yrbe hypothetical 27.9 kd protein in murz-rpon intergenic region (cl:conserved hypothetical protein hi1086) (db:pir2.dat) D65110 D65110 Escherichia coli 562 -11535801 7500952616 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f260) (le:119218) (re:120000) (di:complement) ECOUW67 U18997 g606132 Escherichia coli 562 -11535801 236431 yrbe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:f260; 100 pct identical amino acid sequence and) (le:9739) (re:10521) (di:complement) AE000399 AE000399 g1789585 Escherichia coli 562 -11535801 5000693433 (de:(ecoli_3116) (pn:hypothetical 27) (gn:yrbe) (gtcfc:13.7:14.1) (ec:) (yrbe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3116 ECOLI_3116 Escherichia coli 562 10057830

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861499	12267	34423	2775	925

Description

6500731944 yrbf:b3195 hypothetical protein:hypothetical abc transporter
atp-binding protein in mura-rpon intergenic region (gtcfc:12.6)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3195 b3195
Escherichia coli 562 -11535802 116106 yrbf (de:intergenic region)
(db:swissprot) YRBF_ECOLI P45393 ESCHERICHIA COLI 562 -11535802 7000688533
hypothetical protein b3195 (cl:unassigned atp-binding cassette
proteins:atp-binding cassette homology) (db:pir2.dat) E65110 E65110
Escherichia coli 562 -11535802 7500952618 (db:genpept-bct1) (de:escherichia
coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f269)
(le:120008) (re:120817) (di:complement) ECOUW67 U18997 g606133 Escherichia
coli 562 -11535802 236432 yrbf putative atp-binding component of a
transport (fn:putative transport; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.)
(nt:f269) (le:10529) (re:11338) (di:complement) AE000399 AE000399 g1789586
Escherichia coli 562 -11535802 5000693434 (de:(ecoli_3117) (pn:hypothetical
abc transporter atp-binding protein in murz-rpon intergenic region:f269)
(gtcfc:13.7:14.1) (ec:) (yrbf_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) ECOLI_3117 ECOLI_3117 Escherichia coli 562
10057832

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861530	12268	34424	1398	465

Description

GTC ORF with score 222 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe
chromosome i cosmid c23h4.) (nt:spac23h4.14, unknown, len:905aa, contains
ps00307) (le:24967:25085:25214:25365) (re:25039:25162:25318:27753)
(di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861533	12269	34425	1188	395

Description

GTC ORF with score 305 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe
chromosome i cosmid c23h4.) (nt:spac23h4.14, unknown, len:905aa, contains
ps00307) (le:24967:25085:25214:25365) (re:25039:25162:25318:27753)
(di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861536	12270	34426	504	167

Description

GTC ORF with score 138 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome i cosmid c23h4.) (nt:spac23h4.14, unknown, len:905aa, contains ps00307) (le:24967:25085:25214:25365) (re:25039:25162:25318:27753) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861548	12271	34427	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861555	12272	34428	330	109

Description

6500731945 yrbg:b3196 hypothetical 34.7 kd protein in murz-rpon intergenic region:hypothetical 34.7 kd protein in mura-rpon intergenic region:o325 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3196 b3196 Escherichia coli 562 -11535803 116108 yrbg (de:hypothetical 34.7 kd protein in mura-rpon intergenic region (o325)) (db:swissprot) YRBG_ECOLI P45394 ESCHERICHIA COLI 562 -11535803 7000688534 yrbg hypothetical 34.7 kd protein in murz-rpon intergenic region (db:pir2.dat) F65110 F65110 Escherichia coli 562 -11535803 7500952620 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o325) (le:121027) (re:122004) (di:direct) ECOUW67 U18997 g606134 Escherichia coli 562 -11535803 236433 yrbg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:o325; 100 pct identical amino acid sequence and) (le:11548) (re:12525) (di:direct) AE000399 AE000399 g1789587 Escherichia coli 562 -11535803 5000693435 (de:(ecoli_3118) (pn:hypothetical 34) (gn:yrbg) (gtcfc:13.7:14.1) (ec:) (yrbg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3118 ECOLI_3118 Escherichia coli 562 10057834

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861558	12273	34429	483	160

Description

6500731946 yrbh:b3197 hypothetical 35.2 kd protein in murz-rpon intergenic region:hypothetical 35.2 kd protein in mura-rpon intergenic region:o328 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3197 b3197 Escherichia coli 562 -11535804 116109 yrbh (de:hypothetical 35.2 kd protein in mura-rpon intergenic region (o328)) (db:swissprot) YRBH_ECOLI P45395 ESCHERICHIA COLI 562 -11535804 7000688535 yrbh hypothetical 35.2 kd protein in murz-rpon intergenic region (cl:probable atp-binding protein gutq) (db:pir2.dat) G65110 G65110 Escherichia coli 562 -11535804 7500952621 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o328) (le:122018) (re:123004) (di:direct) ECOUW67 U18997 g606135 Escherichia coli 562 -11535804 236434 yrbh putative isomerase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:o328; 100 pct identical amino acid sequence and) (le:12539) (re:13525) (di:direct) AE000399 AE000399 g1789588 Escherichia coli 562 -11535804 5000693436 (de:(ecoli_3119) (pn:hypothetical 35) (gn:yrbh) (gtcfc:13.7:14.1) (ec:) (yrbh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3119 ECOLI_3119 Escherichia coli 562 10057835

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861560	12274	34430	786	261

Description

6500731947 yrbi:b3198 hypothetical 20.0 kd protein in murz-rpon intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b3198 b3198 Escherichia coli 562 -11535805 7500952623 yrbi (de:hypothetical 20.0 kd protein in mura-rpon intergenic region) (db:swissprot) YRBI_ECOLI P45396 ESCHERICHIA COLI 562 -11535805 7000690922 yrbi hypothetical 20.0 kd protein in murz-rpon intergenic region (cl:hypothetical protein h11679) (db:pir2.dat) H65110 H65110 Escherichia coli 562 -11535805 7500952625 yrbi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:o188; sequence change joins orfs yrbi and yrbj from) (le:13546) (re:14112) (di:direct) AE000399 AE000399 g2367202 Escherichia coli 562 -11535805

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861562	12275	34431	210	69

Description

6500731948 yrbk:b3199 hypothetical 21.7 kd protein in murz-rpon intergenic region:hypothetical 21.7 kd protein in mura-rpon intergenic region:o191 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3199 b3199 Escherichia coli 562 -11535806 116114 yrbk (de:hypothetical 21.7 kd protein in mura-rpon intergenic region (o191)) (db:swissprot) YRBK_ECOLI P45397 ESCHERICHIA COLI 562 -11535806 7000688536 yrbk hypothetical 21.7 kd protein in murz-rpon intergenic region (db:pir2.dat) A65111 A65111 Escherichia coli 562 -11535806 7500952627 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o191) (le:123587) (re:124162) (di:direct) ECOUW67 U18997 g606138 Escherichia coli 562 -11535806 236437 yrbk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:o191; 100 pct identical amino acid sequence and) (le:14109) (re:14684) (di:direct) AE000399 AE000399 g1789591 Escherichia coli 562 -11535806 5000693439 (de:(ecoli_3122) (pn:hypothetical 21) (gn:yrbk) (gtcfc:13.7:14.1) (ec:) (yrbk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3122 ECOLI_3122 Escherichia coli 562 10057840

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861565	12276	34432	471	156

Description

6500731949 yhbj:b3205 hypothetical protein:hypothetical 32.5 kd protein in ptsn-ptso intergenic region:orf4:orf284 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3205 b3205 Escherichia coli 562 -11535807 238607 yhbj (de:(orf284)) (db:swissprot) YHBJ_ECOLI P33995 ESCHERICHIA COLI 562 -11535807 163702 hypothetical protein b3205 (cl:bacillus subtilis conserved hypothetical protein yvcj) (db:pir2.dat) I76721 I76721 Escherichia coli 562 -11535807 238259 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o284) (le:127866) (re:128720) (di:direct) ECOUW67 U18997 g606144 Escherichia coli 562 -11535807 5000693443 (db:genpept-bct1) (de:e.coli(k12) rpon gene for sigma factor 54.) (nt:orfiv) (le:2491) (re:3345) (di:direct) ECSIG540 Z27094 g414888 Escherichia coli 562 -11535807 7500936772 (fn:unknown, possible atpase) (db:genpept-bct1) (de:escherichia coli rpon operon and adjoining regions includingorf185, orf241, sigma-54 (rpon), orf95, iiantr (ptsn), orf284, andnpr (npr) genes, complete cds.) (nt:orf284) (le:3876) (re:4730) (di:direct) ECU12684 U12684 g551341 Escherichia coli 562 -11535807 236443 yhbj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 290 of 400 of the completegenome.) (nt:o284) (le:645) (re:1499) (di:direct) AE000400 AE000400 g1789598 Escherichia coli 562 -11535807 112637 yhbj (de:(orf284)) (db:swissprot) YHBJ_ECOLI P33995 ESCHERICHIA COLI 562 -11535807

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861566	12277	34433	486	161

Description

6500731950 yrbl:b3207 hypothetical protein:hypothetical 24.3 kd protein in ptso-arch intergenic region:o210 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3207 b3207 Escherichia coli 562 -11535808 116116 yrbl (de:hypothetical 24.3 kd protein in ptso-arch intergenic region (o210)) (db:swissprot) YRBL_ECOLI P46021 ESCHERICHIA COLI 562 -11535808 7000688537 hypothetical protein b3207 (db:pir2.dat) A65112 A65112 Escherichia coli 562 -11535808 7500952629 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o210) (le:129203) (re:129835) (di:direct) ECOUW67 U18997 g606146 Escherichia coli 562 -11535808 236445 yrbl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 290 of 400 of the completegenome.) (nt:o210) (le:1982) (re:2614) (di:direct) AE000400 AE000400 g1789600 Escherichia coli 562 -11535808 5000693445 (de:(ecoli_3130) (pn:hypothetical 24) (gtcfc:13.7:14.1) (ec:) (yrbl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3130 ECOLI_3130 Escherichia coli 562 10057842

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861588	12278	34434	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861624	12279	34435	3168	1055

Description

6500731951 yhcc:b3211 hypothetical 34.6 kd protein in arch-gltb intergenic region:f309 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3211 b3211 Escherichia coli 562 -11535809 7500936805 yhcc (de:hypothetical 34.6 kd protein in arch-gltb intergenic region) (db:swissprot) YHCC_ECOLI P45476 ESCHERICHIA COLI 562 -11535809 7000690937 yhcc hypothetical 34.6 kd protein in arch-gltb intergenic region (cl:methanococcus jannaschii conserved hypothetical protein mj0486) (db:pir2.dat) E65112 E65112 Escherichia coli 562 -11535809 7500936807 yhcc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 290 of 400 of the completegenome.) (nt:f309; 99 pct identical to yhcc_ecoli sw: p45476) (le:6645) (re:7574) (di:complement) AE000400 AE000400 g2367204 Escherichia coli 562 -11535809

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861632	12280	34436	483	160

Description

6500731952 yhca:b3215 hypothetical 25.3 kd fimbrial chaperone in gltf-nant intergenic region:hypothetical 25.3 kd fimbrial chaperone in gltf-nant intergenic region precursor:o224 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3215 b3215 Escherichia coli 562 -11535810 112664 yhca (de:precursor) (db:swissprot) YHCA_ECOLI P28722 ESCHERICHIA COLI 562 -11535810 7000687914 yhca hypothetical 25.3 kd fimbrial chaperone:gltf-nant intergenic region (db:pir2.dat) A65113 A65113 Escherichia coli 562 -11535810 7500936802 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o224) (le:142857) (re:143531) (di:direct) ECOUW67 U18997 g606154 Escherichia coli 562 -11535810 236453 yhca putative chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 291 of 400 of the completengenome.) (nt:o224; 100 pct identical amino acid sequence and) (le:1399) (re:2073) (di:direct) AE000401 AE000401 g1789609 Escherichia coli 562 -11535810 5000693449 (de:(ecoli_3138) (pn:hypothetical 25) (gn:yhca) (gtcfc:13.7:14.1) (ec:) (yhca_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3138 ECOLI_3138 Escherichia coli 562 10054392

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861640	12281	34437	615	204

Description

6500731953 yhcd:b3216 hypothetical outer membrane usher protein in gltf-nant intergenic region:hypothetical outer membrane usher protein in gltf-nant intergenic region precursor:o793 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3216 b3216 Escherichia coli 562 -11535811 112671 yhcd (de:region precursor) (db:swissprot) YHCD_ECOLI P45420 ESCHERICHIA COLI 562 -11535811 7000687919 yhcd hypothetical outer membrane usher protein in gltf-nant intergenic region (db:pir2.dat) B65113 B65113 Escherichia coli 562 -11535811 7500936808 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o793) (le:143552) (re:145933) (di:direct) ECOUW67 U18997 g606155 Escherichia coli 562 -11535811 236454 yhcd putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 291 of 400 of the completengenome.) (nt:o793; 100 pct identical amino acid sequence and) (le:2094) (re:4475) (di:direct) AE000401 AE000401 g1789610 Escherichia coli 562 -11535811 5000693450 (de:(ecoli_3139) (pn:hypothetical outer membrane usher protein in gltf-nant intergenic region precursor:o793) (gn:yhcd) (gtcfc:13.7:14.1) (ec:) (yhcd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3139 ECOLI_3139 Escherichia coli 562 10054399

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861652	12282	34438	534	177

Description

6500731954 yhcf:b3219 hypothetical protein:hypothetical 24.9 kd protein in gltf-nant intergenic region precursor:o238 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3219 b3219 Escherichia coli 562 -11535812 112675 yhcf (de:(o238)) (db:swissprot) YHCF_ECOLI P45422 ESCHERICHIA COLI 562 -11535812 7000687922 hypothetical protein b3219 (db:pir2.dat) E65113 E65113 Escherichia coli 562 -11535812 7500936809 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o238) (le:147671) (re:148387) (di:direct) ECOUW67 U18997 g606158 Escherichia coli 562 -11535812 236457 yhcf putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 291 of 400 of the completengenome.) (nt:o238) (le:6213) (re:6929) (di:direct) AE000401 AE000401 g1789613 Escherichia coli 562 -11535812 5000693452 (de:(ecoli_3142) (pn:hypothetical 24) (gtcfc:13.7:14.1) (ec:) (yhcf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3142 ECOLI_3142 Escherichia coli 562 10054403

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861653	12283	34439	1701	566

Description

6500731955 yhcg:b3220 hypothetical 43.3 kd protein in gltf-nant intergenic region:o375 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3220 b3220 Escherichia coli 562 -11535813 112677 yhcg (de:hypothetical 43.3 kd protein in gltf-nant intergenic region (o375)) (db:swissprot) YHCG_ECOLI P45423 ESCHERICHIA COLI 562 -11535813 7000687924 yhcg hypothetical 43.3 kd protein in gltf-nant intergenic region (db:pir2.dat) F65113 F65113 Escherichia coli 562 -11535813 7500936810 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o375) (le:148572) (re:149699) (di:direct) ECOUW67 U18997 g606159 Escherichia coli 562 -11535813 236458 yhcg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 291 of 400 of the completengenome.) (nt:o375; 100 pct identical amino acid sequence and) (le:7114) (re:8241) (di:direct) AE000401 AE000401 g1789614 Escherichia coli 562 -11535813 5000693453 (de:(ecoli_3143) (pn:hypothetical 43) (gn:yhcg) (gtcfc:13.7:14.1) (ec:) (yhcg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3143 ECOLI_3143 Escherichia coli 562 10054405

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861655	12284	34440	282	93

Description

6500731956 yhch:b3221 hypothetical protein:hypothetical 17.0 kd protein in gltf-nant intergenic region:f154 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3221 b3221 Escherichia coli 562 -11535814 112679 yhch (de:hypothetical 17.0 kd protein in gltf-nant intergenic region (f154)) (db:swissprot) YHCH_ECOLI P45424 ESCHERICHIA COLI 562 -11535814 7000687926 hypothetical protein b3221 (cl:hypothetical protein hi0227) (db:pir2.dat) G65113 G65113 Escherichia coli 562 -11535814 7500936811 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f154; 1st of 3 start codons) (le:149759) (re:150223) (di:complement) ECOUW67 U18997 g606160 Escherichia coli 562 -11535814 236459 yhch orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 291 of 400 of the completegenome.) (nt:f154) (le:8301) (re:8765) (di:complement) AE000401 AE000401 g1789615 Escherichia coli 562 -11535814 5000693454 (de:(ecoli_3144) (pn:hypothetical 17) (gtcfc:13.7:14.1) (ec:) (yhch_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3144 ECOLI_3144 Escherichia coli 562 10054407

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861663	12285	34441	846	281

Description

6500731957 yhci:b3222 hypothetical 30.8 kd protein in gltf-nant intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3222 b3222 Escherichia coli 562 -11535815 7000687928 yhci hypothetical 30.8 kd protein in gltf-nant intergenic region (cl:haemophilus probable glucose kinase:glucose kinase homology) (db:pir2.dat) H65113 H65113 Escherichia coli 562 -11535815 7500936813 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f302) (le:150220) (re:151128) (di:complement) ECOUW67 U18997 g606161 Escherichia coli 562 -11535815 236460 yhci putative nagc-like transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 291 of 400 of the completegenome.) (nt:f302; 100 pct identical amino acid sequence and) (le:8762) (re:9670) (di:complement) AE000401 AE000401 g1789616 Escherichia coli 562 -11535815 112682 yhci (de:hypothetical 30.8 kd protein in gltf-nant intergenic region) (db:swissprot) YHCI_ECOLI P45425 ESCHERICHIA COLI 562 -11535815 5000693455 (de:(ecoli_3145) (pn:hypothetical 30) (gn:yhci) (gtcfc:13.7:14.1) (ec:) (yhci_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3145 ECOLI_3145 Escherichia coli 562 10054410

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861680	12286	34442	1650	549

Description

6500731958 yhcj:b3223 hypothetical protein:hypothetical 24.1 kd protein in gltf-nant intergenic region:f229 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3223 b3223 Escherichia coli 562 -11535816 112685 yhcj (de:hypothetical 24.1 kd protein in gltf-nant intergenic region (f229)) (db:swissprot) YHCJ_ECOLI P45426 ESCHERICHIA COLI 562 -11535816 7000687930 hypothetical protein b3223 (db:pir2.dat) A65114 A65114 Escherichia coli 562 -11535816 7500936815 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f229) (le:151092) (re:151781) (di:complement) ECOUW67 U18997 g606162 Escherichia coli 562 -11535816 236461 yhcj putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 291 of 400 of the completegenome.) (nt:f229) (le:9634) (re:10323) (di:complement) AE000401 AE000401 g1789617 Escherichia coli 562 -11535816 5000693456 (de:(ecoli_3146) (pn:hypothetical 24) (gtcfc:13.7:14.1) (ec:) (yhcj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3146 ECOLI_3146 Escherichia coli 562 10054413

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861697	12287	34443	360	119

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861704	12288	34444	294	98

Description

6500731959 yhck:b3226 hypothetical protein:hypothetical transcriptional regulator in nana-sspb intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3226 b3226 Escherichia coli 562 -11535817 112687 yhck (de:hypothetical transcriptional regulator in nana-sspb intergenic region) (db:swissprot) YHCK_ECOLI P45427 ESCHERICHIA COLI 562 -11535817 7000687932 hypothetical protein b3226 (cl:regulatory protein fadr) (db:pir2.dat) D65114 D65114 Escherichia coli 562 -11535817 7500936817 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f263) (le:154443) (re:155234) (di:complement) ECOUW67 U18997 g606165 Escherichia coli 562 -11535817 236464 yhck putative fada-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 292 of 400 of the completegenome.) (nt:f263) (le:1085) (re:1876) (di:complement) AE000402 AE000402 g1789621 Escherichia coli 562 -11535817 5000693458 (de:(ecoli_3149) (pn:hypothetical transcriptional regulator in nana-sspb intergenic region:f263) (gtcfc:13.7:14.1) (ec:)(yhck_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3149 ECOLI_3149 Escherichia coli 562 10054415

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861713	12289	34445	738	245

Description

GTC ORF with score 112 to: (sr:kaposi's sarcoma-associated herpesvirus - human herpesvirus 8) (db:genpept-vr1) (de:kaposi's sarcoma-associated herpesvirus glycoprotein m, dnareplication protein, glycoprotein, dna replication protein, fliceinhibitory ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861722	12290	34446	768	256

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861741	12291	34447	537	178

Description

6500731960 yhcl:b3227 hypothetical 48.8 kd protein in nana-sspb intergenic region:o455 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3227 b3227 Escherichia coli 562 -11535818 112689 yhcl (de:hypothetical 48.8 kd protein in nana-sspb intergenic region (o455)) (db:swissprot) YHCL_ECOLI P45428 ESCHERICHIA COLI 562 -11535818 7000687934 yhcl hypothetical 48.8 kd protein in nana-sspb intergenic region (cl:dcuc protein) (db:pir2.dat) E65114 E65114 Escherichia coli 562 -11535818 7500936818 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o455) (le:155614) (re:156981) (di:direct) ECOUW67 U18997 g606166 Escherichia coli 562 -11535818 236465 yhcl putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 292 of 400 of the completegenome.) (nt:o455; 100 pct identical amino acid sequence and) (le:2256) (re:3623) (di:direct) AE000402 AE000402 g1789622 Escherichia coli 562 -11535818 5000693459 (de:(ecoli_3150) (pn:hypothetical 48) (gn:yhcl) (gtcfc:13.7:14.1) (ec:) (yhcl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3150 ECOLI_3150 Escherichia coli 562 10054417

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861743	12292	34448	357	118

Description

6500731961 yhcm:b3232 hypothetical 43.1 kd protein in rplm-hhoa intergenic region:f375 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3232 b3232 Escherichia coli 562 -11535819 112691 yhcm (de:hypothetical 43.1 kd protein in rplm-hhoa intergenic region (f375)) (db:swissprot) YHCM_ECOLI P46442 ESCHERICHIA COLI 562 -11535819 7000687936 yhcm hypothetical 43.1 kd protein in rplm-hhoa intergenic region (db:pir2.dat) B65115 B65115 Escherichia coli 562 -11535819 7500936819 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f375) (le:159615) (re:160742) (di:complement) ECOUW67 U18997 g606171 Escherichia coli 562 -11535819 236470 yhcm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 292 of 400 of the completegenome.) (nt:f375; 100 pct identical amino acid sequence and) (le:6257) (re:7384) (di:complement) AE000402 AE000402 g1789627 Escherichia coli 562 -11535819 5000693460 (de:(ecoli_3155) (pn:hypothetical 43) (gn:yhcm) (gtcfc:13.7:14.1) (ec:) (yhcm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3155 ECOLI_3155 Escherichia coli 562 10054419

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861746	12293	34449	549	182

Description

6500731962 yhcb:b3233 hypothetical 15.2 kd protein in rplm-hhoa intergenic region:o134 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3233 b3233 Escherichia coli 562 -11535820 112666 yhcb (de:hypothetical 15.2 kd protein in rplm-hhoa intergenic region (o134)) (db:swissprot) YHCB_ECOLI P39436 ESCHERICHIA COLI 562 -11535820 7000687916 yhcb hypothetical 15.2 kd protein in rplm-hhoa intergenic region (cl:hypothetical protein hi1628) (db:pir2.dat) C65115 C65115 Escherichia coli 562 -11535820 7500936803 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o134) (le:160930) (re:161334) (di:direct) ECOUW67 U18997 g606172 Escherichia coli 562 -11535820 236471 yhcb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 292 of 400 of the completegenome.) (nt:o134; 100 pct identical amino acid sequence and) (le:7572) (re:7976) (di:direct) AE000402 AE000402 g1789628 Escherichia coli 562 -11535820 5000693461 (de:(ecoli_3156) (pn:hypothetical 15) (gn:yhcb) (gtcfc:13.7:14.1) (ec:) (yhcb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3156 ECOLI_3156 Escherichia coli 562 10054394

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861764	12294	34450	285	94

Description

6500731963 yhcn:b3238 hypothetical protein:hypothetical 11.2 kd protein in argr-cafa intergenic region:o104 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3238 b3238 Escherichia coli 562 -11535821 7000687938 hypothetical protein b3238 (cl:conserved hypothetical protein b3238) (db:pir2.dat) H65115 H65115 Escherichia coli 562 -11535821 236476 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o104) (le:166232) (re:166546) (di:direct) ECOUW67 U18997 g606177 Escherichia coli 562 -11535821 7500960315 yhcn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 293 of 400 of the completegenome.) (nt:o104) (le:2219) (re:2533) (di:direct) AE000403 AE000403 g1789634 Escherichia coli 562 -11535821 112693 yhcn_ecoli (de:hypothetical 11.2 kd protein in argr-cafa intergenic region (o104).) P46477 P46477 Escherichia coli 562 -11535821 5000693464 (de:(ecoli_3161) (pn:hypothetical 11) (gtcfc:13.7:14.1) (ec:) (yhcn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3161 ECOLI_3161 Escherichia coli 562 10054421

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861768	12295	34451	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861770	12296	34452	297	98

Description

GTC ORF with score 352 to: (fn:converts 4-hydroxyphenylpyruvate to) (db:genpept-pln1) (ec:1.13.11.27) (de:mycosphaerella graminicola 4-hydroxyphenylpyruvate dioxygenase(hppd) gene, complete cds.) (nt:tyrosine catabolic pathway.) (le:1079) (re:2338) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861790	12297	34453	2244	747

Description

6500731964 yhco:b3239 hypothetical protein:hypothetical 10.8 kd protein in argr-cafa intergenic region:f90 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3239 b3239 Escherichia coli 562 -11535822 112695 yhco (de:hypothetical 10.8 kd protein in argr-cafa intergenic region (f90)) (db:swissprot) YHCO_ECOLI P46480 ESCHERICHIA COLI 562 -11535822 7000687940 hypothetical protein b3239 (db:pir2.dat) A65116 A65116 Escherichia coli 562 -11535822 7500936821 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f90; small but good stats) (le:166602) (re:166874) (di:complement) ECOUW67 U18997 g606178 Escherichia coli 562 -11535822 236477 yhco orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 293 of 400 of the completegenome.) (nt:f90; small but good stats) (le:2589) (re:2861) (di:complement) AE000403 AE000403 g1789635 Escherichia coli 562 -11535822 5000693465 (de:(ecoli_3162) (pn:hypothetical 10) (gtcfc:13.7:14.1) (ec:) (yhco_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3162 ECOLI_3162 Escherichia coli 562 10054423

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861795	12298	34454	1986	662

Description

6500731965 yhcp:b3240 hypothetical 73.6 kd protein in argr-cafa intergenic region:f655 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3240 b3240 Escherichia coli 562 -11535823 112697 yhcp (de:hypothetical 73.6 kd protein in argr-cafa intergenic region (f655)) (db:swissprot) YHCP_ECOLI P46481 ESCHERICHIA COLI 562 -11535823 7000687942 yhcp hypothetical 73.6 kd protein in argr-cafa intergenic region (db:pir2.dat) B65116 B65116 Escherichia coli 562 -11535823 7500936822 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f655) (le:166966) (re:168933) (di:complement) ECOUW67 U18997 g606179 Escherichia coli 562 -11535823 236478 yhcp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 293 of 400 of the completegenome.) (nt:f655; 100 pct identical amino acid sequence and) (le:2953) (re:4920) (di:complement) AE000403 AE000403 g1789636 Escherichia coli 562 -11535823 5000693466 (de:(ecoli_3163) (pn:hypothetical 73) (gn:yhcp) (gtcfc:13.7:14.1) (ec:) (ychcp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3163 ECOLI_3163 Escherichia coli 562 10054425

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861803	12299	34455	243	80

Description

6500731966 yhcq:b3241 hypothetical 34.8 kd protein in argr-cafa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3241 b3241 Escherichia coli 562 -11535824 112699 yhcq (de:hypothetical 34.8 kd protein in argr-cafa intergenic region) (db:swissprot) YHCQ_ECOLI P46482 ESCHERICHIA COLI 562 -11535824 7000687944 yhcq hypothetical 34.8 kd protein in argr-cafa intergenic region (cl:escherichia coli hypothetical protein b1644) (db:pir2.dat) C65116 C65116 Escherichia coli 562 -11535824 7500936823 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f310) (le:168939) (re:169871) (di:complement) ECOUW67 U18997 g606180 Escherichia coli 562 -11535824 236479 yhcq putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 293 of 400 of the completegenome.) (nt:f310; 100 pct identical amino acid sequence and) (le:4926) (re:5858) (di:complement) AE000403 AE000403 g1789637 Escherichia coli 562 -11535824 5000693467 (de:(ecoli_3164) (pn:hypothetical 34) (gn:yhcq) (gtcfc:13.7:14.1) (ec:) (yhqcq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3164 ECOLI_3164 Escherichia coli 562 10054427

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861808	12300	34456	1254	417

Description

GTC ORF with score 1244 to: (de:(yhr019c) (pn:putative asparaginyl-trna synthetase :asparagine-- trna ligase:asnrs:asparaginyl-trna-synthetase) (gn:ded81) (gtcfc:5.2:10.6) (ec:6.1.1.22) (de81_yeast) (keggfc:5.2:10.1:10.2) (sgdfc:5.4.0) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861815	12301	34457	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861817	12302	34458	660	219

Description

6500731967 yhcr:b3242 hypothetical protein: hypothetical 10.3 kd protein in argr-cafa intergenic region:f90 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3242 b3242 Escherichia coli 562 -11535825 112701 yhcr (de:hypothetical 10.3 kd protein in argr-cafa intergenic region (f90)) (db:swissprot) YHCR_ECOLI P46478 ESCHERICHIA COLI 562 -11535825 7000687946 hypothetical protein b3242 (db:pir2.dat) D65116 D65116 Escherichia coli 562 -11535825 7500936824 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f90) (le:169879) (re:170151) (di:complement) ECOUW67 U18997 g606181 Escherichia coli 562 -11535825 236480 yhcr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 293 of 400 of the completegenome.) (nt:f90) (le:5866) (re:6138) (di:complement) AE000403 AE000403 g1789638 Escherichia coli 562 -11535825 5000693468 (de:(ecoli_3165) (pn:hypothetical 10) (gtcfc:13.7:14.1) (ec:) (yhcr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3165 ECOLI_3165 Escherichia coli 562 10054429

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861839	12303	34459	417	138

Description

6500731968 yhcs:b3243 hypothetical protein:hypothetical transcriptional regulator in argr-cafa intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3243 b3243 Escherichia coli 562 -11535826 112703 yhcs (de:hypothetical transcriptional regulator in argr-cafa intergenic region) (db:swissprot) YHCS_ECOLI P45691 ESCHERICHIA COLI 562 -11535826 7000687948 hypothetical protein b3243 (cl:conserved hypothetical protein hil364) (db:pir2.dat) E65116 E65116 Escherichia coli 562 -11535826 7500936825 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o309) (le:170265) (re:171194) (di:direct) ECOUW67 U18997 g606182 Escherichia coli 562 -11535826 236481 yhcs putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 293 of 400 of the completegenome.) (nt:o309) (le:6252) (re:7181) (di:direct) AE000403 AE000403 g1789639 Escherichia coli 562 -11535826 5000693469 (de:(ecoli_3166) (pn:hypothetical transcriptional regulator in argr-cafa intergenic region:o309) (gtcfc:13.7:14.1) (ec:)(yhcs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3166 ECOLI_3166 Escherichia coli 562 10054431

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861840	12304	34460	222	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861843	12305	34461	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861850	12306	34462	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861852	12307	34463	246	81

Description

6500731969 hypothetical 107.7 kd protein in argr-cafa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b3245 b3245 Escherichia coli 562 -11535827 7500936849 yhdp (de:hypothetical 107.7 kd protein in argr-cafa intergenic region) (db:swissprot) YHDP_ECOLI P46474 ESCHERICHIA COLI 562 -11535827 7000690907 hypothetical 107.7 kd protein in argr-cafa intergenic region (db:pir2.dat) G65116 G65116 Escherichia coli 562 -11535827 7500936851 yhdp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 293 of 400 of the completegenome.) (nt:f986; sequence change joins orfs yhdp and yhdq from) (le:9191) (re:12151) (di:complement) AE000403 AE000403 g2367206 Escherichia coli 562 -11535827

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861859	12308	34464	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861862	12309	34465	453	150

Description

6500731970 yhdr:b3246 hypothetical 31.5 kd protein in argr-cafa intergenic region:hypothetical 31.5 kd protein in argr-cafa intergenic region precursor:f282 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3246 b3246 Escherichia coli 562 -11535828 112731 yhdr (de:hypothetical 31.5 kd protein in argr-cafa intergenic region precursor) (db:swissprot) YHDR_ECOLI P46476 ESCHERICHIA COLI 562 -11535828 7000687956 yhdr hypothetical 31.5 kd protein in argr-cafa intergenic region (db:pir2.dat) H65116 H65116 Escherichia coli 562 -11535828 7500936852 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f282) (le:176155) (re:177003) (di:complement) ECOUW67 U18997 g606186 Escherichia coli 562 -11535828 236485 yhdr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 293 of 400 of the completegenome.) (nt:f282; 100 pct identical amino acid sequence and) (le:12144) (re:12992) (di:complement) AE000403 AE000403 g1789643 Escherichia coli 562 -11535828 5000693473 (de:(ecoli_3170) (pn:hypothetical 31) (gn:yhdr) (gtcfc:13.7:14.1) (ec:) (yhdr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3170 ECOLI_3170 Escherichia coli 562 10054459

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861886	12310	34466	333	110

Description

6500731971 yhde:b3248 hypothetical 21.5 kd protein in cafa-mred intergenic region:orfe (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3248 b3248 Escherichia coli 562 -11535829 7500936832 yhde (de:hypothetical 21.5 kd protein in cafa-mred intergenic region (orfe)) (db:swissprot) YHDE_ECOLI P25536 ESCHERICHIA COLI 562 -11535829 163255 yhde hypothetical 21.5k protein cafa-mred intergenic region:orfe protein (cl:septum formation protein maf) (db:pir2.dat) JQ1271 JQ1271 Escherichia coli 562 -11535829 5000693474 (db:genpept-bct1) (de:e.coli mred gene, orfe and orff.) (nt:orfe) (le:44) (re:637) (di:direct) ECMRED X57166 g48825 Escherichia coli 562 -11535829 233403 yhde orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 294 of 400 of the completgenome.) (nt:f197; 100 pct identical to yhde_ecoli sw: p25536) (le:1523) (re:2116) (di:complement) AE000404 AE000404 g1789646 Escherichia coli 562 -11535829 112718 yhde (de:hypothetical 21.5 kd protein in cafa-mred intergenic region (orfe)) (db:swissprot) YHDE_ECOLI P25536 ESCHERICHIA COLI 562 -11535829

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861891	12311	34467	2340	779

Description

GTC ORF with score 1134 to: (db:genpept-pln1) (de:glomerella cingulata two-component histidine kinase chk-1 (chk-1)gene, complete cds.) (nt:similar to bacterial two-component histidine) (le:929:3085) (re:3031:3219) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861892	12312	34468	315	104

Description

6500731972 yhda:b3252 hypothetical 73.3 kd protein in mreB-acbB intergenic region:f646 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3252 b3252 Escherichia coli 562 -11535830 112716 yhda (de:hypothetical 73.3 kd protein in mreB-acbB intergenic region (f646)) (db:swissprot) YHDA_ECOLI P13518 ESCHERICHIA COLI 562 -11535830 7000687954 yhda hypothetical 73.3 kd protein:mreB-acbB intergenic region:hypothetical protein 102 envB 5 region (db:pir1.dat) (mp:71 min) QQECE5 F65117 Escherichia coli 562 -11535830 7500936831 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f646) (le:182137) (re:184077) (di:complement) ECOUW67 U18997 g606192 Escherichia coli 562 -11535830 236491 yhda orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 294 of 400 of the complete genome.) (nt:f646; 100 pct identical amino acid sequence and) (le:5130) (re:7070) (di:complement) AE000404 AE000404 g1789650 Escherichia coli 562 -11535830 5000693475 (de:(ecoli_3176) (pn:hypothetical 73) (gn:yhda) (gtcfc:13.7:14.1) (ec:) (yhda_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3176 ECOLI_3176 Escherichia coli 562 10054444

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861905	12313	34469	1998	665

Description

5000693477 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3254 b3254 Escherichia coli 562 -11535831 7000691810 hypothetical protein b3254 (db:pir2.dat) H65117 H65117 Escherichia coli 562 -11535831 7500960316 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f33) (le:185261) (re:185362) (di:complement) ECOUW67 U18997 g606194 Escherichia coli 562 -11535831 236493 b3254 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 294 of 400 of the complete genome.) (nt:f33; this 33 aa orf is 57 pct identical (1 gap)) (le:8254) (re:8355) (di:complement) AE000404 AE000404 g1789652 Escherichia coli 562 -11535831 6500731973 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3254 b3254 Escherichia coli 562 -11535831

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861921	12314	34470	729	242

Description

6500731974 yhdt:b3257 hypothetical 9.1 kd protein in accc-panf intergenic region:o80 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3257 b3257 Escherichia coli 562 -11535832 112732 yhdt (de:hypothetical 9.1 kd protein in accc-panf intergenic region (o80)) (db:swissprot) YHDT_ECOLI P45566 ESCHERICHIA COLI 562 -11535832 7000687957 yhdt hypothetical 9.1 kd protein in accc-panf intergenic region (db:pir2.dat) C65118 C65118 Escherichia coli 562 -11535832 7500936857 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o80) (le:188120) (re:188362) (di:direct) ECOUW67 U18997 g606197 Escherichia coli 562 -11535832 236496 yhdt orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 294 of 400 of the completegenome.) (nt:o80; 100 pct identical amino acid sequence and) (le:11113) (re:11355) (di:direct) AE000404 AE000404 g1789655 Escherichia coli 562 -11535832 5000693478 (de:(ecoli_3181) (pn:hypothetical 9) (gn:yhdt) (gtcfc:13.7:14.1) (ec:) (yhdt_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3181 ECOLI_3181 Escherichia coli 562 10054460

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861924	12315	34471	354	117

Description

6500731975 yhdg:b3260 hypothetical 35.9 kd protein in pmra-fis intergenic region:orf1 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3260 b3260 Escherichia coli 562 -11535833 112719 yhdg (de:hypothetical 35.9 kd protein in pmra-fis intergenic region (orf1)) (db:swissprot) YHDG_ECOLI P25717 ESCHERICHIA COLI 562 -11535833 164194 yhdg hypothetical 35.9k protein pmra-fis intergenic region:hypothetical 35.8k protein fis 5 region (cl:conserved hypothetical protein hi0979) (db:pir2.dat) B47043 B47043 Escherichia coli 562 -11535833 236500 (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli fis protein gene, orf3, 3'end; orf1, complete cds;orf2, 5'end.) (nt:'orf1') (le:794) (re:1759) (di:direct) ECOFISORFS M95784 g145976 Escherichia coli 562 -11535833 7500936837 yhdg (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o321) (le:191026) (re:191991) (di:direct) ECOUW67 U18997 g606201 Escherichia coli 562 -11535833 234356 yhdg putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 295 of 400 of the completegenome.) (nt:o321; 100 pct identical amino acid sequence and) (le:76) (re:1041) (di:direct) AE000405 AE000405 g1789660 Escherichia coli 562 -11535833 5000693480 (de:(ecoli_3185) (pn:hypothetical 35) (gn:yhdg) (gtcfc:13.7:14.1) (ec:) (yhdg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3185 ECOLI_3185 Escherichia coli 562 10054447

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861925	12316	34472	360	119

Description

6500731976 yhdj:b3262 hypothetical adenine-specific methylase in fis-envr
intergenic region:hypothetical adenine-specific methylase in fis-envr
intergenic region:orf2 (gtcfc:14.1) (ec:2.1.1.72) (keggfc:14.1)
(rileyfc:5.7.0) (db:gtc-escherichia coli) b3262 b3262 Escherichia coli 562
-11535834 7000687955 yhdj hypothetical adenine-specific methylase in
fis-envr intergenic region (cl:site-specific dna-methyltransferase
(adenine-specific) hpai) (db:pir2.dat) H65118 H65118 Escherichia coli 562
-11535834 7500936840 yhdj (db:genpept-bct1) (de:escherichia coli k-12
chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o296) (le:192393)
(re:193283) (di:direct) ECOUW67 U18997 g606203 Escherichia coli 562
-11535834 236502 yhdj putative methyltransferase (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 295
of 400 of the completegenome.) (nt:o296; 100 pct identical amino acid
sequence and) (le:1443) (re:2333) (di:direct) AE000405 AE000405 g1789662
Escherichia coli 562 -11535834 112723 yhdj (ec:2.1.1.72) (de:(ec 2.1.1.72)
(orf2)) (db:swissprot) YHDJ_ECOLI P28638 ESCHERICHIA COLI 562 -11535834
5000693481 (de:(ecoli_3187) (pn:hypothetical adenine-specific methylase in
fis-envr intergenic region:orf2:o296) (gn:yhdj) (gtcfc:13.7:14.1) (ec:)
(yhdj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_3187 ECOLI_3187 Escherichia coli 562 10054451

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861926	12317	34473	354	117

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501861937	12318	34474	684	227

Description

6500731977 yhdu:b3263 hypothetical protein:hypothetical 7.2 kd protein in fis-envr intergenic region:o59 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3263 b3263 Escherichia coli 562 -11535835 112734 yhdu (de:hypothetical 7.2 kd protein in fis-envr intergenic region (o59)) (db:swissprot) YH DU_ECOLI P45764 ESCHERICHIA COLI 562 -11535835 7000687958 hypothetical protein b3263 (db:pir2.dat) A65119 A65119 Escherichia coli 562 -11535835 7500936859 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o59) (le:193367) (re:193546) (di:direct) ECOUW67 U18997 g606204 Escherichia coli 562 -11535835 236503 yhdu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 295 of 400 of the completengenome.) (nt:o59) (le:2417) (re:2596) (di:direct) AE000405 AE000405 g1789663 Escherichia coli 562 -11535835 5000693482 (de:(ecoli_3188) (pn:hypothetical 7) (gtcfc:13.7:14.1) (ec:) (yhdu_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3188 ECOLI_3188 Escherichia coli 562 10054462

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501861946	12319	34475	276	91

Description

6500731978 yhdv:b3267 hypothetical 7.5 kd protein in acrf-rrnd intergenic region:o73 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3267 b3267 Escherichia coli 562 -11535836 112735 yhdv (de:hypothetical 7.5 kd protein in acrf-rrnd intergenic region (o73)) (db:swissprot) YH DV_ECOLI P45765 ESCHERICHIA COLI 562 -11535836 7000687959 yhdv hypothetical 7.5 kd protein in acrf-rrnd intergenic region (db:pir2.dat) E65119 E65119 Escherichia coli 562 -11535836 7500936860 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o73) (le:199136) (re:199357) (di:direct) ECOUW67 U18997 g606208 Escherichia coli 562 -11535836 236507 yhdv orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 295 of 400 of the completengenome.) (nt:o73; 100 pct identical amino acid sequence and) (le:8186) (re:8407) (di:direct) AE000405 AE000405 g1789667 Escherichia coli 562 -11535836 5000693485 (de:(ecoli_3192) (pn:hypothetical 7) (gn:yhdv) (gtcfc:13.7:14.1) (ec:) (yhdv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3192 ECOLI_3192 Escherichia coli 562 10054463

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861955	12320	34476	510	169

Description

6500731979 yhdw:b3268 hypothetical amino-acid abc transporter in acrf-rrnd intergenic region:hypothetical amino-acid abc transporter binding protein in acrf-rrnd intergenic region precursor (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3268 b3268 Escherichia coli 562 -11535837 112736 yhdw (de:intergenic region precursor) (db:swissprot) YHDW_ECOLI P45766 ESCHERICHIA COLI 562 -11535837 7000687960 yhdw hypothetical amino-acid abc transporter in acrf-rrnd intergenic region (db:pir2.dat) F65119 F65119 Escherichia coli 562 -11535837 7500936861 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o305; frameshift upstream would extend start) (le:199895) (re:200812) (di:direct) ECOUW67 U18997 g606209 Escherichia coli 562 -11535837 236508 yhdw putative periplasmic binding transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 295 of 400 of the completegenome.) (nt:o305; o305; frameshift upstream would extend) (le:8945) (re:9862) (di:direct) AE000405 AE000405 g1789668 Escherichia coli 562 -11535837 5000693486 (de:(ecoli_3193) (pn:hypothetical amino-acid abc transporter binding protein in acrf-rrnd intergenic region precursor:o305) (gn:yhdw) (gtcfc:13.7:14.1) (ec:) (yhdw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3193 ECOLI_3193 Escherichia coli 562 10054464

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861957	12321	34477	435	144

Description

6500731980 yhdx:b3269 hypothetical 40.4 kd protein in acrf-rrnd intergenic region:hypothetical abc transporter permease protein yhdx (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3269 b3269 Escherichia coli 562 -11535838 7000687961 yhdx hypothetical 40.4 kd protein in acrf-rrnd intergenic region (db:pir2.dat) G65119 G65119 Escherichia coli 562 -11535838 7500936862 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o368a; frameshift at end might extend) (le:200862) (re:201968) (di:direct) ECOUW67 U18997 g606210 Escherichia coli 562 -11535838 236509 yhdx putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 295 of 400 of the completegenome.) (nt:o368; o368a; frameshift at end might extend; 100) (le:9912) (re:11018) (di:direct) AE000405 AE000405 g1789669 Escherichia coli 562 -11535838 112737 yhdx (de:hypothetical amino-acid abc transporter permease protein yhdx) (db:swissprot) YHDX_ECOLI P45767 ESCHERICHIA COLI 562 -11535838 5000693487 (de:(ecoli_3194) (pn:hypothetical 40) (gn:yhdx) (gtcfc:13.7:14.1) (ec:) (yhdx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3194 ECOLI_3194 Escherichia coli 562 10054465

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861958	12322	34478	366	121

Description

6500731981 yhdy:b3270 hypothetical 41.6 kd protein in acrf-rrnd intergenic region:hypothetical abc transporter permease protein yhdy (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3270 b3270 Escherichia coli 562 -11535839 7000687962 yhdy hypothetical 41.6 kd protein in acrf-rrnd intergenic region (db:pir2.dat) H65119 H65119 Escherichia coli 562 -11535839 7500936863 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o368b) (le:202067) (re:203173) (di:direct) ECOUW67 U18997 g606211 Escherichia coli 562 -11535839 236510 yhdy putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 296 of 400 of the completegenome.) (nt:o368; 100 pct identical amino acid sequence and) (le:80) (re:1186) (di:direct) AE000406 AE000406 g1789671 Escherichia coli 562 -11535839 112738 yhdy (de:hypothetical amino-acid abc transporter permease protein yhdy) (db:swissprot) YHDY_ECOLI P45768 ESCHERICHIA COLI 562 -11535839 5000693488 (de:(ecoli_3195) (pn:hypothetical 41) (gn:yhdy) (gtcfc:13.7:14.1) (ec:)) (yhdy_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3195 ECOLI_3195 Escherichia coli 562 10054466

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861960	12323	34479	297	98

Description

6500731982 yhdz:b3271 hypothetical abc transporter in acrf-rrnd intergenic region:hypothetical abc transporter atp-binding protein in acrf-rrnd intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3271 b3271 Escherichia coli 562 -11535840 112739 yhdz (de:hypothetical amino-acid abc transporter atp-binding protein yhdz) (db:swissprot) YHDZ_ECOLI P45769 ESCHERICHIA COLI 562 -11535840 7000687963 yhdz abc-type transport protein yhdz (cl:inner membrane protein malk:atp-binding cassette homology) (db:pir2.dat) A65120 A65120 Escherichia coli 562 -11535840 7500936864 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o252) (le:203181) (re:203939) (di:direct) ECOUW67 U18997 g606212 Escherichia coli 562 -11535840 236511 yhdz putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 296 of 400 of the completegenome.) (nt:o252; 100 pct identical amino acid sequence and) (le:1194) (re:1952) (di:direct) AE000406 AE000406 g1789672 Escherichia coli 562 -11535840 5000693489 (de:(ecoli_3196) (pn:hypothetical abc transporter atp-binding protein in acrf-rrnd intergenic region:o252) (gn:yhdz) (gtcfc:13.7:14.1) (ec:)) (yhdz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3196 ECOLI_3196 Escherichia coli 562 10054467

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861962	12324	34480	378	125

Description

6500731983 yrda:b3279 hypothetical protein:hypothetical 28.4 kd protein in rrnd-aroe intergenic region:o256 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3279 b3279 Escherichia coli 562 -11535841 116125 yrda (de:hypothetical 28.4 kd protein in rrnd-aroe intergenic region (o256)) (db:swissprot) YRDA_ECOLI P45770 ESCHERICHIA COLI 562 -11535841 7000688538 hypothetical protein b3279 (db:pir2.dat) B65120 B65120 Escherichia coli 562 -11535841 7500952630 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o256) (le:209766) (re:210536) (di:direct) ECOUW67 U18997 g606213 Escherichia coli 562 -11535841 236512 yrda putative transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 296 of 400 of the completegenome.) (nt:o256) (le:7779) (re:8549) (di:direct) AE000406 AE000406 g1789673 Escherichia coli 562 -11535841 5000693490 (de:(ecoli_3197) (pn:hypothetical 28) (gtcfc:13.7:14.1) (ec:) (yrda_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3197 ECOLI_3197 Escherichia coli 562 10057851

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861965	12325	34481	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861968	12326	34482	432	143

Description

6500731984 yrdb:b3280 hypothetical 10.0 kd protein in rrnd-aroe intergenic region:f85 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3280 b3280 Escherichia coli 562 -11535842 116126 yrdb (de:hypothetical 10.0 kd protein in rrnd-aroe intergenic region (f85)) (db:swissprot) YRDB_ECOLI P45795 ESCHERICHIA COLI 562 -11535842 7000688539 yrdb hypothetical 10.0 kd protein in rrnd-aroe intergenic region (db:pir2.dat) C65120 C65120 Escherichia coli 562 -11535842 7500952631 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f85) (le:210512) (re:210769) (di:complement) ECOUW67 U18997 g606214 Escherichia coli 562 -11535842 236513 yrdb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 296 of 400 of the completegenome.) (nt:f85; 100 pct identical amino acid sequence and) (le:8525) (re:8782) (di:complement) AE000406 AE000406 g1789674 Escherichia coli 562 -11535842 5000693491 (de:(ecoli_3198) (pn:hypothetical 10) (gn:yrdb) (gtcfc:13.7:14.1) (ec:) (yrdb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3198 ECOLI_3198 Escherichia coli 562 10057852

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861971	12327	34483	618	205

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861975	12328	34484	501	166

Description

6500731985 yrdc:b3282 hypothetical protein in aroe-smg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3282 b3282 Escherichia coli 562 -11535843 7500952632 yrdc (de:hypothetical 20.8 kd protein in aroe-smg intergenic region) (db:swissprot) YRDC_ECOLI P45748 ESCHERICHIA COLI 562 -11535843 7000691825 yrdc hypothetical protein in aroe-smg intergenic region (db:pir2.dat) E65120 E65120 Escherichia coli 562 -11535843 7500952634 yrdc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 296 of 400 of the completegenome.) (nt:f190; sequence change lengthens n-terminus relative) (le:9602) (re:10174) (di:complement) AE000406 AE000406 g2367210 Escherichia coli 562 -11535843

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501861977	12329	34485	417	138

Description

6500731986 yrdd:b3283 hypothetical 18.6 kd protein in aroe-smg intergenic region:f169 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3283 b3283 Escherichia coli 562 -11535844 116129 yrdd (de:hypothetical 18.6 kd protein in aroe-smg intergenic region (f169)) (db:swissprot) YRDD_ECOLI P45771 ESCHERICHIA COLI 562 -11535844 7000688540 yrdd hypothetical 18.6 kd protein in aroe-smg intergenic region (db:pir2.dat) F65120 F65120 Escherichia coli 562 -11535844 7500952636 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f169) (le:212167) (re:212676) (di:complement) ECOUW67 U18997 g606217 Escherichia coli 562 -11535844 236516 yrdd putative dna topoisomerase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 296 of 400 of the completegenome.) (nt:f169; 100 pct identical amino acid sequence and) (le:10179) (re:10688) (di:complement) AE000406 AE000406 g1789677 Escherichia coli 562 -11535844 5000693493 (de:(ecoli_3201) (pn:hypothetical 18) (gn:yrdd) (gtcfc:13.7:14.1) (ec:) (yrdd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3201 ECOLI_3201 Escherichia coli 562 10057855

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861978	12330	34486	630	210

Description

5000693496 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b3286 b3286 Escherichia coli
562 -11535845 7000691917 smf smf protein (db:pir2.dat) (mp:72 min) A65121
A65121 Escherichia coli 562 -11535845 7500960463 smf (db:genpept-bct1)
(de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.)
(nt:different end due to fs difference) (le:213546) (re:214307)
(di:complement) ECOUW67 U18997 g606220 Escherichia coli 562 -11535845
236519 smf_1 orf:fragment 1 (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 297 of 400 of the completegenome.)
(nt:f253; 100 pct identical to n-terminal 248 residues) (le:869) (re:1630)
(di:complement) AE000407 AE000407 g1789681 Escherichia coli 562 -11535845
6500731987 hypothetical protein (gtcfc:14.1) (keggfc:14.2)
(rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b3286 b3286 Escherichia coli
562 -11535845

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861990	12331	34487	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861996	12332	34488	1176	392

Description

6500731988 yhdm:b3292 hypothetical transcriptional regulator in mscl-rplq
intergenic region:hypothetical transcriptional regulator in mscl-rplq
intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3292 b3292 Escherichia coli 562 -11535846 112726
zntr (de:zn(ii)-responsive regulator of znta) (db:swissprot) ZNTR_ECOLI
P36676 ESCHERICHIA COLI 562 -11535846 163188 yhdm hypothetical
transcription regulator mscl-rplq intergenic region:hg resistance protein
homolog (cl:transcription repressor glnr) (db:pir2.dat) I67892 I67892
Escherichia coli 562 -11535846 237656 yhdm (db:genpept-bct1)
(de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.)
(le:219453) (re:219878) (di:complement) ECOUW67 U18997 g606226 Escherichia
coli 562 -11535846 7500936842 yhdm (sr:escherichia coli dna)
(db:genpept-bct1) (de:escherichia coli (pn02530) yhdc, yhdl, yhdm and yhdn
genes,complete cds's.) (nt:similar to merr (hg resistance) proteins)
(le:682) (re:1107) (di:complement) ECOYHDM L29458 g473422 Escherichia coli
562 -11535846 236525 yhdm putative transcriptional regulator (fn:putative
regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 297 of 400 of the completegenome.) (nt:f141; 100 pct
identical amino acid sequence and) (le:6775) (re:7200) (di:complement)
AE000407 AE000407 g1789687 Escherichia coli 562 -11535846 5000693498
(de:(ecoli_3210) (pn:hypothetical transcriptional regulator in mscl-rplq
intergenic region) (gn:yhdm) (gtcfc:13.7:14.1) (ec:) (yhdm_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3210
ECOLI_3210 Escherichia coli 562 10054454

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501861997	12333	34489	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862011	12334	34490	297	98

Description

6500731989 yhdn:b3293 hypothetical 13.9 kd protein in mscl-rplq intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3293 b3293 Escherichia coli 562 -11535847 112728 yhdn (de:hypothetical 13.9 kd protein in mscl-rplq intergenic region) (db:swissprot) YHDN_ECOLI P36677 ESCHERICHIA COLI 562 -11535847 164847 yhdn hypothetical 13.9k protein mscl-rplq intergenic region:yhdn protein (db:pir2.dat) I67893 I67893 Escherichia coli 562 -11535847 237657 yhdn (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:219889) (re:220257) (di:complement) ECOUW67 U18997 g606227 Escherichia coli 562 -11535847 7500936844 yhdn (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli (pn02530) yhdc, yhdl, yhdm and yhdn genes,complete cds's.) (le:1118) (re:1486) (di:complement) ECOYHDM L29458 g473423 Escherichia coli 562 -11535847 236526 yhdn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 297 of 400 of the completegenome.) (nt:f122; 100 pct identical amino acid sequence and) (le:7211) (re:7579) (di:complement) AE000407 AE000407 g1789688 Escherichia coli 562 -11535847 5000693499 (de:(ecoli_3211) (pn:hypothetical 13) (gn:yhdn) (gtcfc:13.7:14.1) (ec:) (yhdn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3211 ECOLI_3211 Escherichia coli 562 10054456

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862014	12335	34491	237	78

Description

6500731990 yheb:b3338 hypothetical 97.1 kd protein in bfr-tufa intergenic region:hypothetical 97.1 kd protein in bfr-tufa intergenic region precursor:gen24:f897 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3338 b3338 Escherichia coli 562 -11535848 112754 yheb (de:(gen24') (f897)) (db:swissprot) YHEB_ECOLI P13656 ESCHERICHIA COLI 562 -11535848 7000687964 yheb hypothetical 97.1 kd protein bfr-tufa intergenic region (db:pir2.dat) (mp:73 min) E65127 E65127 Escherichia coli 562 -11535848 7500936874 yheb (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f897) (le:247908) (re:250601) (di:complement) ECOUW67 U18997 g606272 Escherichia coli 562 -11535848 236571 yheb putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 300 of 400 of the completegenome.) (nt:f897; 100 pct identical amino acid sequence and) (le:429) (re:3122) (di:complement) AE000410 AE000410 g1789736 Escherichia coli 562 -11535848 5000693515 (de:(ecoli_3256) (pn:hypothetical 97) (gn:yheb) (gtcfc:13.7:14.1) (ec:) (yheb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3256 ECOLI_3256 Escherichia coli 562 10054482

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862015	12336	34492	405	134

Description

6500731991 yhel:b3343 hypothetical 10.7 kd protein in rpsl-fkpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3343 b3343 Escherichia coli 562 -11535849 112755 yhel (de:hypothetical 10.7 kd protein in rpsl-fkpa intergenic region) (db:swissprot) YHEL_ECOLI P45530 ESCHERICHIA COLI 562 -11535849 7000687965 yhel hypothetical 10.7 kd protein in rpsl-fkpa intergenic region (db:pir2.dat) B65128 B65128 Escherichia coli 562 -11535849 7500936875 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f95) (le:255426) (re:255713) (di:complement) ECOUW67 U18997 g606277 Escherichia coli 562 -11535849 236576 yhel orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 300 of 400 of the completegenome.) (nt:f95; 100 pct identical amino acid sequence and) (le:7947) (re:8234) (di:complement) AE000410 AE000410 g1789741 Escherichia coli 562 -11535849 5000693516 (de:(ecoli_3261) (pn:hypothetical 10) (gn:yhel) (gtcfc:13.7:14.1) (ec:) (yhel_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3261 ECOLI_3261 Escherichia coli 562 10054483

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862017	12337	34493	198	65

Description

6500731992 yhem:b3344 hypothetical protein:hypothetical 13.0 kd protein in rpsl-fkpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3344 b3344 Escherichia coli 562 -11535850 112756 yhem (de:hypothetical 13.0 kd protein in rpsl-fkpa intergenic region) (db:swissprot) YHEM_ECOLI P45531 ESCHERICHIA COLI 562 -11535850 7000687966 hypothetical protein b3344 (db:pir2.dat) C65128 C65128 Escherichia coli 562 -11535850 7500936876 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f119) (le:255721) (re:256080) (di:complement) ECOUW67 U18997 g606278 Escherichia coli 562 -11535850 236577 yhem orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 300 of 400 of the completegenome.) (nt:f119) (le:8242) (re:8601) (di:complement) AE000410 AE000410 g1789742 Escherichia coli 562 -11535850 5000693517 (de:(ecoli_3262) (pn:hypothetical 13) (gtcfc:13.7:14.1) (ec:) (yhem_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3262 ECOLI_3262 Escherichia coli 562 10054484

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862020	12338	34494	294	97

Description

6500731993 yhen:b3345 hypothetical 13.6 kd protein in rpsl-fkpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3345 b3345 Escherichia coli 562 -11535851 112757 yhen (de:hypothetical 13.6 kd protein in rpsl-fkpa intergenic region) (db:swissprot) YHEN_ECOLI P45532 ESCHERICHIA COLI 562 -11535851 7000687967 yhen hypothetical 13.6 kd protein in rpsl-fkpa intergenic region (cl:hypothetical protein hi0576) (db:pir2.dat) D65128 D65128 Escherichia coli 562 -11535851 7500936878 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f128) (le:256080) (re:256466) (di:complement) ECOUW67 U18997 g606279 Escherichia coli 562 -11535851 236578 yhen orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 300 of 400 of the completegenome.) (nt:f128; 100 pct identical amino acid sequence and) (le:8601) (re:8987) (di:complement) AE000410 AE000410 g1789743 Escherichia coli 562 -11535851 5000693518 (de:(ecoli_3263) (pn:hypothetical 13) (gn:yhen) (gtcfc:13.7:14.1) (ec:) (yhen_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3263 ECOLI_3263 Escherichia coli 562 10054485

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862022	12339	34495	309	102

Description

6500731994 yheo:b3346 hypothetical protein:hypothetical 27.4 kd protein in rpsl-fkpa intergenic region:f244 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3346 b3346 Escherichia coli 562 -11535852 7000687968 hypothetical protein b3346 (db:pir2.dat) E65128 E65128 Escherichia coli 562 -11535852 7500936880 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f244; gtg start) (le:256466) (re:257200) (di:complement) ECOUW67 U18997 g606280 Escherichia coli 562 -11535852 236579 yheo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 300 of 400 of the completegenome.) (nt:f244; gtg start) (le:8987) (re:9721) (di:complement) AE000410 AE000410 g1789744 Escherichia coli 562 -11535852 112759 yheo (de:hypothetical 27.4 kd protein in rpsl-fkpa intergenic region (f244)) (db:swissprot) YHEO_ECOLI P45533 ESCHERICHIA COLI 562 -11535852 5000693519 (de:(ecoli_3264) (pn:hypothetical 27) (gtcfc:13.7:14.1) (ec:) (yheo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3264 ECOLI_3264 Escherichia coli 562 10054487

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862025	12340	34496	645	214

Description

6500731995 yher:b3351 hypothetical nadph oxidoreductase in kifb-prkb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3351 b3351 Escherichia coli 562 -11535853 112761 yher (ec:1.6.99.-) (de:putative nad(p)h oxidoreductase yher,) (db:swissprot) YHER_ECOLI P45534 ESCHERICHIA COLI 562 -11535853 7000687969 yher hypothetical nad p h oxidoreductase in kifb-prkb intergenic region (cl:probable nad(p)h oxidoreductase yabf) (db:pir2.dat) B65129 B65129 Escherichia coli 562 -11535853 7500936882 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f184; frameshift near start not found) (le:261355) (re:261909) (di:complement) ECOUW67 U18997 g606285 Escherichia coli 562 -11535853 236584 yher putative nad p h oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 301 of 400 of the completegenome.) (nt:f184; f184; frameshift near start not found; 100) (le:3108) (re:3662) (di:complement) AE000411 AE000411 g1789750 Escherichia coli 562 -11535853 5000693522 (de:(ecoli_3269) (pn:hypothetical nad:ph oxidoreductase in kifb-prkb intergenic region) (gn:yher) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3269 ECOLI_3269 Escherichia coli 562 10054489

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862030	12341	34497	408	135

Description

6500731996 yhes:b3352 hypothetical abc transporter in kifb-prkb intergenic region:hypothetical abc transporter atp-binding protein in kifb-prkb intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3352 b3352 Escherichia coli 562 -11535854 112762 yhes (de:hypothetical abc transporter atp-binding protein yhes) (db:swissprot) YHES_ECOLI P45535 ESCHERICHIA COLI 562 -11535854 7000687970 yhes hypothetical abc transporter in kifb-prkb intergenic region (cl:atp-binding cassette homology) (db:pir2.dat) C65129 C65129 Escherichia coli 562 -11535854 7500936883 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o637) (le:262037) (re:263950) (di:direct) ECOUW67 U18997 g606286 Escherichia coli 562 -11535854 236585 yhes putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 301 of 400 of the completegenome.) (nt:o637; 100 pct identical amino acid sequence and) (le:3790) (re:5703) (di:direct) AE000411 AE000411 g1789751 Escherichia coli 562 -11535854 5000693523 (de:(ecoli_3270) (pn:hypothetical abc transporter in kifb-prkb intergenic region) (gn:yhes) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3270 ECOLI_3270 Escherichia coli 562 10054490

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862035	12342	34498	315	104

Description

GTC ORF with score 90 to: (or:Macaca mulatta) (sr:rhesus monkey)
(db:genpept-pri2) (de:macaca mulatta platelet and t cell activation antigen
1 (ptal)mrna, complete cds.) (nt:t lineage-specific activation antigen 1;
tlisal) (le:1) (re:1011) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862043	12343	34499	291	96

Description

6500731997 yhet:b3353 hypothetical 38.5 kd protein in kifb-prkb intergenic
region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)
b3353 b3353 Escherichia coli 562 -11535855 112765 yhet (de:hypothetical
38.5 kd protein in kifb-prkb intergenic region) (db:swissprot) YHET_ECOLI
P45524 ESCHERICHIA COLI 562 -11535855 7000687971 yhet hypothetical 38.5 kd
protein in kifb-prkb intergenic region (db:pir2.dat) D65129 D65129
Escherichia coli 562 -11535855 7500936885 (db:genpept-bct1) (de:escherichia
coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o340)
(le:263950) (re:264972) (di:direct) ECOUW67 U18997 g606287 Escherichia coli
562 -11535855 236586 yhet orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 301 of 400 of the
completegenome.) (nt:o340; 100 pct identical amino acid sequence and)
(le:5703) (re:6725) (di:direct) AE000411 AE000411 g1789752 Escherichia coli
562 -11535855 5000693524 (de:(ecoli_3271) (pn:hypothetical 38) (gn:yhet)
(gtcfc:13.7:14.1) (ec:) (yhet_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_3271 ECOLI_3271 Escherichia coli 562
10054493

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862064	12344	34500	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862065	12345	34501	765	254

Description

6500731998 yheu:b3354 hypothetical 8.5 kd protein in kifb-prkb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3354 b3354 Escherichia coli 562 -11535856 112766 yheu (de:hypothetical 8.5 kd protein in kifb-prkb intergenic region) (db:swissprot) YHEU_ECOLI P45536 ESCHERICHIA COLI 562 -11535856 7000687972 yheu hypothetical 8.5 kd protein in kifb-prkb intergenic region (cl:hypothetical protein hi0956) (db:pir2.dat) E65129 E65129 Escherichia coli 562 -11535856 7500936886 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o72; alternate orf with good statistics, no) (le:264966) (re:265184) (di:direct) ECOUW67 U18997 g606288 Escherichia coli 562 -11535856 236587 yheu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 301 of 400 of the completegenome.) (nt:o72; o72; alternate orf with good statistics,) (le:6719) (re:6937) (di:direct) AE000411 AE000411 g1789753 Escherichia coli 562 -11535856 5000693525 (de:(ecoli_3272) (pn:hypothetical 8) (gn:yheu) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3272 ECOLI_3272 Escherichia coli 562 10054494

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862067	12346	34502	417	138

Description

6500731999 yhfa:b3356 hypothetical protein:hypothetical 14.5 kd protein in prkb-crp intergenic region:f134 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3356 b3356 Escherichia coli 562 -11535857 112769 yhfa (de:hypothetical 14.5 kd protein in prkb-crp intergenic region (f134)) (db:swissprot) YHFA_ECOLI P24246 ESCHERICHIA COLI 562 -11535857 7000687973 hypothetical protein b3356:14k hypothetical protein crp region (db:pir2.dat) G65129 G65129 Escherichia coli 562 -11535857 7500936889 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f134) (le:266161) (re:266565) (di:complement) ECOUW67 U18997 g606290 Escherichia coli 562 -11535857 236589 yhfa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 301 of 400 of the completegenome.) (nt:f134) (le:7915) (re:8319) (di:complement) AE000411 AE000411 g1789755 Escherichia coli 562 -11535857 5000693526 (de:(ecoli_3274) (pn:hypothetical 14) (gtcfc:13.7:14.1) (ec:) (yhfa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3274 ECOLI_3274 Escherichia coli 562 10054497

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862070	12347	34503	735	244

Description

6500732000 yhfk:b3358 hypothetical 79.5 kd protein in crp-argd intergenic region:o696 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3358 b3358 Escherichia coli 562 -11535858 112775 yhfk (de:hypothetical 79.5 kd protein in crp-argd intergenic region (o696)) (db:swissprot) YHFK_ECOLI P45537 ESCHERICHIA COLI 562 -11535858 7000687975 yhfk hypothetical 79.5 kd protein in crp-argd intergenic region (db:pir2.dat) A65130 A65130 Escherichia coli 562 -11535858 7500936892 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o696) (le:267550) (re:269640) (di:direct) ECOUW67 U18997 g606292 Escherichia coli 562 -11535858 236591 yhfk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 301 of 400 of the completegenome.) (nt:o696; 100 pct identical amino acid sequence and) (le:9304) (re:11394) (di:direct) AE000411 AE000411 g1789757 Escherichia coli 562 -11535858 5000693527 (de:(ecoli_3276) (pn:hypothetical 79) (gn:yhfk) (gtcfc:13.7:14.1) (ec:) (yhfk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3276 ECOLI_3276 Escherichia coli 562 10054503

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862078	12348	34504	873	291

Description

GTC ORF with score 191 to: (sr:agrobacterium tumefaciens dna) (db:genpept-bct2) (de:agrobacterium tumefaciens cela, celb, celc, celd, cele genes,complete cdss; fixr gene, partial cds.) (nt:alternate start for cela) (le:9535) (re:11724) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862096	12349	34505	1065	354

Description

6500732001 yhfg:b3362 f5:hypothetical 6.6 kd protein in fic-ppia intergenic region:f55 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3362 b3362 Escherichia coli 562 -11535859 112771 yhfg (de:hypothetical 6.6 kd protein in fic-ppia intergenic region (f55)) (db:swissprot) YHFG_ECOLI P37770 ESCHERICHIA COLI 562 -11535859 163289 yhfg hypothetical 6k protein ppia-fic intergenic region (db:pir2.dat) (mp:74 min) JV0064 JV0064 Escherichia coli 562 -11535859 236595 (sr:e.coli dna, clone pszd3) (db:genpept-bct1) (de:e.coli glutamine amidotransferase subunit of para-aminobenzoatesynthase (paba) and pot. cell division protein (fic) genes,complete cds.) (nt:orf1 (gtg start codon)) (le:572) (re:739) (di:direct) ECOPABAA M32354 g147053 Escherichia coli 562 -11535859 7500936891 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f55) (le:272200) (re:272367) (di:complement) ECOUW67 U18997 g606296 Escherichia coli 562 -11535859 235320 yhfg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 302 of 400 of the completegenome.) (nt:f55; 100 pct identical amino acid sequence and) (le:2557) (re:2724) (di:complement) AE000412 AE000412 g1789762 Escherichia coli 562 -11535859 5000693528 (de:(ecoli_3280) (pn:hypothetical 6) (gn:yhfg) (gtcfc:13.7:14.1) (ec:) (yhfg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3280 ECOLI_3280 Escherichia coli 562 10054499

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862105	12350	34506	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862120	12351	34507	375	124

Description

6500732002 yhfc:b3364 hypothetical 43.2 kd protein in ppia-nirb intergenic region:o393 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3364 b3364 Escherichia coli 562 -11535860 112770 yhfc (de:hypothetical 43.2 kd protein in ppia-nirb intergenic region (o393)) (db:swissprot) YHFC_ECOLI P21229 ESCHERICHIA COLI 562 -11535860 7000687974 yhfc hypothetical 43.2k protein ppia-nirb intergenic region (db:pir2.dat) G65130 G65130 Escherichia coli 562 -11535860 7500936890 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o393) (le:273315) (re:274496) (di:direct) ECOUW67 U18997 g606298 Escherichia coli 562 -11535860 236597 yhfc putative transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 302 of 400 of the completegenome.) (nt:o393; 100 pct identical amino acid sequence and) (le:3672) (re:4853) (di:direct) AE000412 AE000412 g1789764 Escherichia coli 562 -11535860 5000693529 (de:(ecoli_3282) (pn:hypothetical 43) (gn:yhfc) (gtcfc:13.7:14.1) (ec:) (yhfc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3282 ECOLI_3282 Escherichia coli 562 10054498

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862121	12352	34508	549	182

Description

6500732003 yhfl:b3369 hypothetical 5.8 kd protein in cysg-trps intergenic region:o55 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3369 b3369 Escherichia coli 562 -11535861 112777 yhfl (de:hypothetical 5.8 kd protein in cysg-trps intergenic region (o55)) (db:swissprot) YHFL_ECOLI P45538 ESCHERICHIA COLI 562 -11535861 7000687976 yhfl hypothetical 5.8 kd protein in cysg-trps intergenic region (db:pir2.dat) D65131 D65131 Escherichia coli 562 -11535861 7500936893 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o55) (le:280195) (re:280362) (di:direct) ECOUW67 U18997 g606303 Escherichia coli 562 -11535861 236602 yhfl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:o55; 100 pct identical amino acid sequence and) (le:154) (re:321) (di:direct) AE000413 AE000413 g1789770 Escherichia coli 562 -11535861 5000693530 (de:(ecoli_3287) (pn:hypothetical 5) (gn:yhfl) (gtcfc:13.7:14.1) (ec:) (yhfl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3287 ECOLI_3287 Escherichia coli 562 10054505

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862129	12353	34509	612	203

Description

6500732004 yhfm:b3370 hypothetical 47.5 kd protein in cysg-trps intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3370 b3370 Escherichia coli 562 -11535862 7000690951 yhfm hypothetical 47.5 kd protein in cysg-trps intergenic region (db:pir2.dat) E65131 E65131 Escherichia coli 562 -11535862 7500959816 yhfm putative amino acid/amine transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:o462; 99 pct identical to 445 amino acids of) (le:565) (re:1953) (di:direct) AE000413 AE000413 g2367216 Escherichia coli 562 -11535862

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862132	12354	34510	453	150

Description

6500732005 yhfn:b3371 hypothetical 39.3 kd protein in cysg-trps intergenic region:o347 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3371 b3371 Escherichia coli 562 -11535863 112779 yhfn (de:hypothetical 39.3 kd protein in cysg-trps intergenic region) (db:swissprot) YHFN_ECOLI P45540 ESCHERICHIA COLI 562 -11535863 7000687977 yhfn hypothetical 39.3 kd protein in cysg-trps intergenic region (db:pir2.dat) F65131 F65131 Escherichia coli 562 -11535863 7500936895 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o347) (le:281994) (re:283037) (di:direct) ECOUW67 U18997 g606305 Escherichia coli 562 -11535863 236604 yhfn putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:o347; 100 pct identical amino acid sequence and) (le:1953) (re:2996) (di:direct) AE000413 AE000413 g1789772 Escherichia coli 562 -11535863 5000693532 (de:(ecoli_3289) (pn:hypothetical 39) (gn:yhfn) (gtcfc:13.7:14.1) (ec:) (yhfn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3289 ECOLI_3289 Escherichia coli 562 10054507

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862135	12355	34511	621	206

Description

6500732006 yhf0:b3372 hypothetical 16.5 kd protein in cysg-trps intergenic region:o149 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3372 b3372 Escherichia coli 562 -11535864 7000687978 yhf0 hypothetical 16.5 kd protein in cysg-trps intergenic region (db:pir2.dat) G65131 G65131 Escherichia coli 562 -11535864 7500936896 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o149) (le:283000) (re:283449) (di:direct) ECOUW67 U18997 g606306 Escherichia coli 562 -11535864 236605 yhf0 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:o149; 100 pct identical amino acid sequence and) (le:2959) (re:3408) (di:direct) AE000413 AE000413 g1789773 Escherichia coli 562 -11535864 112780 yhf0 (de:hypothetical 16.5 kd protein in cysg-trps intergenic region (o149)) (db:swissprot) YHFO_ECOLI P45541 ESCHERICHIA COLI 562 -11535864 5000693533 (de:(ecoli_3290) (pn:hypothetical 16) (gn:yhf0) (gtcfc:13.7:14.1) (ec:) (yhf0_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3290 ECOLI_3290 Escherichia coli 562 10054508

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862142	12356	34512	564	187

Description

6500732007 yhfP:b3373 hypothetical 14.6 kd protein in cysg-trps intergenic region:o132 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3373 b3373 Escherichia coli 562 -11535865 7500936897 yhfP (de:hypothetical 15.4 kd protein in cysg-trps intergenic region) (db:swissprot) YHFP_ECOLI P45542 ESCHERICHIA COLI 562 -11535865 7000690918 yhfP hypothetical 14.6 kd protein in cysg-trps intergenic region (db:pir2.dat) H65131 H65131 Escherichia coli 562 -11535865 7500936899 yhfP orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:o134; sequence change alters c-term relative) (le:3473) (re:3877) (di:direct) AE000413 AE000413 g2367217 Escherichia coli 562 -11535865

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862145	12357	34513	1788	595

Description

GTC ORF with score 100 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862147	12358	34514	471	156

Description

GTC ORF with score 184 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid c36a4, complete sequence.) (nt:similar to acetyl-coenzyme a synthetase; cdna est) (le:35918:36028:36863:37037) (re:35977:36738:36978:37363) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862171	12359	34515	246	81

Description

6500732008 yhfq:b3374 hypothetical 28.3 kd protein in cysg-trps intergenic region:o261 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3374 b3374 Escherichia coli 562 -11535866 112782 yhfq (de:hypothetical sugar kinase in cysg-trps intergenic region) (db:swissprot) YHFQ_ECOLI P45543 ESCHERICHIA COLI 562 -11535866 7000687979 yhfq hypothetical 28.3 kd protein in cysg-trps intergenic region (db:pir2.dat) A65132 A65132 Escherichia coli 562 -11535866 7500936900 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o261) (le:283916) (re:284701) (di:direct) ECOUW67 U18997 g606308 Escherichia coli 562 -11535866 236607 yhfq putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:o261; 100 pct identical amino acid sequence and) (le:3874) (re:4659) (di:direct) AE000413 AE000413 g1789775 Escherichia coli 562 -11535866 5000693535 (de:(ecoli_3292) (pn:hypothetical 28) (gn:yhfq) (gtcfc:13.7:14.1) (ec:) (yhfq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3292 ECOLI_3292 Escherichia coli 562 10054510

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862172	12360	34516	1482	493

Description

6500732009 yhfr:b3375 hypothetical transcriptional regulator in cysg-trps intergenic region:hypothetical transcriptional regulator in cysg-trps intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3375 b3375 Escherichia coli 562 -11535867
7000687980 yhfr hypothetical transcription regulator:cysg-trps intergenic region (cl:transcription regulator gntr) (db:pir2.dat) B65132 B65132 Escherichia coli 562 -11535867 7500936901 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o265; gtg start) (le:284735) (re:285532) (di:direct) ECOUW67 U18997 g606309 Escherichia coli 562 -11535867 236608 yhfr putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:o265; o265; gtg start; 100 pct identical amino) (le:4693) (re:5490) (di:direct) AE000413 AE000413 g1789776 Escherichia coli 562 -11535867 112783 yhfr (de:hypothetical transcriptional regulator in cysg-trps intergenic region) (db:swissprot) YHFR_ECOLI P45544 ESCHERICHIA COLI 562 -11535867 5000693536 (de:(ecoli_3293) (pn:hypothetical transcriptional regulator in cysg-trps intergenic region:o265) (gn:yhfr) (gtcfc:13.7:14.1) (ec:) (yhfr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3293 ECOLI_3293 Escherichia coli 562 10054511

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862180	12361	34517	843	280

Description

6500732010 yhfs:b3376 hypothetical 38.6 kd protein in cysg-trps intergenic region:f361 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3376 b3376 Escherichia coli 562 -11535868 112784 yhfs (de:hypothetical 38.6 kd protein in cysg-trps intergenic region (f361)) (db:swissprot) YHFS_ECOLI P45545 ESCHERICHIA COLI 562 -11535868 7000687981 yhfs hypothetical 38.6 kd protein in cysg-trps intergenic region (db:pir2.dat) C65132 C65132 Escherichia coli 562 -11535868 7500936902 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f361) (le:285684) (re:286769) (di:complement) ECOUW67 U18997 g606310 Escherichia coli 562 -11535868 236609 yhfs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:f361; 100 pct identical amino acid sequence and) (le:5642) (re:6727) (di:complement) AE000413 AE000413 g1789777 Escherichia coli 562 -11535868 5000693537 (de:(ecoli_3294) (pn:hypothetical 38) (gn:yhfs) (gtcfc:13.7:14.1) (ec:) (yhfs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3294 ECOLI_3294 Escherichia coli 562 10054512

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862182	12362	34518	513	170

Description

6500732011 yhft:b3377 hypothetical 46.5 kd protein in cysg-trps intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3377 b3377 Escherichia coli 562 -11535869 7500936903 yhft (de:hypothetical 46.5 kd protein in cysg-trps intergenic region) (db:swissprot) YHFT_ECOLI P45546 ESCHERICHIA COLI 562 -11535869 7000690946 yhft hypothetical 46.5 kd protein in cysg-trps intergenic region (db:pir2.dat) D65132 D65132 Escherichia coli 562 -11535869 7500936905 yhft putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:f434; sequence change alters n-term relative) (le:6739) (re:8043) (di:complement) AE000413 AE000413 g2367218 Escherichia coli 562 -11535869

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862202	12363	34519	531	177

Description

6500732012 yhfub3378 hypothetical 14.0 kd protein in cysg-trps intergenic region:f130 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3378 b3378 Escherichia coli 562 -11535870 112786 yhfub (de:hypothetical 14.0 kd protein in cysg-trps intergenic region (f130)) (db:swissprot) YHFU_ECOLI P45547 ESCHERICHIA COLI 562 -11535870 7000687982 yhfub hypothetical 14.0 kd protein in cysg-trps intergenic region (db:pir2.dat) E65132 E65132 Escherichia coli 562 -11535870 7500936906 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f130; gtg start) (le:288096) (re:288488) (di:complement) ECOUW67 U18997 g606312 Escherichia coli 562 -11535870 236611 yhfub orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:f130; gtg start; 100 pct identical amino) (le:8055) (re:8447) (di:complement) AE000413 AE000413 g1789779 Escherichia coli 562 -11535870 5000693539 (de:(ecoli_3296) (pn:hypothetical 14) (gn:yhfub) (gtcfc:13.7:14.1) (ec:) (yhfub_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3296 ECOLI_3296 Escherichia coli 562 10054514

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862208	12364	34520	522	173

Description

6500732013 yhfv:b3379 hypothetical 32.9 kd protein in cysg-trps intergenic region:f292 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3379 b3379 Escherichia coli 562 -11535871 112787 php (de:phosphotriesterase homology protein) (db:swissprot) PHP_ECOLI P45548 ESCHERICHIA COLI 562 -11535871 7000687983 yhfv hypothetical 32.9 kd protein in cysg-trps intergenic region (db:pir2.dat) F65132 F65132 Escherichia coli 562 -11535871 7500936907 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f292) (le:288460) (re:289338) (di:complement) ECOUW67 U18997 g606313 Escherichia coli 562 -11535871 236612 yhfv putative hydrolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completegenome.) (nt:f292; 100 pct identical amino acid sequence and) (le:8419) (re:9297) (di:complement) AE000413 AE000413 g1789780 Escherichia coli 562 -11535871 5000693540 (de:(ecoli_3297) (pn:hypothetical 32) (gn:yhfv) (gtcfc:13.7:14.1) (ec:) (yhfv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3297 ECOLI_3297 Escherichia coli 562 10054515

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862212	12365	34521	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862221	12366	34522	447	148

Description

6500732014 yhfw:b3380 hypothetical 44.6 kd protein in cysg-trps intergenic region:f408 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3380 b3380 Escherichia coli 562 -11535872 112788 yhfw (de:hypothetical 44.6 kd protein in cysg-trps intergenic region) (db:swissprot) YHFW_ECOLI P45549 ESCHERICHIA COLI 562 -11535872 7000687984 yhfw hypothetical 44.6 kd protein in cysg-trps intergenic region (cl:phosphopentomutase) (db:pir2.dat) G65132 G65132 Escherichia coli 562 -11535872 7500936908 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f408) (le:289335) (re:290561) (di:complement) ECOUW67 U18997 g606314 Escherichia coli 562 -11535872 236613 yhfw putative mutase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completengenome.) (nt:f408; 100 pct identical amino acid sequence and) (le:9294) (re:10520) (di:complement) AE000413 AE000413 g1789781 Escherichia coli 562 -11535872 5000693541 (de:(ecoli_3298) (pn:hypothetical 44) (gn:yhfw) (gtcfc:13.7:14.1) (ec:) (yhfw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3298 ECOLI_3298 Escherichia coli 562 10054516

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862234	12367	34523	1866	621

Description

6500732015 yhfx:b3381 hypothetical 44.3 kd protein in cysg-trps intergenic region:f387 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3381 b3381 Escherichia coli 562 -11535873 112789 yhfx (de:hypothetical 44.3 kd protein in cysg-trps intergenic region (f387)) (db:swissprot) YHFX_ECOLI P45550 ESCHERICHIA COLI 562 -11535873 7000687985 yhfx hypothetical 44.3 kd protein in cysg-trps intergenic region (db:pir2.dat) H65132 H65132 Escherichia coli 562 -11535873 7500936909 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f387) (le:290561) (re:291724) (di:complement) ECOUW67 U18997 g606315 Escherichia coli 562 -11535873 236614 yhfx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 303 of 400 of the completengenome.) (nt:f387; 100 pct identical amino acid sequence and) (le:10520) (re:11683) (di:complement) AE000413 AE000413 g1789782 Escherichia coli 562 -11535873 5000693542 (de:(ecoli_3299) (pn:hypothetical 44) (gn:yhfx) (gtcfc:13.7:14.1) (ec:) (yhfx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3299 ECOLI_3299 Escherichia coli 562 10054517

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862246	12368	34524	939	312

Description

6500732016 yhfy:b3382 hypothetical 15.2 kd protein in cysg-trps intergenic region:f134 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3382 b3382 Escherichia coli 562 -11535874 7000687986 yhfy hypothetical 15.2 kd protein in cysg-trps intergenic region (db:pir2.dat) A65133 A65133 Escherichia coli 562 -11535874 7500936910 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f134; gtg start) (le:291808) (re:292212) (di:complement) ECOUW67 U18997 g606316 Escherichia coli 562 -11535874 236615 yhfy orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f134; gtg start; 100 pct identical amino) (le:72) (re:476) (di:complement) AE000414 AE000414 g1789784 Escherichia coli 562 -11535874 112790 yhfy (de:hypothetical 15.2 kd protein in cysg-trps intergenic region (f134)) (db:swissprot) YHFY_ECOLI P45551 ESCHERICHIA COLI 562 -11535874 5000693543 (de:(ecoli_3300) (pn:hypothetical 15) (gn:yhfy) (gtcfc:13.7:14.1) (ec:) (yhfy_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3300 ECOLI_3300 Escherichia coli 562 10054518

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862247	12369	34525	795	264

Description

6500732017 yhfz:b3383 hypothetical 25.4 kd protein in cysg-trps intergenic region:f228 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3383 b3383 Escherichia coli 562 -11535875 112792 yhfz (de:hypothetical 25.4 kd protein in cysg-trps intergenic region (f228)) (db:swissprot) YHFZ_ECOLI P45552 ESCHERICHIA COLI 562 -11535875 7000687987 yhfz hypothetical 25.4 kd protein in cysg-trps intergenic region (db:pir2.dat) B65133 B65133 Escherichia coli 562 -11535875 7500936912 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f228) (le:292187) (re:292873) (di:complement) ECOUW67 U18997 g606317 Escherichia coli 562 -11535875 236616 yhfz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f228; 100 pct identical amino acid sequence and) (le:451) (re:1137) (di:complement) AE000414 AE000414 g1789785 Escherichia coli 562 -11535875 5000693544 (de:(ecoli_3301) (pn:hypothetical 25) (gn:yhfz) (gtcfc:13.7:14.1) (ec:) (yhfz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3301 ECOLI_3301 Escherichia coli 562 10054520

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862253	12370	34526	546	181

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862254	12371	34527	189	63

Description

6500732018 yrfa:b3392 hypothetical 16.9 kd protein in hofq-mrca intergenic region:f147 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3392 b3392 Escherichia coli 562 -11535876 116140 yrfa (de:hypothetical 16.9 kd protein in hofq-mrca intergenic region (f147)) (db:swissprot) YRFA_ECOLI P45750 ESCHERICHIA COLI 562 -11535876 7000688542 yrfa hypothetical 16.9 kd protein in hofq-mrca intergenic region (db:pir2.dat) C65134 C65134 Escherichia coli 562 -11535876 7500952644 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f147; gtg start) (le:301363) (re:301806) (di:complement) ECOUW67 U18997 g606326 Escherichia coli 562 -11535876 236625 yrfa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 304 of 400 of the completegenome.) (nt:f147; gtg start; 100 pct identical amino) (le:9627) (re:10070) (di:complement) AE000414 AE000414 g1789794 Escherichia coli 562 -11535876 5000693546 (de:(ecoli_3310) (pn:hypothetical 16) (gn:yrfa) (gtcfc:13.7:14.1) (ec:) (yrfa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3310 ECOLI_3310 Escherichia coli 562 10057866

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862274	12372	34528	660	219

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862275	12373	34529	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862276	12374	34530	855	284

Description

6500732019 yrfb:b3393 hypothetical 16.8 kd protein in hofq-mrca intergenic region:f146 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3393 b3393 Escherichia coli 562 -11535877 116141 yrfb (de:hypothetical 16.8 kd protein in hofq-mrca intergenic region (f146)) (db:swissprot) YRFB_ECOLI P45751 ESCHERICHIA COLI 562 -11535877 7000688543 yrfb hypothetical 16.8 kd protein in hofq-mrca intergenic region (db:pir2.dat) D65134 D65134 Escherichia coli 562 -11535877 7500952645 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f146; overlaps next orf, downstream starts) (le:301757) (re:302197) (di:complement) ECOUW67 U18997 g606327 Escherichia coli 562 -11535877 236626 yrfb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f146; overlaps next orf, downstream starts) (le:10021) (re:10461) (di:complement) AE000414 AE000414 g1789795 Escherichia coli 562 -11535877 5000693547 (de:(ecoli_3311) (pn:hypothetical 16) (gn:yrfb) (gtcfc:13.7:14.1) (ec:) (yrfb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3311 ECOLI_3311 Escherichia coli 562 10057867

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862278	12375	34531	957	318

Description

GTC ORF with score 247 to: (sr:homo sapiens male bone marrow myeloblast cell_line:kg-1 cdna t) (db:genpept-pri2) (de:human mrna for kiaa0248 gene, partial cds.) (nt:similar to s.cerevisiae sec7 protein (a31068)) (le:<1) (re:5078) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862279	12376	34532	609	202

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862299	12377	34533	2277	758

Description

6500732020 yrfc:b3394 hypothetical 20.8 kd protein in hofq-mrca intergenic region:f179 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3394 b3394 Escherichia coli 562 -11535878 116142 yrfc (de:hypothetical 20.8 kd protein in hofq-mrca intergenic region (f179)) (db:swissprot) YRFC_ECOLI P45752 ESCHERICHIA COLI 562 -11535878 7000688544 yrfc hypothetical 20.8 kd protein in hofq-mrca intergenic region (db:pir2.dat) E65134 E65134 Escherichia coli 562 -11535878 7500952646 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f179; overlaps next orf, downstream starts) (le:302181) (re:302720) (di:complement) ECOUW67 U18997 g606328 Escherichia coli 562 -11535878 236627 yrfc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f179; overlaps next orf, downstream starts) (le:10445) (re:10984) (di:complement) AE000414 AE000414 g1789796 Escherichia coli 562 -11535878 5000693548 (de:(ecoli_3312) (pn:hypothetical 20) (gn:yrfc) (gtcfc:13.7:14.1) (ec:) (yrfc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3312 ECOLI_3312 Escherichia coli 562 10057868

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862314	12378	34534	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862323	12379	34535	840	279

Description

6500732021 yrfd:b3395 hypothetical 30.0 kd protein in hofq-mrca intergenic region:f268 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3395 b3395 Escherichia coli 562 -11535879 116143 yrfd (de:hypothetical 30.0 kd protein in hofq-mrca intergenic region (f268)) (db:swissprot) YRFD_ECOLI P45753 ESCHERICHIA COLI 562 -11535879 7000688545 yrfd hypothetical 30.0 kd protein in hofq-mrca intergenic region (db:pir2.dat) F65134 F65134 Escherichia coli 562 -11535879 7500952647 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f268; gtg start, overlaps next gene) (le:302720) (re:303526) (di:complement) ECOUW67 U18997 g606329 Escherichia coli 562 -11535879 236628 yrfd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f268; gtg start, overlaps next gene; 100 pct) (le:10984) (re:11790) (di:complement) AE000414 AE000414 g1789797 Escherichia coli 562 -11535879 5000693549 (de:(ecoli_3313) (pn:hypothetical 30) (gn:yrfd) (gtcfc:13.7:14.1) (ec:) (yrfd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3313 ECOLI_3313 Escherichia coli 562 10057869

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862324	12380	34536	486	161

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862335	12381	34537	285	94

Description

6500732022 yrfe:b3397 hypothetical 21.2 kd protein in mrca-pcka intergenic region:f186 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3397 b3397 Escherichia coli 562 -11535880 116144 yrfe (de:hypothetical 21.2 kd protein in mrca-pcka intergenic region (f186)) (db:swissprot) YRFE_ECOLI P45799 ESCHERICHIA COLI 562 -11535880 7000688546 yrfe hypothetical 21.2 kd protein in mrca-pcka intergenic region (db:pir2.dat) H65134 H65134 Escherichia coli 562 -11535880 7500952648 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f186) (le:306337) (re:306897) (di:complement) ECOUW67 U18997 g606331 Escherichia coli 562 -11535880 236630 yrfe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 305 of 400 of the completengenome.) (nt:f186; 100 pct identical amino acid sequence and) (le:2807) (re:3367) (di:complement) AE000415 AE000415 g1789800 Escherichia coli 562 -11535880 5000693550 (de:(ecoli_3315) (pn:hypothetical 21) (gn:yrfe) (gtcfc:13.7:14.1) (ec:) (yrfe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3315 ECOLI_3315 Escherichia coli 562 10057870

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862337	12382	34538	192	63

Description

6500732023 yrff:b3398 hypothetical 79.5 kd protein in mrca-pcka intergenic region:o711 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3398 b3398 Escherichia coli 562 -11535881 116145 yrff (de:hypothetical 79.5 kd protein in mrca-pcka intergenic region (o711)) (db:swissprot) YRFF_ECOLI P45800 ESCHERICHIA COLI 562 -11535881 7000688547 yrff hypothetical 79.5 kd protein in mrca-pcka intergenic region (db:pir2.dat) A65135 A65135 Escherichia coli 562 -11535881 7500952649 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o711) (le:307217) (re:309352) (di:direct) ECOUW67 U18997 g606332 Escherichia coli 562 -11535881 236631 yrff putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 305 of 400 of the completengenome.) (nt:o711; 100 pct identical amino acid sequence and) (le:3687) (re:5822) (di:direct) AE000415 AE000415 g1789801 Escherichia coli 562 -11535881 5000693551 (de:(ecoli_3316) (pn:hypothetical 79) (gn:yrff) (gtcfc:13.7:14.1) (ec:) (yrff_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3316 ECOLI_3316 Escherichia coli 562 10057871

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862345	12383	34539	384	127

Description

6500732024 yrfg:b3399 hypothetical 27.1 kd protein in mrca-pcka intergenic region:o237 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3399 b3399 Escherichia coli 562 -11535882 7000688548 yrfg hypothetical 27.1 kd protein in mrca-pcka intergenic region (db:pir2.dat) B65135 B65135 Escherichia coli 562 -11535882 236632 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o237) (le:309372) (re:310085) (di:direct) ECOUW67 U18997 g606333 Escherichia coli 562 -11535882 7500959803 yrfg putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 305 of 400 of the completegenome.) (nt:o237; 100 pct identical amino acid sequence and) (le:5842) (re:6555) (di:direct) AE000415 AE000415 g1789802 Escherichia coli 562 -11535882 116146 yrfg_ecoli (de:hypothetical 27.1 kd protein in mrca-pcka intergenic region (o237).) P45801 P45801 Escherichia coli 562 -11535882 5000693552 (de:(ecoli_3317) (pn:hypothetical 27) (gn:yrfg) (gtcfc:13.7:14.1) (ec:) (yrfg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3317 ECOLI_3317 Escherichia coli 562 10057872

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862349	12384	34540	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862355	12385	34541	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862367	12386	34542	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862373	12387	34543	489	162

Description

6500732025 yrfh:b3400 hypothetical 15.5 kd protein in mrca-pcka intergenic region:o133 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3400 b3400 Escherichia coli 562 -11535883 116147 yrfh (de:hypothetical 15.5 kd protein in mrca-pcka intergenic region (o133)) (db:swissprot) YRFH_ECOLI P45802 ESCHERICHIA COLI 562 -11535883 7000688549 yrfh hypothetical 15.5 kd protein in mrca-pcka intergenic region (db:pir2.dat) C65135 C65135 Escherichia coli 562 -11535883 7500952651 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o133) (le:310096) (re:310497) (di:direct) ECOUW67 U18997 g606334 Escherichia coli 562 -11535883 236633 yrfh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 305 of 400 of the completegenome.) (nt:o133; 100 pct identical amino acid sequence and) (le:6566) (re:6967) (di:direct) AE000415 AE000415 g1789803 Escherichia coli 562 -11535883 5000693553 (de:(ecoli_3318) (pn:hypothetical 15) (gn:yrfh) (gtcfc:13.7:14.1) (ec:) (yrfh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3318 ECOLI_3318 Escherichia coli 562 10057873

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862381	12388	34544	1278	425

Description

6500732026 yrfi:b3401 hypothetical 32.8 kd protein in mrca-pcka intergenic region:o294 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3401 b3401 Escherichia coli 562 -11535884 7000688550 yrfi hypothetical 32.8 kd protein in mrca-pcka intergenic region (db:pir2.dat) D65135 D65135 Escherichia coli 562 -11535884 236634 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o294) (le:310516) (re:311400) (di:direct) ECOUW67 U18997 g606335 Escherichia coli 562 -11535884 7500959807 yrfi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 305 of 400 of the completegenome.) (nt:o294; 100 pct identical amino acid sequence and) (le:6986) (re:7870) (di:direct) AE000415 AE000415 g1789804 Escherichia coli 562 -11535884 116149 yrfi_ecoli (de:hypothetical 32.8 kd protein in mrca-pcka intergenic region (o294).) P45803 P45803 Escherichia coli 562 -11535884 5000693554 (de:(ecoli_3319) (pn:hypothetical 32) (gn:yrfi) (gtcfc:13.7:14.1) (ec:) (yrfi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3319 ECOLI_3319 Escherichia coli 562 10057875

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862395	12389	34545	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862401	12390	34546	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862418	12391	34547	780	259

Description

6500732027 yhge:b3402 hypothetical 64.6 kd protein in mrca-pcka intergenic region:f574 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3402 b3402 Escherichia coli 562 -11535885 112802 yhge (de:hypothetical 64.6 kd protein in mrca-pcka intergenic region (f574)) (db:swissprot) YHGE_ECOLI P45804 ESCHERICHIA COLI 562 -11535885 7000687989 yhge hypothetical 64.6 kd protein in mrca-pcka intergenic region (db:pir2.dat) E65135 E65135 Escherichia coli 562 -11535885 7500936934 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f574) (le:311463) (re:313187) (di:complement) ECOUW67 U18997 g606336 Escherichia coli 562 -11535885 236635 yhge putative transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 305 of 400 of the completegenome.) (nt:f574; 100 pct identical amino acid sequence and) (le:7933) (re:9657) (di:complement) AE000415 AE000415 g1789805 Escherichia coli 562 -11535885 5000693555 (de:(ecoli_3320) (pn:hypothetical 64) (gn:yhge) (gtcfc:13.7:14.1) (ec:) (yhge_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3320 ECOLI_3320 Escherichia coli 562 10054530

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862427	12392	34548	1212	404

Description

6500732028 yhgg:b3410 hypothetical 8.7 kd protein in feob-bioh intergenic region:o78 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3410 b3410 Escherichia coli 562 -11535886 112804 yhgg (de:hypothetical 8.7 kd protein in feob-bioh intergenic region (o78)) (db:swissprot) YHGG_ECOLI P46845 ESCHERICHIA COLI 562 -11535886 7000687991 yhgg hypothetical 8.7 kd protein in feob-bioh intergenic region (db:pir2.dat) E65136 E65136 Escherichia coli 562 -11535886 7500936937 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o78) (le:323471) (re:323707) (di:direct) ECOUW67 U18997 g606345 Escherichia coli 562 -11535886 236644 yhgg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 306 of 400 of the completengenome.) (nt:o78; 100 pct identical amino acid sequence and) (le:9983) (re:10219) (di:direct) AE000416 AE000416 g1789814 Escherichia coli 562 -11535886 5000693557 (de:(ecoli_3328) (pn:hypothetical 8) (gn:yhgg) (gtcfc:13.7:14.1) (ec:) (yhgg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3328 ECOLI_3328 Escherichia coli 562 10054532

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862428	12393	34549	516	171

Description

6500732029 yhga:b3411 hypothetical 33.3 kd protein in feob-bioh intergenic region:o292 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3411 b3411 Escherichia coli 562 -11535887 112799 yhga (de:hypothetical 33.3 kd protein in feob-bioh intergenic region (o292)) (db:swissprot) YHGA_ECOLI P31667 ESCHERICHIA COLI 562 -11535887 7000687988 yhga hypothetical 33.3 kd protein in feob-bioh intergenic region (db:pir2.dat) F65136 F65136 Escherichia coli 562 -11535887 7500936923 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o292) (le:323910) (re:324788) (di:direct) ECOUW67 U18997 g606346 Escherichia coli 562 -11535887 236645 yhga orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 307 of 400 of the completengenome.) (nt:o292; 100 pct identical amino acid sequence and) (le:132) (re:1010) (di:direct) AE000417 AE000417 g1789816 Escherichia coli 562 -11535887 5000693558 (de:(ecoli_3329) (pn:hypothetical 33) (gn:yhga) (gtcfc:13.7:14.1) (ec:) (yhga_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3329 ECOLI_3329 Escherichia coli 562 10054527

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862441	12394	34550	750	249

Description

6500732030 yhgh:b3413 hypothetical 27.7 kd protein in bioh-gntt intergenic region:o243 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3413 b3413 Escherichia coli 562 -11535888 112805 yhgh (de:hypothetical 27.7 kd protein in bioh-gntt intergenic region (o243)) (db:swissprot) YHGH_ECOLI P46846 ESCHERICHIA COLI 562 -11535888 7000687992 yhgh hypothetical 27.7 kd protein in bioh-gntt intergenic region (cl:transformation competence-related protein comf) (db:pir2.dat) H65136 H65136 Escherichia coli 562 -11535888 7500936938 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o243) (le:325577) (re:326308) (di:direct) ECOUW67 U18997 g606348 Escherichia coli 562 -11535888 236647 yhgh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 307 of 400 of the completegenome.) (nt:o243; 100 pct identical amino acid sequence and) (le:1799) (re:2530) (di:direct) AE000417 AE000417 g1789818 Escherichia coli 562 -11535888 5000693559 (de:(ecoli_3331) (pn:hypothetical 27) (gn:yhgh) (gtcfc:13.7:14.1) (ec:) (yhgh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3331 ECOLI_3331 Escherichia coli 562 10054533

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862442	12395	34551	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862462	12396	34552	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862464	12397	34553	597	198

Description

6500732031 yhgi:b3414 hypothetical 21.0 kd protein in bioh-gntt intergenic region:o191 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3414 b3414 Escherichia coli 562 -11535889 112806 yhgi (de:hypothetical 21.0 kd protein in bioh-gntt intergenic region (o191)) (db:swissprot) YHGI_ECOLI P46847 ESCHERICHIA COLI 562 -11535889 7000687993 yhgi hypothetical 21.0 kd protein in bioh-gntt intergenic region (db:pir2.dat) A65137 A65137 Escherichia coli 562 -11535889 7500936939 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o191) (le:326367) (re:326942) (di:direct) ECOUW67 U18997 g606349 Escherichia coli 562 -11535889 236648 yhgi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 307 of 400 of the completegenome.) (nt:o191; 100 pct identical amino acid sequence and) (le:2589) (re:3164) (di:direct) AE000417 AE000417 g1789819 Escherichia coli 562 -11535889 5000693560 (de:(ecoli_3332) (pn:hypothetical 21) (gn:yhgi) (gtcfc:13.7:14.1) (ec:) (yhgi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3332 ECOLI_3332 Escherichia coli 562 10054534

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862474	12398	34554	1047	348

Description

6500732032 yhgj:b3419 hypothetical 21.7 kd protein in malt-glpr intergenic region:f201 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3419 b3419 Escherichia coli 562 -11535890 7000690925 yhgj hypothetical 21.7 kd protein in malt-glpr intergenic region (db:pir2.dat) F65137 F65137 Escherichia coli 562 -11535890 236653 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f201) (le:336572) (re:337177) (di:complement) ECOUW67 U18997 g606354 Escherichia coli 562 -11535890 7500959796 yhgj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 308 of 400 of the completegenome.) (nt:f201; 100 pct identical amino acid sequence and) (le:2960) (re:3565) (di:complement) AE000418 AE000418 g1789825 Escherichia coli 562 -11535890 112808 yhgj_ecoli (de:hypothetical 21.7 kd protein in malt-glpr intergenic region (f201).) P46848 P46848 Escherichia coli 562 -11535890 5000693561 (de:(ecoli_3337) (pn:hypothetical 21) (gn:yhgj) (gtcfc:13.7:14.1) (ec:) (yhgj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3337 ECOLI_3337 Escherichia coli 562 10054536

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862494	12399	34555	339	112

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862502	12400	34556	390	129

Description

GTC ORF with score 256 to: (sr:spinach (s.oleraceai, american hybrid 424) leaf, cdna to mrna) (db:genpept-pln1) (de:spinach (s.oleracea) glycolate oxidase mrna, complete cds.) (nt:glycolate oxidase (ec 1.1.3.15)) (le:135) (re:1244) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862503	12401	34557	204	67

Description

GTC ORF with score 92 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f4le6.) (nt:similar to glycolate oxidase; coded for by c.) (le:11477:11792:12101:12438) (re:11616:12053:12387:12570) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862505	12402	34558	333	110

Description

6500732033 yhgk:b3420 hypothetical 15.4 kd protein in malt-glpr intergenic region:f146 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3420 b3420 Escherichia coli 562 -11535891 7000690919 yhgk hypothetical 15.4 kd protein in malt-glpr intergenic region (db:pir2.dat) G65137 G65137 Escherichia coli 562 -11535891 7500959784 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f146) (le:337150) (re:337590) (di:complement) ECOUW67 U18997 g606355 Escherichia coli 562 -11535891 236654 rtca rna 3-terminal phosphate cyclase (fn:enzyme; rna synthesis, modification, dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 308 of 400 of the completgenome.) (nt:f146; formerly designated yhgk) (le:3538) (re:3978) (di:complement) AE000418 AE000418 g1789826 Escherichia coli 562 -11535891 5000693562 (de:(ecoli_3338) (pn:hypothetical 15) (gn:yhgk) (gtcfc:13.7:14.1) (ec:) (yhgc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3338 ECOLI_3338 Escherichia coli 562 10054537

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862506	12403	34559	315	105

Description

6500732034 yhg1:b3421 hypothetical 45.1 kd protein in malt-glpr intergenic region:f408 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3421 b3421 Escherichia coli 562 -11535892 7500891199 rtcb (de:rtcb protein) (db:swissprot) RTCB_ECOLI P46850 ESCHERICHIA COLI 562 -11535892 7000690944 yhg1 hypothetical 45.1 kd protein in malt-glpr intergenic region (db:pir2.dat) H65137 H65137 Escherichia coli 562 -11535892 7500891201 rtcb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 308 of 400 of the completegenome.) (nt:f408; formerly designated yhg1) (le:3979) (re:5205) (di:complement) AE000418 AE000418 g2367224 Escherichia coli 562 -11535892

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862522	12404	34560	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862530	12405	34561	1392	463

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862539	12406	34562	627	208

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862542	12407	34563	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862547	12408	34564	2493	830

Description

6500732035 yhgb:b3422 hypothetical 60.3 kd protein in malt-glpr intergenic region:o532 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3422 b3422 Escherichia coli 562 -11535893 112800 rtcr (de:transcriptional regulatory protein rtcr) (db:swissprot) RTCR_ECOLI P38035 ESCHERICHIA COLI 562 -11535893 7000686528 yhgb hypothetical 60.3 kd protein in malt-glpr intergenic region (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) A65138 A65138 Escherichia coli 562 -11535893 7500891202 rtcr putative 2-component regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 308 of 400 of the completegenome.) (nt:o532; formerly designated yhgb) (le:5394) (re:6992) (di:direct) AE000418 AE000418 g1789828 Escherichia coli 562 -11535893 5000693564 (de:(ecoli_3340) (pn:hypothetical 60) (gn:yhgb) (gtcfc:13.7:14.1) (ec:) (yhgb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3340 ECOLI_3340 Escherichia coli 562 10054528

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862566	12409	34565	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862575	12410	34566	273	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862611	12411	34567	1245	415

Description

6500732036 yzgl:b3427 very hypothetical 10.7 kd protein in glpd-glpg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3427 b3427 Escherichia coli 562 -11535894
7000688999 yzgl hypothetical 10.7k protein in glpd-glpg intergenic region (db:pir1.dat) (mp:75 min) Q4ECGG F65138 Escherichia coli 562 -11535894
7500953703 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f97) (le:344463) (re:344756) (di:complement) ECOUW67 U18997 g606362 Escherichia coli 562 -11535894
236661 yzgl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 309 of 400 of the completgenome.) (nt:f97; 100 pct identical amino acid sequence and) (le:133) (re:426) (di:complement) AE000419 AE000419 g1789834 Escherichia coli 562 -11535894
5000693565 (de:(ecoli_3345) (pn:very hypothetical 10) (gn:yzgl) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3345 ECOLI_3345 Escherichia coli 562 10124031

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862632	12412	34568	258	85

Description

6500732037 yhgn:b3434 hypothetical protein:hypothetical 21.5 kd protein in asd-gntu intergenic region:o197 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3434 b3434 Escherichia coli 562 -11535895 112811
yhgn (de:hypothetical 21.5 kd protein in asd-gntu intergenic region (o197)) (db:swissprot) YHGN_ECOLI P46851 ESCHERICHIA COLI 562 -11535895 7000687994
hypothetical protein b3434 (cl:conserved hypothetical protein mj1677) (db:pir2.dat) E65139 E65139 Escherichia coli 562 -11535895 7500936941
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o197) (le:355810) (re:356403) (di:direct) ECOUW67 U18997 g606369 Escherichia coli 562 -11535895 236668 yhgn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completgenome.) (nt:o197) (le:1463) (re:2056) (di:direct) AE000420 AE000420 g1789842 Escherichia coli 562 -11535895
5000693566 (de:(ecoli_3352) (pn:hypothetical 21) (gtcfc:13.7:14.1) (ec:) (yhgn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3352 ECOLI_3352 Escherichia coli 562 10054539

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862633	12413	34569	441	146

Description

6500732038 yhhw:b3439 hypothetical 26.3 kd protein in gntr-ggt intergenic region:f231 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3439 b3439 Escherichia coli 562 -11535896 112839 yhhw (de:hypothetical 26.3 kd protein in gntr-ggt intergenic region (f231)) (db:swissprot) YHHW_ECOLI P46852 ESCHERICHIA COLI 562 -11535896 7000687996 yhhw hypothetical 26.3 kd protein in gntr-ggt intergenic region (cl:conserved hypothetical protein sll1773) (db:pir2.dat) B65140 B65140 Escherichia coli 562 -11535896 7500936959 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f231) (le:359687) (re:360382) (di:complement) ECOUW67 U18997 g606374 Escherichia coli 562 -11535896 236673 yhhw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completegenome.) (nt:f231; 100 pct identical amino acid sequence and) (le:5340) (re:6035) (di:complement) AE000420 AE000420 g1789847 Escherichia coli 562 -11535896 5000693569 (de:(ecoli_3357) (pn:hypothetical 26) (gn:yhhw) (gtcfc:13.7:14.1) (ec:) (yhhw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3357 ECOLI_3357 Escherichia coli 562 10054567

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862634	12414	34570	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862635	12415	34571	381	126

Description

6500732039 yhhx:b3440 hypothetical 38.8 kd protein in gntr-ggt intergenic region:f345 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3440 b3440 Escherichia coli 562 -11535897 112840 yhhx (de:hypothetical oxidoreductase in gntr-ggt intergenic region) (db:swissprot) YHHX_ECOLI P46853 ESCHERICHIA COLI 562 -11535897 7000687997 yhhx hypothetical 38.8 kd protein in gntr-ggt intergenic region (cl:conserved hypothetical protein b1624) (db:pir2.dat) C65140 C65140 Escherichia coli 562 -11535897 7500936960 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f345) (le:360505) (re:361542) (di:complement) ECOUW67 U18997 g606375 Escherichia coli 562 -11535897 236674 yhhx putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completegenome.) (nt:f345; 100 pct identical amino acid sequence and) (le:6158) (re:7195) (di:complement) AE000420 AE000420 g1789848 Escherichia coli 562 -11535897 5000693570 (de:(ecoli_3358) (pn:hypothetical 38) (gn:yhhx) (gtcfc:13.7:14.1) (ec:) (yhhx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3358 ECOLI_3358 Escherichia coli 562 10054568

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862639	12416	34572	1299	432

Description

6500732040 yhhx:b3441 hypothetical protein:hypothetical 18.8 kd protein in gntr-ggt intergenic region:o162 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3441 b3441 Escherichia coli 562 -11535898 112841 yhhx (de:hypothetical 18.8 kd protein in gntr-ggt intergenic region (o162)) (db:swissprot) YHHY_ECOLI P46854 ESCHERICHIA COLI 562 -11535898 7000687998 hypothetical protein b3441 (db:pir2.dat) D65140 D65140 Escherichia coli 562 -11535898 7500936961 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o162) (le:361875) (re:362363) (di:direct) ECOUW67 U18997 g606376 Escherichia coli 562 -11535898 236675 yhhx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completegenome.) (nt:o162) (le:7528) (re:8016) (di:direct) AE000420 AE000420 g1789849 Escherichia coli 562 -11535898 5000693571 (de:(ecoli_3359) (pn:hypothetical 18) (gtcfc:13.7:14.1) (ec:) (yhhx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3359 ECOLI_3359 Escherichia coli 562 10054569

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862644	12417	34573	318	105

Description

6500732041 yhhz:b3442 hypothetical 44.2 kd protein in gntr-ggt intergenic region:o392 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3442 b3442 Escherichia coli 562 -11535899 112842 yhhz (de:hypothetical 44.2 kd protein in gntr-ggt intergenic region (o392)) (db:swissprot) YHHZ_ECOLI P46855 ESCHERICHIA COLI 562 -11535899 7000687999 yhhz hypothetical 44.2 kd protein in gntr-ggt intergenic region (db:pir2.dat) E65140 E65140 Escherichia coli 562 -11535899 7500936962 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o392; poor e. coli, good phage statistics) (le:362600) (re:363778) (di:direct) ECOUW67 U18997 g606377 Escherichia coli 562 -11535899 236676 yhhz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completegenome.) (nt:o392; 100 pct identical amino acid sequence and) (le:8253) (re:9431) (di:direct) AE000420 AE000420 g1789850 Escherichia coli 562 -11535899 5000693572 (de:(ecoli_3360) (pn:hypothetical 44) (gn:yhhz) (gtcfc:13.7:14.1) (ec:) (yhhz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3360 ECOLI_3360 Escherichia coli 562 10054570

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862645	12418	34574	231	76

Description

6500732042 yrha:b3443 hypothetical protein:hypothetical 16.0 kd protein in gntr-ggt intergenic region:o138 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3443 b3443 Escherichia coli 562 -11535900 116154 yrha (de:hypothetical 16.0 kd protein in gntr-ggt intergenic region (o138)) (db:swissprot) YRHA_ECOLI P46856 ESCHERICHIA COLI 562 -11535900 7000688551 hypothetical protein b3443 (db:pir2.dat) F65140 F65140 Escherichia coli 562 -11535900 7500952657 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o138; poor e. coli, good phage statistics) (le:363775) (re:364191) (di:direct) ECOUW67 U18997 g606378 Escherichia coli 562 -11535900 236677 yrha orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completegenome.) (nt:o138) (le:9428) (re:9844) (di:direct) AE000420 AE000420 g1789851 Escherichia coli 562 -11535900 5000693573 (de:(ecoli_3361) (pn:hypothetical 16) (gtcfc:13.7:14.1) (ec:) (yrha_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3361 ECOLI_3361 Escherichia coli 562 10057880

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862646	12419	34575	234	77

Description

GTC ORF with score 148 to: (or:Caenorhabditis elegans) (db:genpept-inv)
(de:caenorhabditis elegans cosmid f58e10, complete sequence.) (nt:similar to
atp-dependent helicase (dead box); cdna) (le:24571:24722:24982)
(re:24622:24936:25079) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862647	12420	34576	777	258

Description

6500732043 yrhb:b3446 hypothetical 10.6 kd protein in gntr-ggt intergenic
region:o94 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia
coli) b3446 b3446 Escherichia coli 562 -11535901 116155 yrhb
(de:hypothetical 10.6 kd protein in gntr-ggt intergenic region (o94))
(db:swissprot) YRHB_ECOLI P46857 ESCHERICHIA COLI 562 -11535901 7000688552
yrhb hypothetical 10.6 kd protein in gntr-ggt intergenic region
(db:pir2.dat) A65141 A65141 Escherichia coli 562 -11535901 7500952658
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to
76.0 minutes.) (nt:orf_o94) (le:365496) (re:365780) (di:direct) ECOUW67
U18997 g606381 Escherichia coli 562 -11535901 236680 yrhb orf:hypothetical
protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
section 311 of 400 of the completengenome.) (nt:o94; 100 pct identical amino
acid sequence and) (le:312) (re:596) (di:direct) AE000421 AE000421 g1789855
Escherichia coli 562 -11535901 5000693574 (de:(ecoli_3364) (pn:hypothetical
10) (gn:yrhb) (gtcfc:13.7:14.1) (ec:) (yrhb_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3364 ECOLI_3364 Escherichia
coli 562 10057881

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862649	12421	34577	1164	387

Description

6500732044 yhhk:b3459 hypothetical 14.5 kd protein in livk-livj intergenic region:ol27 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3459 b3459 Escherichia coli 562 -11535902 112824 yhhk (de:hypothetical 14.5 kd protein in livk-livj intergenic region (ol27)) (db:swissprot) YHHK_ECOLI P37613 ESCHERICHIA COLI 562 -11535902 163722 yhhk hypothetical 14.5k protein livk-livj intergenic region:hypothetical protein ol27 (db:pir2.dat) S47678 S47678 Escherichia coli 562 -11535902 7500936949 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:12246) (re:12629) (di:direct) ECOUW76 U00039 g466595 Escherichia coli 562 -11535902 236694 yhhk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 312 of 400 of the completegenome.) (nt:ol27; 100 pct identical amino acid sequence and) (le:104) (re:487) (di:direct) AE000422 AE000422 g1789869 Escherichia coli 562 -11535902 5000693576 (de:(ecoli_3377) (pn:hypothetical 14) (gn:yhhk) (gtcfc:13.7:14.1) (ec:) (yhhk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3377 ECOLI_3377 Escherichia coli 562 10054552

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862667	12422	34578	186	61

Description

6500732045 yhhf:b3465 hypothetical 21.7 kd protein in ftsy-nika intergenic region:21.7 kd protein in ftsy-nika intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3465 b3465 Escherichia coli 562 -11535903 236700 yhhf (de:21.7 kd protein in ftsy-nika intergenic region) (db:swissprot) YHHF_ECOLI P10120 ESCHERICHIA COLI 562 -11535903 135222 yhhf hypothetical 21.7k protein ftsy-nika intergenic region (db:pir1.dat) (mp:76 min) QQECX3 S03129 Escherichia coli 562 -11535903 5000693577 (db:genpept-bct1) (de:e.coli ftsyex genes for cell division control.) (nt:orf 4 (aa 1-198); 20 kd) (le:401) (re:997) (di:complement) ECFTSYEX X04398 g41497 Escherichia coli 562 -11535903 7500936947 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:cg site no. 18301; orf4 of x04398; alternate gene) (le:18655) (re:19251) (di:direct) ECOUW76 U00039 g466601 Escherichia coli 562 -11535903 232925 yhhf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 312 of 400 of the completegenome.) (nt:ol98; 100 pct identical to yhhf_ecoli sw:) (le:6513) (re:7109) (di:direct) AE000422 AE000422 g1789875 Escherichia coli 562 -11535903 112818 yhhf (de:21.7 kd protein in ftsy-nika intergenic region) (db:swissprot) YHHF_ECOLI P10120 ESCHERICHIA COLI 562 -11535903

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862668	12423	34579	381	126
<u>Description</u>				

6500732046 yhhl:b3466 hypothetical 10.3 kd protein in ftsy-nika intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3466 b3466 Escherichia coli 562 -11535904 112825 yhhl (de:hypothetical 10.3 kd protein in ftsy-nika intergenic region) (db:swissprot) YHHL_ECOLI P37614 ESCHERICHIA COLI 562 -11535904 7000687995 hypothetical 10.3k protein ftsy-nika intergenic region (db:pir2.dat) E65143 E65143 Escherichia coli 562 -11535904 7500936950 yhhl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 312 of 400 of the completegenome.) (nt:o89; 100 pct identical to yhhl_ecoli sw: p37614) (le:7099) (re:7368) (di:direct) AE000422 AE000422 g1789876 Escherichia coli 562 -11535904 5000693578 (de:(ecoli_3384) (pn:hypothetical 10) (gtcfc:13.7:14.1) (ec:) (yhhl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3384 ECOLI_3384 Escherichia coli 562 10054553

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862672	12424	34580	1017	338
<u>Description</u>				

6500732047 yhhm:b3467 hypothetical 13.5 kd protein in ftsy-nika intergenic region:f119 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3467 b3467 Escherichia coli 562 -11535905 112826 yhhm (de:hypothetical 13.5 kd protein in ftsy-nika intergenic region (f119)) (db:swissprot) YHHM_ECOLI P37615 ESCHERICHIA COLI 562 -11535905 163553 yhhm hypothetical 13.5k protein ftsy-nika intergenic region:hypothetical protein f119 (db:pir2.dat) S47686 S47686 Escherichia coli 562 -11535905 7500936951 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:19513) (re:19872) (di:complement) ECOUW76 U00039 g466603 Escherichia coli 562 -11535905 236702 yhhm putative receptor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 312 of 400 of the completegenome.) (nt:f119; 100 pct identical amino acid sequence and) (le:7371) (re:7730) (di:complement) AE000422 AE000422 g1789877 Escherichia coli 562 -11535905 5000693579 (de:(ecoli_3385) (pn:hypothetical 13) (gn:yhhm) (gtcfc:13.7:14.1) (ec:) (yhhm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3385 ECOLI_3385 Escherichia coli 562 10054554

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862692	12425	34581	1032	343

Description

6500732048 yhhn:b3468 hypothetical protein:hypothetical 23.8 kd protein in ftsy-nika intergenic region:o208 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3468 b3468 Escherichia coli 562 -11535906 112827 yhhn (de:hypothetical 23.8 kd protein in ftsy-nika intergenic region (o208)) (db:swissprot) YHHN_ECOLI P37616 ESCHERICHIA COLI 562 -11535906 163764 hypothetical protein o208:hypothetical protein b3468 (db:pir2.dat) S47687 S47687 Escherichia coli 562 -11535906 7500936952 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:20013) (re:20639) (di:direct) ECOUW76 U00039 g466604 Escherichia coli 562 -11535906 236703 yhhn putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 312 of 400 of the completengenome.) (nt:o208) (le:7871) (re:8497) (di:direct) AE000422 AE000422 g1789878 Escherichia coli 562 -11535906 5000693580 (de:(ecoli_3386) (pn:hypothetical 23) (gtcfc:13.7:14.1) (ec:) (yhhn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3386 ECOLI_3386 Escherichia coli 562 10054555

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862693	12426	34582	549	182

Description

6500732049 yhhp:b3470 hypothetical 9.1 kd protein in ftsy-nika intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3470 b3470 Escherichia coli 562 -11535907 112829 yhhp (de:hypothetical 9.1 kd protein in ftsy-nika intergenic region) (db:swissprot) YHHP_ECOLI P37618 ESCHERICHIA COLI 562 -11535907 163691 yhhp hypothetical 9.1k protein ftsy-nika intergenic region:hypothetical protein f81 (cl:conserved hypothetical protein hi0721) (db:pir2.dat) S47689 S47689 Escherichia coli 562 -11535907 7500936953 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:23013) (re:23258) (di:complement) ECOUW76 U00039 g466606 Escherichia coli 562 -11535907 236705 yhhp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 313 of 400 of the completengenome.) (nt:f81; 100 pct identical amino acid sequence and) (le:65) (re:310) (di:complement) AE000423 AE000423 g1789881 Escherichia coli 562 -11535907 5000693581 (de:(ecoli_3388) (pn:hypothetical 9) (gn:yhhp) (gtcfc:13.7:14.1) (ec:) (yhhp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3388 ECOLI_3388 Escherichia coli 562 10054557

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862697	12427	34583	690	229

Description

6500732050 yhhq:b3471 hypothetical 25.3 kd protein in ftsy-nika intergenic region:o221 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3471 b3471 Escherichia coli 562 -11535908 112831 yhhq (de:hypothetical 25.3 kd protein in ftsy-nika intergenic region (o221)) (db:swissprot) YHHQ_ECOLI P37619 ESCHERICHIA COLI 562 -11535908 163773 yhhq hypothetical 25.3k protein ftsy-nika intergenic region:hypothetical protein o221 (db:pir2.dat) S47690 S47690 Escherichia coli 562 -11535908 7500936954 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:23479) (re:24144) (di:direct) ECOUW76 U00039 g466607 Escherichia coli 562 -11535908 236706 yhhq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.) (nt:o221; 100 pct identical amino acid sequence and) (le:531) (re:1196) (di:direct) AE000423 AE000423 g1789882 Escherichia coli 562 -11535908 5000693582 (de:(ecoli_3389) (pn:hypothetical 25) (gn:yhhq) (gtcfc:13.7:14.1) (ec:) (yhhq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3389 ECOLI_3389 Escherichia coli 562 10054559

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862702	12428	34584	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862705	12429	34585	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501862724	12430	34586	3198	1066

Description

5000693583 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3472 b3472 Escherichia coli 562 -11535909 163759 hypothetical protein b3472:hypothetical protein o203 (db:pir2.dat) S47691 S47691 Escherichia coli 562 -11535909 7500960317 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:24163) (re:24774) (di:direct) ECOUW76 U00039 g912458 Escherichia coli 562 -11535909 236707 b3472 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.) (nt:o203) (le:1215) (re:1826) (di:direct) AE000423 AE000423 g1789883 Escherichia coli 562 -11535909 6500732051 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3472 b3472 Escherichia coli 562 -11535909

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501862732	12431	34587	297	98

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501862733	12432	34588	366	121

Description

6500732052 yhhs:b3473 hypothetical 43.8 kd protein in ftsy-nika intergenic region:f419 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3473 b3473 Escherichia coli 562 -11535910 112834 yhhs (de:hypothetical 43.8 kd protein in ftsy-nika intergenic region (f419)) (db:swissprot) YHHS_ECOLI P37621 ESCHERICHIA COLI 562 -11535910 163661 yhhs hypothetical 43.8k protein ftsy-nika intergenic region:hypothetical protein f419 (cl:hypothetical protein b2322) (db:pir2.dat) S47692 S47692 Escherichia coli 562 -11535910 7500936956 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:24778) (re:26037) (di:complement) ECOUW76 U00039 g912459 Escherichia coli 562 -11535910 236708 yhhs putative transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.) (nt:f419; 100 pct identical amino acid sequence and) (le:1830) (re:3089) (di:complement) AE000423 AE000423 g1789884 Escherichia coli 562 -11535910 5000693584 (de:(ecoli_3391) (pn:hypothetical 43) (gn:yhhs) (gtcfc:13.7:14.1) (ec:) (yhhs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3391 ECOLI_3391 Escherichia coli 562 10054562

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862734	12433	34589	639	212

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862739	12434	34590	270	89

Description

6500732053 yhht:b3474 hypothetical 38.5 kd protein in ftsy-nika intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3474 b3474 Escherichia coli 562 -11535911 163826 yhht hypothetical 38.5k protein ftsy-nika intergenic region:hypothetical protein o376 (cl:conserved hypothetical protein hi0338) (db:pir2.dat) S47693 S47693 Escherichia coli 562 -11535911 7500959810 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:26046) (re:27176) (di:direct) ECOUW76 U00039 g912460 Escherichia coli 562 -11535911 236709 yhht orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.) (nt:o376; 100 pct identical to 349 amino acids of) (le:3098) (re:4228) (di:direct) AE000423 AE000423 g1789885 Escherichia coli 562 -11535911 5000693585 (de:(ecoli_3392) (pn:hypothetical 38) (gn:yhht) (gtcfc:13.7:14.1) (ec:) (yhht_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3392 ECOLI_3392 Escherichia coli 562 10087056

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862753	12435	34591	993	330

Description

6500732054 yhhu:b3475 hypothetical 21.8 kd protein in ftsy-nika intergenic region:o195 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3475 b3475 Escherichia coli 562 -11535912 112837 yhhu (de:hypothetical 21.8 kd protein in ftsy-nika intergenic region (o195)) (db:swissprot) YHHU_ECOLI P37623 ESCHERICHIA COLI 562 -11535912 163756 yhhu hypothetical 21.8k protein ftsy-nika intergenic region:hypothetical protein o195 (db:pir2.dat) S47694 S47694 Escherichia coli 562 -11535912 7500936958 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:27231) (re:27818) (di:direct) ECOUW76 U00039 g466611 Escherichia coli 562 -11535912 236710 yhhu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.) (nt:o195; 100 pct identical amino acid sequence and) (le:4283) (re:4870) (di:direct) AE000423 AE000423 g1789886 Escherichia coli 562 -11535912 5000693586 (de:(ecoli_3393) (pn:hypothetical 21) (gn:yhhu) (gtcfc:13.7:14.1) (ec:) (yhhu_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3393 ECOLI_3393 Escherichia coli 562 10054565

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862754	12436	34592	261	86

Description

GTC ORF with score 94 to: (or:Daucus carota) (sr:daucus carota (cultivar:kurodagosa) hypocotil cdna to mrna) (db:genpept-pln1) (de:carrot mrna for hypocotil specific gene, complete cds.) (nt:unnamed protein product) (le:38) (re:1081) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862779	12437	34593	561	186

Description

6500732055 yhhg:b3481 hypothetical 15.1 kd protein in nike-rhsb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3481 b3481 Escherichia coli 562 -11535913 112820 yhhg (de:hypothetical 15.1 kd protein in nike-rhsb intergenic region) (db:swissprot) YHHG_ECOLI P28910 ESCHERICHIA COLI 562 -11535913 164848 yhhg hypothetical 15.1k protein nike-rhsb intergenic region:yhhg protein (cl:conserved hypothetical protein mj0080) (db:pir2.dat) S47700 S47700 Escherichia coli 562 -11535913 236716 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yhhg) (le:32850) (re:33251) (di:direct) ECOUW76 U00039 g466617 Escherichia coli 562 -11535913 235807 yhhg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 313 of 400 of the completegenome.) (nt:o133; 100 pct identical to yhhg_ecoli sw: p28910) (le:9902) (re:10303) (di:direct) AE000423 AE000423 g1789892 Escherichia coli 562 -11535913 300038 unknown (db:genpept-bct2) (de:escherichia coli rhs core protein, rhsb accessory element-encodedprotein (rhsb), and h repeat-associated protein genes, completeds; and unknown genes.) (le:122) (re:523) (di:direct) ECORHSBAA L02370 g147625 Escherichia coli 562 -11535913 5000693587 (de:(ecoli_3399) (pn:hypothetical 15) (gn:yhhg) (gtcfc:13.7:14.1) (ec:) (yhhg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3399 ECOLI_3399 Escherichia coli 562 10054548

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862788	12438	34594	378	126

Description

6500732056 yhhj:b3485 hypothetical 41.1 kd protein in rhsb-pit intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3485 b3485 Escherichia coli 562 -11535914 164851 yhhj hypothetical 41.1k protein rhsb-pit intergenic region:yhhj protein (db:pir2.dat) S47704 S47704 Escherichia coli 562 -11535914 7500959814 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yhhj) (le:39941) (re:41068) (di:complement) ECOUW76 U00039 g466621 Escherichia coli 562 -11535914 236720 yhhj putative transporter (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 314 of 400 of the completegenome.) (nt:f375; 100 pct identical amino acid sequence and) (le:6552) (re:7679) (di:complement) AE000424 AE000424 g1789897 Escherichia coli 562 -11535914 5000693591 (de:(ecoli_3403) (pn:hypothetical 41) (gn:yhhj) (gtcfc:13.7:14.1) (ec:) (yhhj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3403 ECOLI_3403 Escherichia coli 562 10087488

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862807	12439	34595	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862811	12440	34596	744	247

Description

6500732057 hypothetical abc transporter in rhsb-pit intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3486 b3486 Escherichia coli 562 -11535915 7500936972 yhih (de:hypothetical abc transporter atp-binding protein yhih) (db:swissprot) YHIH_ECOLI P37624 ESCHERICHIA COLI 562 -11535915 7000690978 hypothetical abc transporter in rhsb-pit intergenic region (cl:atp-binding cassette homology) (db:pir2.dat) A65146 A65146 Escherichia coli 562 -11535915 7500936974 yhih putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 314 of 400 of the completegenome.) (nt:f894; sequence change joins orfs yhih and yhih from) (le:7676) (re:10360) (di:complement) AE000424 AE000424 g2367231 Escherichia coli 562 -11535915

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862819	12441	34597	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862824	12442	34598	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862830	12443	34599	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862833	12444	34600	522	173

Description

6500732058 yhii:b3487 hypothetical 38.8 kd protein in rhsb-pit intergenic region:hypothetical 38.8 kd protein in rhsb-pit intergenic region precursor:f355 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3487 b3487 Escherichia coli 562 -11535916 112866 yhii (de:(f355)) (db:swissprot) YHII_ECOLI P37626 ESCHERICHIA COLI 562 -11535916 163643 yhii hypothetical 38.8k protein rhsb-pit intergenic region (cl:lipoyl/biotin-binding homology) (db:pir2.dat) S47707 S47707 Escherichia coli 562 -11535916 7500936975 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:43795) (re:44862) (di:complement) ECOUW76 U00039 g466624 Escherichia coli 562 -11535916 236723 yhii putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 314 of 400 of the completegenome.) (nt:f355; 100 pct identical amino acid sequence and) (le:10407) (re:11474) (di:complement) AE000424 AE000424 g1789900 Escherichia coli 562 -11535916 5000693594 (de:(ecoli_3406) (pn:hypothetical 38) (gn:yhii) (gtcfc:13.7:14.1) (ec:) (yhii_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3406 ECOLI_3406 Escherichia coli 562 10054594

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862839	12445	34601	2622	874

Description

6500732059 yhi:j:b3488 hypothetical 61.2 kd protein in rhsb-pit intergenic region:f540 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3488 b3488 Escherichia coli 562 -11535917 112867 yhi:j (de:hypothetical 61.2 kd protein in rhsb-pit intergenic region (f540)) (db:swissprot) YHIJ_ECOLI P37627 ESCHERICHIA COLI 562 -11535917 163676 yhi:j hypothetical 61.2k protein rhsb-pit intergenic region:hypothetical protein f540 (db:pir2.dat) S47708 S47708 Escherichia coli 562 -11535917 7500936976 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:45228) (re:46850) (di:complement) ECOUW76 U00039 g466625 Escherichia coli 562 -11535917 236724 yhi:j orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 315 of 400 of the completegenome.) (nt:f540; 100 pct identical amino acid sequence and) (le:229) (re:1851) (di:complement) AE000425 AE000425 g1789902 Escherichia coli 562 -11535917 5000693595 (de:(ecoli_3407) (pn:hypothetical 61) (gn:yhi:j) (gtcfc:13.7:14.1) (ec:) (yhi:j_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3407 ECOLI_3407 Escherichia coli 562 10054595

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862841	12446	34602	519	172

Description

6500732060 yhik:b3489 hypothetical 14.2 kd protein in rhsb-pit intergenic region:f123 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3489 b3489 Escherichia coli 562 -11535918 112868 yhik (de:hypothetical 14.2 kd protein in rhsb-pit intergenic region (f123)) (db:swissprot) YHIK_ECOLI P37628 ESCHERICHIA COLI 562 -11535918 163556 yhik hypothetical 14.2k protein rhsb-pit intergenic region:hypothetical protein f123 (db:pir2.dat) S47709 S47709 Escherichia coli 562 -11535918 7500936977 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:47112) (re:47483) (di:complement) ECOUW76 U00039 g466626 Escherichia coli 562 -11535918 236725 yhik orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 315 of 400 of the completengenome.) (nt:f123; 100 pct identical amino acid sequence and) (le:2113) (re:2484) (di:complement) AE000425 AE000425 g1789903 Escherichia coli 562 -11535918 5000693596 (de:(ecoli_3408) (pn:hypothetical 14) (gn:yhik) (gtcfc:13.7:14.1) (ec:) (yhik_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3408 ECOLI_3408 Escherichia coli 562 10054596

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862847	12447	34603	816	271

Description

6500732061 yhil:b3490 hypothetical 47.4 kd protein in rhsb-pit intergenic region:hypothetical 47.0 kd protein in rhsb-pit intergenic region:f409 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3490 b3490 Escherichia coli 562 -11535919 7500936978 yhil (de:hypothetical 47.4 kd protein in rhsb-pit intergenic region) (db:swissprot) YHIL_ECOLI P37629 ESCHERICHIA COLI 562 -11535919 7000690950 yhil hypothetical 47.4 kd protein in rhsb-pit intergenic region:hypothetical protein f409 (db:pir2.dat) E65146 E65146 Escherichia coli 562 -11535919 7500936980 yhil orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 315 of 400 of the completengenome.) (nt:f413; sequence change lengthens c-terminus relative) (le:2481) (re:3719) (di:complement) AE000425 AE000425 g2367233 Escherichia coli 562 -11535919

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862860	12448	34604	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862864	12449	34605	507	168

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862866	12450	34606	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862874	12451	34607	1719	572

Description

GTC ORF with score 250 to: (sr:human) (db:genpept) (de:homo sapiens dna sequence from pac 454m7 on chromosome xq25-26.3.contains the ocr11 gene for lowe oculocerebrorenal syndrome proteinocr1-1. contains ests, stss and gsss, complete sequence.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862884	12452	34608	990	329

Description

6500732062 yhim:b3491 hypothetical 39.2 kd protein in rhsb-pit intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3491 b3491 Escherichia coli 562 -11535920 163830 yhim hypothetical 39.2k protein rhsb-pit intergenic region:hypothetical protein o383 (db:pir2.dat) S47711 S47711 Escherichia coli 562 -11535920 7500959811 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:49001) (re:50152) (di:direct) ECOUW76 U00039 g466628 Escherichia coli 562 -11535920 236727 yhim orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 315 of 400 of the completegenome.) (nt:o383; 100 pct identical to 364 amino acids of) (le:4003) (re:5154) (di:direct) AE000425 AE000425 g1789905 Escherichia coli 562 -11535920 5000693598 (de:(ecoli_3410) (pn:hypothetical 39) (gn:yhim) (gtcfc:13.7:14.1) (ec:) (yhim_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3410 ECOLI_3410 Escherichia coli 562 10087059

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862892	12453	34609	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862907	12454	34610	441	146

Description

6500732063 yhin:b3492 hypothetical 43.8 kd protein in rhsb-pit intergenic region:f400 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3492 b3492 Escherichia coli 562 -11535921 7500936981 yhin (de:hypothetical 43.8 kd protein in rhsb-pit intergenic region) (db:swissprot) YHIN_ECOLI P37631 ESCHERICHIA COLI 562 -11535921 7000690942 yhin hypothetical 43.8 kd protein in rhsb-pit intergenic region (db:pir2.dat) G65146 G65146 Escherichia coli 562 -11535921 7500936983 yhin orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 315 of 400 of the completegenome.) (nt:f400; 99 pct identical amino acid sequence and) (le:5469) (re:6671) (di:complement) AE000425 AE000425 g2367234 Escherichia coli 562 -11535921

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862911	12455	34611	906	301

Description

6500732064 yhio:b3494 hypothetical 13.0 kd protein in pit-uspa intergenic region:f111 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3494 b3494 Escherichia coli 562 -11535922 112873 uspb (de:universal stress protein b) (db:swissprot) USPB_ECOLI P37632 ESCHERICHIA COLI 562 -11535922 163551 yhio hypothetical 13k protein pit-uspa intergenic region:hypothetical protein f111 (db:pir2.dat) S47714 S47714 Escherichia coli 562 -11535922 7500936985 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:53644) (re:53979) (di:complement) ECUW76 U00039 g466631 Escherichia coli 562 -11535922 236730 yhio orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 315 of 400 of the completegenome.) (nt:f111; 100 pct identical to yhio_ecoli sw: p37632) (le:8646) (re:8981) (di:complement) AE000425 AE000425 g1789908 Escherichia coli 562 -11535922 5000693600 (de:(ecoli_3413) (pn:hypothetical 13) (gn:yhio) (gtcfc:13.7:14.1) (ec:) (yhio_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3413 ECOLI_3413 Escherichia coli 562 10054601

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862914	12456	34612	450	149

Description

6500732065 yhip:b3496 hypothetical 53.7 kd protein in uspa-prlc intergenic region:o489 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3496 Escherichia coli 562 -11535923 112874 yhip (de:hypothetical 53.7 kd protein in uspa-prlc intergenic region) (db:swissprot) YHIP_ECOLI P36837 ESCHERICHIA COLI 562 -11535923 7000688000 yhip hypothetical 53.7 kd protein in uspa-prlc intergenic region:hypothetical protein o489 (cl:peptide transporter protein) (db:pir2.dat) C65147 C65147 Escherichia coli 562 -11535923 7500936986 yhip putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 316 of 400 of the completegenome.) (nt:o489; 99 pct identical amino acid sequence and) (le:161) (re:1630) (di:direct) AE000426 AE000426 g1789911 Escherichia coli 562 -11535923 5000693601 (de:(ecoli_3415) (pn:hypothetical 53) (gn:yhip) (gtcfc:13.7:14.1) (ec:) (yhip_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3415 ECOLI_3415 Escherichia coli 562 10124041

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862915	12457	34613	549	182

Description

6500732066 yhiq:b3497 hypothetical protein in uspa-prlc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3497 b3497 Escherichia coli 562 -11535924 7500936987 yhiq (de:hypothetical 26.9 kd protein in uspa-prlc intergenic region) (db:swissprot) YHIQ_ECOLI P37633 ESCHERICHIA COLI 562 -11535924 7000691844 yhiq hypothetical protein uspa-prlc intergenic region (db:pir2.dat) D65147 D65147 Escherichia coli 562 -11535924 7500936989 yhiq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 316 of 400 of the completegenome.) (nt:f250; 100 pct identical to 218 amino acids of) (le:1679) (re:2431) (di:complement) AE000426 AE000426 g1789912 Escherichia coli 562 -11535924 5000693602 (de:(ecoli_3416) (pn:hypothetical 23) (gn:yhiq) (gtcfc:13.7:14.1) (ec:) (yhiq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3416 ECOLI_3416 Escherichia coli 562 10124042

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862916	12458	34614	543	180

Description

6500732067 yhir:b3499 hypothetical 31.9 kd protein in prlc-gor intergenic region:o280a (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3499 b3499 Escherichia coli 562 -11535925 112877 yhir (de:hypothetical 31.9 kd protein in prlc-gor intergenic region (o280a)) (db:swissprot) YHIR_ECOLI P37634 ESCHERICHIA COLI 562 -11535925 163790 yhir hypothetical 31.9k protein prlc-gor intergenic region:hypothetical protein o280a (db:pir2.dat) S47719 S47719 Escherichia coli 562 -11535925 7500936994 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:59644) (re:60486) (di:direct) ECOUW76 U00039 g466636 Escherichia coli 562 -11535925 236735 yhir orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 316 of 400 of the completegenome.) (nt:o280; 100 pct identical amino acid sequence and) (le:4684) (re:5526) (di:direct) AE000426 AE000426 g1789914 Escherichia coli 562 -11535925 5000693603 (de:(ecoli_3418) (pn:hypothetical 31) (gn:yhir) (gtcfc:13.7:14.1) (ec:) (yhir_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3418 ECOLI_3418 Escherichia coli 562 10054605

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862918	12459	34615	576	191

Description

GTC ORF with score 275 to: (db:genpept) (de:burkholderia pseudomallei strain 1026b dbhb (dbhb), generalsecretory pathway protein d (gspe), general secretory pathwayprotein e (gspe), general secretory pathway protein f (gspe), gspe(gspe), general ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862921	12460	34616	354	117

Description

6500732068 yhis:b3504 hypothetical 29.5 kd protein in arsg-slp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3504 b3504 Escherichia coli 562 -11535926 112879 yhis (de:hypothetical 29.5 kd protein in arsg-slp intergenic region) (db:swissprot) YHIS_ECOLI P37635 ESCHERICHIA COLI 562 -11535926 163787 yhis hypothetical 29.5k protein arsg-slp intergenic region:hypothetical protein o260 (db:pir2.dat) S47724 S47724 Escherichia coli 562 -11535926 7500936996 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:65550) (re:66332) (di:direct) ECOUW76 U00039 g466641 Escherichia coli 562 -11535926 236740 yhis orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 317 of 400 of the completegenome.) (nt:o260; 100 pct identical amino acid sequence and) (le:408) (re:1190) (di:direct) AE000427 AE000427 g1789920 Escherichia coli 562 -11535926 5000693607 (de:(ecoli_3423) (pn:hypothetical 29) (gn:yhis) (gtcfc:13.7:14.1) (ec:) (yhis_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3423 ECOLI_3423 Escherichia coli 562 10054607

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862923	12461	34617	927	308

Description

GTC ORF with score 183 to: (db:genpept) (de:burkholderia pseudomallei strain 1026b dbhb (dbhb), generalsecretory pathway protein d (gspe), general secretory pathwayprotein e (gspe), general secretory pathway protein f (gspe), gspe(gspe), general ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862943	12462	34618	324	107

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862951	12463	34619	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862953	12464	34620	561	186

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862961	12465	34621	378	125

Description

GTC ORF with score 181 to: (sr:fission yeast) (db:genpept-pln1)
(de:schizosaccharomyces pombe (clone: 16h3) protein kinase (skp1+)gene,
complete cds.) (nt:glycogen synthase kinase-3 homologue) (le:217:283)
(re:234:1329) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862964	12466	34622	324	107

Description

6500732069 yhif:b3507 hypothetical transcriptional regulator in slp-hdeb
intergenic region:hypothetical transcriptional regulator in slp-hdeb
intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3507 b3507 Escherichia coli 562 -11535927 112863
yhif (de:hypothetical transcriptional regulator in slp-hdeb intergenic
region) (db:swissprot) YHIF_ECOLI P37195 ESCHERICHIA COLI 562 -11535927
164854 yhif yhif protein (db:pir2.dat) S47727 S47727 Escherichia coli 562
-11535927 7500936971 (sr:escherichia coli (sub_strain mg1655, strain k-12)
(library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0
to 81.5 minutes.) (nt:alternate gene name yhif) (le:68942) (re:69472)
(di:direct) ECOUW76 U00039 g466644 Escherichia coli 562 -11535927 236743
yhif orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 317 of 400 of the completegenome.)
(nt:o176; 100 pct identical amino acid sequence and) (le:3800) (re:4330)
(di:direct) AE000427 AE000427 g1789923 Escherichia coli 562 -11535927
5000693609 (de:(ecoli_3426) (pn:hypothetical transcriptional regulator in
slp-hdeb intergenic region:o176) (gn:yhif) (gtcfc:13.7:14.1) (ec:)
(yhif_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_3426 ECOLI_3426 Escherichia coli 562 10054591

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862967	12467	34623	207	68

Description

6500732070 yhid:b3508 hypothetical 23.2 kd protein in slp-hdeb intergenic region:orf-c:f215 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3508 b3508 Escherichia coli 562 -11535928 112861 yhid (de:hypothetical 23.2 kd protein in slp-hdeb intergenic region (orf-c)) (db:swissprot) YHID_ECOLI P26606 ESCHERICHIA COLI 562 -11535928 164852 yhid hypothetical 23.2k protein slp-hdeb intergenic region:yhid protein (db:pir2.dat) S47728 S47728 Escherichia coli 562 -11535928 7500936969 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate name yhid; orfc of 123635) (le:69514) (re:70161) (di:complement) ECOUW76 U00039 g466645 Escherichia coli 562 -11535928 236744 yhid putative transport atpase (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 317 of 400 of the completegenome.) (nt:f215; 100 pct identical amino acid sequence and) (le:4372) (re:5019) (di:complement) AE000427 AE000427 g1789924 Escherichia coli 562 -11535928 5000693610 (de:(ecoli_3427) (pn:hypothetical 23) (gn:yhid) (gtcfc:13.7:14.1) (ec:) (yhid_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3427 ECOLI_3427 Escherichia coli 562 10054589

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862968	12468	34624	264	87

Description

GTC ORF with score 234 to: (sr:fission yeast) (db:genpept-pln1) (de:schizosaccharomyces pombe (clone: 16h3) protein kinase (skp1+)gene, complete cds.) (nt:glycogen synthase kinase-3 homologue) (le:217:283) (re:234:1329) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862975	12469	34625	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862984	12470	34626	1632	543

Description

6500732071 yhie:b3512 hypothetical 20.6 kd protein in hded-gada intergenic region:o175 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3512 b3512 Escherichia coli 562 -11535929 112862 yhie (de:hypothetical 20.6 kd protein in hded-gada intergenic region (o175)) (db:swissprot) YHIE_ECOLI P29688 ESCHERICHIA COLI 562 -11535929 163751 yhie hypothetical 20.6k protein hded-gada intergenic region:hypothetical protein o175 (db:pir2.dat) S47732 S47732 Escherichia coli 562 -11535929 7500936970 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:72625) (re:73152) (di:direct) ECOUW76 U00039 g466649 Escherichia coli 562 -11535929 236748 yhie orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 317 of 400 of the completegenome.) (nt:o175; 100 pct identical amino acid sequence and) (le:7483) (re:8010) (di:direct) AE000427 AE000427 g1789928 Escherichia coli 562 -11535929 5000693614 (de:(ecoli_3431) (pn:hypothetical 20) (gn:yhie) (gtcfc:13.7:14.1) (ec:) (yhie_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3431 ECOLI_3431 Escherichia coli 562 10054590

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501862996	12471	34627	387	128

Description

6500732072 yhiu:b3513 hypothetical 41.2 kd lipoprotein in hded-gada intergenic region:hypothetical 41.2 kd lipoprotein in hded-gada intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3513 b3513 Escherichia coli 562 -11535930 112887 yhiu (de:precursor) (db:swissprot) YHIU_ECOLI P37636 ESCHERICHIA COLI 562 -11535930 163831 yhiu yhiu protein precursor (cl:lipoyl/biotin-binding homology) (db:pir2.dat) S47733 S47733 Escherichia coli 562 -11535930 7500937004 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:73491) (re:74648) (di:direct) ECOUW76 U00039 g466650 Escherichia coli 562 -11535930 236749 yhiu putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 317 of 400 of the completegenome.) (nt:o385; 100 pct identical amino acid sequence and) (le:8349) (re:9506) (di:direct) AE000427 AE000427 g1789929 Escherichia coli 562 -11535930 5000693615 (de:(ecoli_3432) (pn:hypothetical 41) (gn:yhiu) (gtcfc:13.7:14.1) (ec:) (yhiu_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3432 ECOLI_3432 Escherichia coli 562 10054615

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501862999	12472	34628	225	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863000	12473	34629	696	231

Description

6500732073 yhiv:b3514 hypothetical 111.5 kd protein in hded-gada intergenic region:o1037 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3514 b3514 Escherichia coli 562 -11535931 112888 yhiv (de:hypothetical 111.5 kd protein in hded-gada intergenic region) (db:swissprot) YHIV_ECOLI P37637 ESCHERICHIA COLI 562 -11535931 163708 yhiv probable membrane protein yhiv (cl:acriflavin resistance protein) (db:pir2.dat) S47734 S47734 Escherichia coli 562 -11535931 7500937005 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:74673) (re:77786) (di:direct) ECOUW76 U00039 g466651 Escherichia coli 562 -11535931 236750 yhiv putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 317 of 400 of the completegenome.) (nt:o1037; 100 pct identical amino acid sequence and) (le:9531) (re:12644) (di:direct) AE000427 AE000427 g1789930 Escherichia coli 562 -11535931 5000693616 (de:(ecoli_3433) (pn:hypothetical 111) (gn:yhiv) (gtcfc:13.7:14.1) (ec:) (yhiv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3433 ECOLI_3433 Escherichia coli 562 10054616

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863009	12474	34630	1287	428
<u>Description</u>				
6500732074 yhiw:b3515 hypothetical protein:hypothetical transcriptional regulator in hded-gada intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3515 b3515 Escherichia coli 562 -11535932 112889 yhiw (de:hypothetical transcriptional regulator in hded-gada intergenic region) (db:swissprot) YHIW_ECOLI P37638 ESCHERICHIA COLI 562 -11535932 163598 transcription regulator homolog b3515:hypothetical protein f242a (cl:hypothetical protein f242a) (db:pir2.dat) S47735 S47735 Escherichia coli 562 -11535932 7500937006 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:78149) (re:78877) (di:complement) ECOUW76 U00039 g466652 Escherichia coli 562 -11535932 236751 yhiw putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 318 of 400 of the completegenome.) (nt:f242) (le:212) (re:940) (di:complement) AE000428 AE000428 g1789932 Escherichia coli 562 -11535932 5000693617 (de:(ecoli_3434) (pn:hypothetical transcriptional regulator in hded-gada intergenic region:f242a) (gtcfc:13.7:14.1) (ec:) (yhiw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3434 ECOLI_3434 Escherichia coli 562 10054617				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863010	12475	34631	450	149

Description

6500732075 yhix:b3516 hypothetical transcriptional regulator in hded-gada intergeni:hypothetical transcriptional regulator in hded-gada intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3516 b3516 Escherichia coli 562 -11535933 112890 yhix (de:hypothetical transcriptional regulator in hded-gada intergenic region) (db:swissprot) YHIX_ECOLI P37639 ESCHERICHIA COLI 562 -11535933 163614 yhix hypothetical transcription regulator:hded-gada intergenic region:hypothetical protein f274a (db:pir2.dat) S47736 S47736 Escherichia coli 562 -11535933 7500937007 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:79245) (re:80069) (di:complement) ECOUW76 U00039 g466653 Escherichia coli 562 -11535933 236752 yhix putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 318 of 400 of the completegenome.) (nt:f274; 100 pct identical amino acid sequence and) (le:1308) (re:2132) (di:complement) AE000428 AE000428 g1789933 Escherichia coli 562 -11535933 5000693618 (de:(ecoli_3435) (pn:hypothetical transcriptional regulator in hded-gada intergenic region:f274a) (gn:yhix) (gtcfc:13.7:14.1) (ec:) (yhix_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3435 ECOLI_3435 Escherichia coli 562 10054618

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863018	12476	34632	1290	429

Description

GTC ORF with score 118 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f59a6.) (nt:similar to glycoproteins) (le:13300:13899:15490:15579) (re:13615:15440:15533:15701) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863034	12477	34633	309	102

Description

GTC ORF with score 97 to: (fn:indole-3-acetonitrile hydrolysis) (sr:nicotiana tabacum (strain:sr1) mature leaf cdna to mrna) (db:genpept-pln1) (ec:3.5.5.1) (de:tobacco mrna for nitrilase, complete cds.) (nt:indole-3-acetonitrile ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863058	12478	34634	1581	526
<u>Description</u>				

GTC ORF with score 174 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c01g8.) (nt:coded for by c. elegans cdna yk7c8.5; coded for by) (le:29275:29808:30204) (re:29412:30154:30315) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863063	12479	34635	186	61
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863073	12480	34636	447	149
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863094	12481	34637	957	319
<u>Description</u>				

6500732076 yhjb:b3520 hypothetical transcriptional regulator in tref-kdgk intergenic region:hypothetical transcriptional regulator in tref-kdgk intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3520 b3520 Escherichia coli 562 -11535934 112900 yhjb (de:hypothetical transcriptional regulator in tref-kdgk intergenic region) (db:swissprot) YHJB_ECOLI P37640 ESCHERICHIA COLI 562 -11535934 163582 yhjb hypothetical transcription regulator tref-kdgk intergenic region:hypothetical protein f200 (db:pir2.dat) S47740 S47740 Escherichia coli 562 -11535934 7500937022 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:85551) (re:86153) (di:complement) ECOUW76 U00039 g466657 Escherichia coli 562 -11535934 236756 yhjb putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 318 of 400 of the completegenome.) (nt:f200; 100 pct identical amino acid sequence and) (le:7614) (re:8216) (di:complement) AE000428 AE000428 g1789937 Escherichia coli 562 -11535934 5000693620 (de:(ecoli_3439) (pn:hypothetical transcriptional regulator in tref-kdgk intergenic region:f200) (gn:yhjb) (gtcfc:13.7:14.1) (ec:) (yhjb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3439 ECOLI_3439 Escherichia coli 562 10054628

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863106	12482	34638	615	204

Description

6500732077 yhjc:b3521 hypothetical transcriptional regulator in tref-kdgc
intergenic region:hypothetical transcriptional regulator in tref-kdgc
intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3521 b3521 Escherichia coli 562 -11535935 163806
yhjc hypothetical transcription regulator tref-kdgc intergenic
region:hypothetical protein o323 (db:pir2.dat) S47741 S47741 Escherichia
coli 562 -11535935 7500937023 (sr:escherichia coli (sub_strain mg1655,
strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal
region from 76.0 to 81.5 minutes.) (le:86601) (re:87572) (di:direct) ECOUW76
U00039 g466658 Escherichia coli 562 -11535935 236757 yhc putative
transcriptional regulator lysr-type (fn:putative regulator; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 318 of 400 of the
completegenome.) (nt:o323; 100 pct identical amino acid sequence and)
(le:8664) (re:9635) (di:direct) AE000428 AE000428 g1789938 Escherichia coli
562 -11535935 112901 yhc (de:hypothetical transcriptional regulator in
tref-kdgc intergenic region) (db:swissprot) YHJC_ECOLI P37641 ESCHERICHIA
COLI 562 -11535935 5000693621 (de:(ecoli_3440) (pn:hypothetical
transcriptional regulator in tref-kdgc intergenic region:o323) (gn:yhc)
(gtcfc:13.7:14.1) (ec:) (yhjc_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_3440 ECOLI_3440 Escherichia coli 562
10054629

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863108	12483	34639	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863111	12484	34640	471	156

Description

6500732078 yhjd:b3522 hypothetical 37.9 kd protein in tref-kdgk intergenic region:o337 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3522 b3522 Escherichia coli 562 -11535936 112902 yhjd (de:hypothetical 37.9 kd protein in tref-kdgk intergenic region (o337)) (db:swissprot) YHJD_ECOLI P37642 ESCHERICHIA COLI 562 -11535936 163815 yhjd hypothetical 37.9k protein tref-kdgk intergenic region:hypothetical protein o337 (db:pir2.dat) S47742 S47742 Escherichia coli 562 -11535936 7500937024 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:87621) (re:88634) (di:direct) ECOUW76 U00039 g466659 Escherichia coli 562 -11535936 236758 yhjd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 318 of 400 of the completegenome.) (nt:o337; 100 pct identical amino acid sequence and) (le:9684) (re:10697) (di:direct) AE000428 AE000428 g1789939 Escherichia coli 562 -11535936 5000693622 (de:(ecoli_3441) (pn:hypothetical 37) (gn:yhjd) (gtcfc:13.7:14.1) (ec:) (yhjd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3441 ECOLI_3441 Escherichia coli 562 10054630

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863114	12485	34641	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863119	12486	34642	183	60

Description

6500732079 yhje:b3523 hypothetical metabolite transport protein in tref-kdgk intergenic region:o440 (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3523 b3523 Escherichia coli 562 -11535937 112904 yhje (de:region (o440)) (db:swissprot) YHJE_ECOLI P37643 ESCHERICHIA COLI 562 -11535937 163842 yhje hypothetical metabolite transport protein tref-kdgk intergenic region:hypothetical protein o440 (cl:citrate utilization determinant) (db:pir2.dat) S47743 S47743 Escherichia coli 562 -11535937 7500937025 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:89045) (re:90367) (di:direct) ECOUW76 U00039 g466660 Escherichia coli 562 -11535937 236759 yhje putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 319 of 400 of the completegenome.) (nt:o440; 100 pct identical amino acid sequence and) (le:272) (re:1594) (di:direct) AE000429 AE000429 g1789941 Escherichia coli 562 -11535937 5000693623 (de:(ecoli_3442) (pn:hypothetical metabolite transport protein in tref-kdgk intergenic region:o440) (gn:yhje) (gtcfc:13.7:14.1) (ec:) (yhje_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3442 ECOLI_3442 Escherichia coli 562 10054632

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863123	12487	34643	468	155

Description

6500732080 hypothetical 75.1 kd protein in tref-kdgk intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b3524 b3524 Escherichia coli 562 -11535938 7500937026 yhjg (de:hypothetical 75.1 kd protein in tref-kdgk intergenic region) (db:swissprot) YHJG_ECOLI P37645 ESCHERICHIA COLI 562 -11535938 7000690972 hypothetical 75.1 kd protein in tref-kdgk intergenic region (db:pir2.dat) G65150 G65150 Escherichia coli 562 -11535938 7500937028 yhjg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 319 of 400 of the completegenome.) (nt:f691; sequence change joins orfs yhjg and yhjg from) (le:1776) (re:3851) (di:complement) AE000429 AE000429 g2367236 Escherichia coli 562 -11535938

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863156	12488	34644	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863157	12489	34645	2259	752

Description

6500732081 yhj:b3525 hypothetical 29.7 kd protein in tref-kdgc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3525 b3525 Escherichia coli 562 -11535939 7000690934 yhj hypothetical 29.7 kd protein in tref-kdgc intergenic region (db:pir2.dat) H65150 H65150 Escherichia coli 562 -11535939 7500937031 yhj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 319 of 400 of the completegenome.) (nt:f256; sequence change lengthens c-terminus relative) (le:3906) (re:4676) (di:complement) AE000429 AE000429 g2367237 Escherichia coli 562 -11535939 7500937029 yhj (de:hypothetical 29.7 kd protein in tref-kdgc intergenic region) (db:swissprot) YHJH_ECOLI P37646 ESCHERICHIA COLI 562 -11535939

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863161	12490	34646	522	173

Description

6500732082 yhj:b3529 hypothetical 73.1 kd protein in dcta-dppf intergenic region:f651 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3529 b3529 Escherichia coli 562 -11535940 112910 yhj (de:hypothetical 73.1 kd protein in dcta-dppf intergenic region (f651)) (db:swissprot) YHJK_ECOLI P37649 ESCHERICHIA COLI 562 -11535940 163683 yhj hypothetical protein dcta-dppf intergenic region:hypothetical protein f651 (db:pir2.dat) S47750 S47750 Escherichia coli 562 -11535940 7500937033 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:97886) (re:99841) (di:complement) ECOUW76 U00039 g466667 Escherichia coli 562 -11535940 236766 yhj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 319 of 400 of the completegenome.) (nt:f651; 100 pct identical amino acid sequence and) (le:9116) (re:11071) (di:complement) AE000429 AE000429 g1789948 Escherichia coli 562 -11535940 5000693628 (de:(ecoli_3449) (pn:hypothetical 73) (gn:yhj) (gtcfc:13.7:14.1) (ec:) (yhjk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3449 ECOLI_3449 Escherichia coli 562 10054638

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863213	12491	34647	1680	559

Description

GTC ORF with score 131 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid zk84.) (nt:final exon in repeat region; similar to long tandem) (le:24170:24288:24411:24654) (re:24234:24357:24597:26737) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863216	12492	34648	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863236	12493	34649	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863244	12494	34650	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863271	12495	34651	717	238

Description

6500732083 yhl:b3530 hypothetical 125.7 kd protein in dcta-dppf intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3530 b3530 Escherichia coli 562 -11535941 7000690911 yhl hypothetical 126k protein dcta-dppf intergenic region:hypothetical protein f1165 (cl:hypothetical protein f1165:tetratricopeptide repeat homology) (db:pir2.dat) E65151 E65151 Escherichia coli 562 -11535941 7500959773 yhl putative oxidoreductase subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 320 of 400 of the completegenome.) (nt:f1166; 100 pct identical to 1139 amino acids of) (le:88) (re:3588) (di:complement) AE000430 AE000430 g2367239 Escherichia coli 562 -11535941

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863276	12496	34652	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863277	12497	34653	399	132

Description

6500732084 yhj:m:b3531 hypothetical 41.7 kd protein in dcta-dppf intergenic region:hypothetical 41.7 kd protein in dcta-dppf intergenic region
precursor:f368 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3531 b3531 Escherichia coli 562 -11535942 112912 yhj:m (de:(f368)) (db:swissprot) YHJM_ECOLI P37651 ESCHERICHIA COLI 562 -11535942 163646 yhj:m hypothetical 41.7k protein dcta-dppf intergenic region:hypothetical protein f368 (db:pir2.dat) S47752 S47752 Escherichia coli 562 -11535942 7500937035 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:103407) (re:104513) (di:complement) ECOUW76 U00039 g466669 Escherichia coli 562 -11535942 236768 yhj:m putative endoglucanase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 320 of 400 of the completegenome.) (nt:f368; 100 pct identical amino acid sequence and) (le:3542) (re:4648) (di:complement) AE000430 AE000430 g1789951 Escherichia coli 562 -11535942 5000693630 (de:(ecoli_3451) (pn:hypothetical 41) (gn:yhj:m) (gtcfc:13.7:14.1) (ec:) (yhj:m_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3451 ECOLI_3451 Escherichia coli 562 10054640

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863281	12498	34654	459	152

Description

6500732085 yhj:n:b3532 hypothetical 86.0 kd protein in dcta-dppf intergenic region:hypothetical 86.0 kd protein in dcta-dppf intergenic region
precursor:f779 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3532 b3532 Escherichia coli 562 -11535943 7000690975 yhj:n hypothetical 86.0 kd protein in dcta-dppf intergenic region (db:pir2.dat) G65151 G65151 Escherichia coli 562 -11535943 7500959835 yhj:n orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 320 of 400 of the completegenome.) (nt:f779; 99 pct identical amino acid sequence and) (le:4655) (re:6994) (di:complement) AE000430 AE000430 g1789952 Escherichia coli 562 -11535943 5000693631 (de:(ecoli_3452) (pn:hypothetical 86) (gn:yhj:n) (gtcfc:13.7:14.1) (ec:) (yhj:n_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3452 ECOLI_3452 Escherichia coli 562 10124043

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863286	12499	34655	741	247

Description

6500732086 hypothetical 101.6 kd protein in dcta-dppf intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b3533 b3533 Escherichia coli 562 -11535944 7500937037 yhjo (de:hypothetical 78.6 kd protein in dcta-dppf intergenic region) (db:swissprot) YHJO_ECOLI P37653 ESCHERICHIA COLI 562 -11535944 7000690906 hypothetical 101.6 kd protein in dcta-dppf intergenic region (db:pir2.dat) H65151 H65151 Escherichia coli 562 -11535944 7500937039 yhjo putative cellulose synthase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 320 of 400 of the completegenome.) (nt:f888; sequence change joins orfs yhjv and yhjo) (le:7005) (re:9671) (di:complement) AE000430 AE000430 g2367240 Escherichia coli 562 -11535944

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863291	12500	34656	1635	544

Description

6500732087 yhjv:b3534 hypothetical protein:hypothetical 27.1 kd protein in dcta-dppf intergenic region:f242b (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3534 b3534 Escherichia coli 562 -11535945 112916 yhjv (de:hypothetical 27.1 kd protein in dcta-dppf intergenic region (f242b)) (db:swissprot) YHJV_ECOLI P37655 ESCHERICHIA COLI 562 -11535945 163599 hypothetical protein f242b:hypothetical protein b3534 (db:pir2.dat) S47756 S47756 Escherichia coli 562 -11535945 7500937040 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:109486) (re:110214) (di:complement) ECOUW76 U00039 g912471 Escherichia coli 562 -11535945 236772 yhjv orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 320 of 400 of the completegenome.) (nt:f242b) (le:9620) (re:10348) (di:complement) AE000430 AE000430 g1789955 Escherichia coli 562 -11535945 5000693634 (de:(ecoli_3455) (pn:hypothetical 27) (gtcfc:13.7:14.1) (ec:) (yhjv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3455 ECOLI_3455 Escherichia coli 562 10054644

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863297	12501	34657	516	171

Description

6500732088 yhjr:b3535 hypothetical protein:hypothetical 7.0 kd protein in dcta-dppf intergenic region:f62 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3535 b3535 Escherichia coli 562 -11535946 112917 yhjr (de:hypothetical 7.0 kd protein in dcta-dppf intergenic region (f62)) (db:swissprot) YHJR_ECOLI P37656 ESCHERICHIA COLI 562 -11535946 163681 hypothetical protein b3535:hypothetical protein f62 (db:pir2.dat) S47757 S47757 Escherichia coli 562 -11535946 7500937041 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:110250) (re:110438) (di:complement) ECOUW76 U00039 g466674 Escherichia coli 562 -11535946 236773 yhjr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 320 of 400 of the completegenome.) (nt:f62) (le:10384) (re:10572) (di:complement) AE000430 AE000430 g1789956 Escherichia coli 562 -11535946 5000693635 (de:(ecoli_3456) (pn:hypothetical 7) (gtcfc:13.7:14.1) (ec:) (yhjr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3456 ECOLI_3456 Escherichia coli 562 10054645

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863315	12502	34658	294	97

Description

6500732089 yhjs:b3536 hypothetical 59.4 kd protein in dcta-dppf intergenic region:o523 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3536 b3536 Escherichia coli 562 -11535947 112918 yhjs (de:hypothetical 59.4 kd protein in dcta-dppf intergenic region (o523)) (db:swissprot) YHJS_ECOLI P37657 ESCHERICHIA COLI 562 -11535947 163858 yhjs hypothetical 59.4k protein dcta-dppf intergenic region:hypothetical protein o523 (db:pir2.dat) S47758 S47758 Escherichia coli 562 -11535947 7500937042 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:110711) (re:112282) (di:direct) ECOUW76 U00039 g466675 Escherichia coli 562 -11535947 236774 yhjs putative protease (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 321 of 400 of the completegenome.) (nt:o523; 100 pct identical amino acid sequence and) (le:214) (re:1785) (di:direct) AE000431 AE000431 g1789958 Escherichia coli 562 -11535947 5000693636 (de:(ecoli_3457) (pn:hypothetical 59) (gn:yhjs) (gtcfc:13.7:14.1) (ec:) (yhjs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3457 ECOLI_3457 Escherichia coli 562 10054646

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863322	12503	34659	417	138

Description

6500732090 yhjt:b3537 hypothetical protein:hypothetical 7.2 kd protein in dcta-dppf intergenic region:o62 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3537 b3537 Escherichia coli 562 -11535948 112919 yhjt (de:hypothetical 7.2 kd protein in dcta-dppf intergenic region (o62)) (db:swissprot) YHJT_ECOLI P37658 ESCHERICHIA COLI 562 -11535948 163864 hypothetical protein o62:hypothetical protein b3537 (db:pir2.dat) S47759 S47759 Escherichia coli 562 -11535948 7500937043 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:112282) (re:112470) (di:direct) ECOUW76 U00039 g466676 Escherichia coli 562 -11535948 236775 yhjt orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 321 of 400 of the completegenome.) (nt:o62) (le:1785) (re:1973) (di:direct) AE000431 AE000431 g1789959 Escherichia coli 562 -11535948 5000693637 (de:(ecoli_3458) (pn:hypothetical 7) (gtcfc:13.7:14.1) (ec:) (yhjt_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3458 ECOLI_3458 Escherichia coli 562 10054647

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863323	12504	34660	258	85

Description

6500732091 yhju:b3538 hypothetical 62.0 kd protein in dcta-dppf intergenic region:o559 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3538 b3538 Escherichia coli 562 -11535949 112920 yhju (de:hypothetical 62.0 kd protein in dcta-dppf intergenic region (o559)) (db:swissprot) YHJU_ECOLI P37659 ESCHERICHIA COLI 562 -11535949 163860 yhju hypothetical 62k protein dcta-dppf intergenic region:hypothetical protein o559 (db:pir2.dat) S47760 S47760 Escherichia coli 562 -11535949 7500937044 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:112467) (re:114146) (di:direct) ECOUW76 U00039 g466677 Escherichia coli 562 -11535949 236776 yhju orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 321 of 400 of the completegenome.) (nt:o559; 100 pct identical amino acid sequence and) (le:1970) (re:3649) (di:direct) AE000431 AE000431 g1789960 Escherichia coli 562 -11535949 5000693638 (de:(ecoli_3459) (pn:hypothetical 62) (gn:yhju) (gtcfc:13.7:14.1) (ec:) (yhju_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3459 ECOLI_3459 Escherichia coli 562 10054648

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863328	12505	34661	612	203

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863368	12506	34662	420	139

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863369	12507	34663	381	126

Description

6500732092 yhjv:b3539 hypothetical 47.3 kd protein in dcta-dppf intergenic region:o423 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3539 b3539 Escherichia coli 562 -11535950 112921 yhjv (de:hypothetical 47.3 kd protein in dcta-dppf intergenic region (o423)) (db:swissprot) YHJV_ECOLI P37660 ESCHERICHIA COLI 562 -11535950 163838 yhjv hypothetical 47.3k protein dcta-dppf intergenic region:hypothetical protein o423 (db:pir2.dat) S47761 S47761 Escherichia coli 562 -11535950 7500937045 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:114816) (re:116087) (di:direct) ECOUW76 U00039 g466678 Escherichia coli 562 -11535950 236777 yhjv putative transporter protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 321 of 400 of the completegenome.) (nt:o423; 100 pct identical amino acid sequence and) (le:4319) (re:5590) (di:direct) AE000431 AE000431 g1789961 Escherichia coli 562 -11535950 5000693639 (de:(ecoli_3460) (pn:hypothetical 47) (gn:yhjv) (gtcfc:13.7:14.1) (ec:) (yhjv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3460 ECOLI_3460 Escherichia coli 562 10054649

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863370	12508	34664	408	135

Description

6500732093 yhjx:b3547 hypothetical 43.0 kd protein in prok-tag intergenic region:f402 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3547 b3547 Escherichia coli 562 -11535951 112924 yhjx (de:hypothetical 43.0 kd protein in prok-tag intergenic region (f402)) (db:swissprot) YHJX_ECOLI P37662 ESCHERICHIA COLI 562 -11535951 163655 yhjx hypothetical 43k protein prok-tag intergenic region:hypothetical protein f402 (cl:hypothetical protein c0103) (db:pir2.dat) S47768 S47768 Escherichia coli 562 -11535951 7500937049 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:125051) (re:126259) (di:complement) ECOUW76 U00039 g466685 Escherichia coli 562 -11535951 236784 yhjx putative resistance protein (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 322 of 400 of the completegenome.) (nt:f402; 100 pct identical amino acid sequence and) (le:3038) (re:4246) (di:complement) AE000432 AE000432 g1789969 Escherichia coli 562 -11535951 5000693645 (de:(ecoli_3467) (pn:hypothetical 43) (gn:yhjx) (gtcfc:13.7:14.1) (ec:) (yhjx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3467 ECOLI_3467 Escherichia coli 562 10054652

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863384	12509	34665	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863392	12510	34666	834	277

Description

6500732094 yhjy:b3548 hypothetical 26.0 kd protein in prok-tag intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3548 b3548 Escherichia coli 562 -11535952 163595 yhjy hypothetical 26k protein prok-tag intergenic region:hypothetical protein f234 (db:pir2.dat) S47769 S47769 Escherichia coli 562 -11535952 7500959801 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:126488) (re:127192) (di:complement) ECOUW76 U00039 g912473 Escherichia coli 562 -11535952 236785 yhjy putative lipase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 322 of 400 of the completegenome.) (nt:f234; 100 pct identical to 232 amino acids of) (le:4475) (re:5179) (di:complement) AE000432 AE000432 g1789970 Escherichia coli 562 -11535952 5000693646 (de:(ecoli_3468) (pn:hypothetical 26) (gn:yhjy) (gtcfc:13.7:14.1) (ec:) (yhjy_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3468 ECOLI_3468 Escherichia coli 562 10087012

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863394	12511	34667	927	308

Description

6500732095 yiac:b3550 hypothetical 17.1 kd protein in tag-bisc intergenic region:o146b (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3550 b3550 Escherichia coli 562 -11535953 113120 yiac (de:hypothetical 17.1 kd protein in tag-bisc intergenic region (o146b)) (db:swissprot) YIAC_ECOLI P37664 ESCHERICHIA COLI 562 -11535953 163737 yiac hypothetical 17.1k protein tag-bisc intergenic region:hypothetical protein o146b (db:pir2.dat) S47771 S47771 Escherichia coli 562 -11535953 7500937283 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:overlaps end of bisc by 31 bases) (le:127904) (re:128344) (di:direct) ECOUW76 U00039 g466688 Escherichia coli 562 -11535953 236787 yiac orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 322 of 400 of the completegenome.) (nt:o146b; 100 pct identical amino acid sequence and) (le:5891) (re:6331) (di:direct) AE000432 AE000432 g1789972 Escherichia coli 562 -11535953 5000693647 (de:(ecoli_3470) (pn:hypothetical 17) (gn:yiac) (gtcfc:13.7:14.1) (ec:) (yiac_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3470 ECOLI_3470 Escherichia coli 562 10054848

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863418	12512	34668	297	98

Description

6500732096 yiad:b3552 hypothetical 22.2 kd lipoprotein in bisc-cspa
intergenic regi:hypothetical 22.2 kd lipoprotein in bisc-cspa intergenic
region precursor:o219 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3552 b3552 Escherichia coli 562 -11535954 113121
yiad (de:precursor (o219)) (db:swissprot) YIAD_ECOLI P37665 ESCHERICHIA COLI
562 -11535954 163770 yiad hypothetical 22.2k lipoprotein bisc-cspa
intergenic region:hypothetical protein o219 (db:pir2.dat) S47773 S47773
Escherichia coli 562 -11535954 7500937284 (sr:escherichia coli (sub_strain
mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli
chromosomal region from 76.0 to 81.5 minutes.) (le:130799) (re:131458)
(di:direct) ECOUW76 U00039 g466690 Escherichia coli 562 -11535954 236789
yiad putative outer membrane protein (fn:putative membrane; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 322 of 400 of the
completegenome.) (nt:o219; 100 pct identical amino acid sequence and)
(le:8786) (re:9445) (di:direct) AE000432 AE000432 g1789974 Escherichia coli
562 -11535954 5000693648 (de:(ecoli_3472) (pn:hypothetical 22) (gn:yiad)
(gtcfc:13.7:14.1) (ec:) (yiad_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_3472 ECOLI_3472 Escherichia coli 562
10054849

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863419	12513	34669	459	152

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863433	12514	34670	210	69

Description

6500732097 yiaf:b3554 hypothetical 30.2 kd protein in bisc-cspa intergenic region:f276 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3554 b3554 Escherichia coli 562 -11535955 113123 yiaf (de:hypothetical 30.2 kd protein in bisc-cspa intergenic region (f276)) (db:swissprot) YIAF_ECOLI P37667 ESCHERICHIA COLI 562 -11535955 163616 yiaf hypothetical 30k protein bisc-cspa intergenic region:hypothetical protein f276 (db:pir2.dat) S47775 S47775 Escherichia coli 562 -11535955 7500937288 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:overlaps end of previous orf) (le:132585) (re:133415) (di:complement) ECOUW76 U00039 g466692 Escherichia coli 562 -11535955 236791 yiaf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 322 of 400 of the completegenome.) (nt:f276; 100 pct identical amino acid sequence and) (le:10573) (re:11403) (di:complement) AE000432 AE000432 g1789976 Escherichia coli 562 -11535955 5000693650 (de:(ecoli_3474) (pn:hypothetical 30) (gn:yiaf) (gtcfc:13.7:14.1) (ec:) (yiaf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3474 ECOLI_3474 Escherichia coli 562 10054851

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863437	12515	34671	540	179

Description

6500732098 yiaq:b3555 hypothetical 11.0 kd protein in bisc-cspa intergenic region:o96 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3555 b3555 Escherichia coli 562 -11535956 113124 yiaq (de:hypothetical 11.0 kd protein in bisc-cspa intergenic region (o96)) (db:swissprot) YIAQ_ECOLI P37668 ESCHERICHIA COLI 562 -11535956 163878 yiaq hypothetical 11k protein bisc-cspa intergenic region:hypothetical protein o96 (db:pir2.dat) S47776 S47776 Escherichia coli 562 -11535956 7500937289 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:133729) (re:134019) (di:direct) ECOUW76 U00039 g466693 Escherichia coli 562 -11535956 236792 yiaq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 323 of 400 of the completegenome.) (nt:o96; 100 pct identical amino acid sequence and) (le:177) (re:467) (di:direct) AE000433 AE000433 g1789978 Escherichia coli 562 -11535956 5000693651 (de:(ecoli_3475) (pn:hypothetical 11) (gn:yiaq) (gtcfc:13.7:14.1) (ec:) (yiaq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3475 ECOLI_3475 Escherichia coli 562 10054852

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863439	12516	34672	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863446	12517	34673	219	72

Description

6500732099 yi5a:b3557 insertion element is150 hypothetical 19.7 kd protein:orfa (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3557 b3557 Escherichia coli 562 -11535957 236794 b3557 (de:insertion element is150 hypothetical 19.7 kd protein (orfa)) (db:swissprot) YI5A_ECOLI P19768 ESCHERICHIA COLI 562 -11535957 163522 yi5a hypothetical protein a (db:pir2.dat) S47778 S47778 Escherichia coli 562 -11535957 5000693652 (db:genpept-bct1) (de:e. coli insertion element is150 complete sequence.) (nt:orf a) (le:48) (re:569) (di:direct) ECIS150 X07037 g48676 Escherichia coli 562 -11535957 304581 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:orfa in is150) (le:134931) (re:135452) (di:direct) ECOUW76 U00039 g466695 Escherichia coli 562 -11535957 233235 yi5a is150 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 323 of 400 of the completegenome.) (nt:o173; 100 pct identical amino acid sequence and) (le:1379) (re:1900) (di:direct) AE000433 AE000433 g1789980 Escherichia coli 562 -11535957 113092 b3557 (de:insertion element is150 hypothetical 19.7 kd protein (orfa)) (db:swissprot) YI5A_ECOLI P19768 ESCHERICHIA COLI 562 -11535957

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863447	12518	34674	342	113

Description

6500732100 yi5b:b3558 insertion element is150 hypothetical 33.3 kd protein:orfb (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3558 b3558 Escherichia coli 562 -11535958 7000691851 yi5b probable transposase:33.3k:hypothetical protein o283:probable transposase b (db:pir2.dat) H65154 H65154 Escherichia coli 562 -11535958 7500960369 t150 is150 putative transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 323 of 400 of the completegenome.) (nt:o283; 99 pct identical amino acid sequence and) (le:1897) (re:2748) (di:direct) AE000433 AE000433 g1789981 Escherichia coli 562 -11535958 5000693653 (de:(ecoli_3478) (pn:insertion element is150 hypothetical 33) (gn:yi5b) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3478 ECOLI_3478 Escherichia coli 562 10124045

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863459	12519	34675	669	222
<u>Description</u>				
<p>6500732101 yiah:b3561 hypothetical 37.6 kd protein in glyq-xylb intergenic region:o331 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3561 b3561 Escherichia coli 562 -11535959 113125 yiah (de:hypothetical 37.6 kd protein in glyq-xylb intergenic region (o331)) (db:swissprot) YIAH_ECOLI P37669 ESCHERICHIA COLI 562 -11535959 163813 yiah hypothetical 37.6k protein glyq-xylb intergenic region:hypothetical protein o331 (db:pir2.dat) S47782 S47782 Escherichia coli 562 -11535959 7500937290 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:140138) (re:141133) (di:direct) ECOUW76 U00039 g466699 Escherichia coli 562 -11535959 236798 yiah orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 323 of 400 of the completegenome.) (nt:o331; 100 pct identical amino acid sequence and) (le:6586) (re:7581) (di:direct) AE000433 AE000433 g1789984 Escherichia coli 562 -11535959 5000693654 (de:(ecoli_3481) (pn:hypothetical 37) (gn:yiah) (gtcfc:13.7:14.1) (ec:) (yiah_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3481 ECOLI_3481 Escherichia coli 562 10054853</p>				
<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863460	12520	34676	969	322
<u>Description</u>				
<p>6500732102 yiaa:b3562 hypothetical 16.1 kd protein in glyq-xylb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3562 b3562 Escherichia coli 562 -11535960 163246 yiaa hypothetical 16k protein xylb 3 region:hypothetical protein in glyq-xylb intergenic region (db:pir2.dat) (mp:80 min) Q3ECX6 S47783 Escherichia coli 562 -11535960 7500959786 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:urf4; alternate gene name yiaa) (le:141175) (re:141615) (di:complement) ECOUW76 U00039 g912475 Escherichia coli 562 -11535960 236799 yiaa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 323 of 400 of the completegenome.) (nt:f146; 100 pct identical amino acid sequence and) (le:7623) (re:8063) (di:complement) AE000433 AE000433 g1789985 Escherichia coli 562 -11535960 5000693655 (de:(ecoli_3482) (pn:hypothetical 16) (gn:yiaa) (gtcfc:13.7:14.1) (ec:) (yiaa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3482 ECOLI_3482 Escherichia coli 562 10086828</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863462	12521	34677	195	64

Description

6500732103 yiab:b3563 hypothetical 13.0 kd protein in glyq-xylb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3563 b3563 Escherichia coli 562 -11535961 113119 yiab (de:hypothetical 13.0 kd protein in glyq-xylb intergenic region) (db:swissprot) YIAB_ECOLI P11286 ESCHERICHIA COLI 562 -11535961 157266 yiab hypothetical 13k protein glyq-xylb intergenic region:hypothetical protein f117 (db:pir1.dat) (mp:80 min) Q3ECX1 S47784 Escherichia coli 562 -11535961 7500937282 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yiab) (le:141658) (re:142011) (di:complement) ECOUW76 U00039 g466701 Escherichia coli 562 -11535961 236800 yiab orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 323 of 400 of the completegenome.) (nt:f117; 100 pct identical amino acid sequence and) (le:8106) (re:8459) (di:complement) AE000433 AE000433 g1789986 Escherichia coli 562 -11535961 5000693656 (de:(ecoli_3483) (pn:hypothetical 13) (gn:yiab) (gtcfc:13.7:14.1) (ec:) (yiab_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3483 ECOLI_3483 Escherichia coli 562 10054847

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863467	12522	34678	207	68

Description

6500732104 bax:b3570 hypothetical protein:protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3570 b3570 Escherichia coli 562 -11535962 61427 bax (de:bax protein) (db:swissprot) BAX_ECOLI P27297 ESCHERICHIA COLI 562 -11535962 163615 hypothetical protein f274b:hypothetical protein b3570 (db:pir2.dat) S47791 S47791 Escherichia coli 562 -11535962 7500877678 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:150604) (re:151428) (di:complement) ECOUW76 U00039 g466708 Escherichia coli 562 -11535962 236807 bax putative atp-binding protein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 324 of 400 of the completegenome.) (nt:f274) (le:5496) (re:6320) (di:complement) AE000434 AE000434 g1789994 Escherichia coli 562 -11535962 5000693657 (de:(ecoli_3490) (pn:bax protein) (gtcfc:13.7:14.1) (ec:) (bax_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3490 ECOLI_3490 Escherichia coli 562 10004136

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863476	12523	34679	654	217

Description

6500732105 hypothetical 17.5 kd protein in avta-selb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3573 b3573 Escherichia coli 562 -11535963 7500952710 ysaa (de:putative electron transport protein ysaa) (db:swissprot) YSAA_ECOLI P56256 ESCHERICHIA COLI 562 -11535963 7000690921 hypothetical 17.5 kd protein in avta-selb intergenic region (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (db:pir2.dat) G65156 G65156 Escherichia coli 562 -11535963 7500952712 yiai orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:f157; replaces an orf (yiai_ecoli sw: p37670) on) (le:146) (re:619) (di:complement) AE000435 AE000435 g2367245 Escherichia coli 562 -11535963

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863483	12524	34680	438	145

Description

6500732106 yiaj:b3574 hypothetical transcriptional regulator in avta-selb intergenic region:hypothetical transcriptional regulator in avta-selb intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3574 b3574 Escherichia coli 562 -11535964 113127 yiaj (de:hypothetical transcriptional regulator in avta-selb intergenic region) (db:swissprot) YIAJ_ECOLI P37671 ESCHERICHIA COLI 562 -11535964 163619 yiaj probable transcription regulator b3574:hypothetical protein f282 (cl:acetate operon repressor) (db:pir2.dat) S47795 S47795 Escherichia coli 562 -11535964 7500937291 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:155936) (re:156784) (di:complement) ECOUW76 U00039 g466712 Escherichia coli 562 -11535964 236811 yiaj putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:f282; 100 pct identical amino acid sequence and) (le:721) (re:1569) (di:complement) AE000435 AE000435 g1789999 Escherichia coli 562 -11535964 5000693659 (de:(ecoli_3494) (pn:hypothetical transcriptional regulator in avta-selb intergenic region:f282) (gn:yiaj) (gtcfc:13.7:14.1) (ec:) (yiaj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3494 ECOLI_3494 Escherichia coli 562 10054855

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863504	12525	34681	606	201

Description

6500732107 yia:b3575 hypothetical protein:hypothetical 36.6 kd protein in avta-selb intergenic region:o332 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3575 b3575 Escherichia coli 562 -11535965 113129 yia:b3575 (de:hypothetical 36.6 kd protein in avta-selb intergenic region (o332)) (db:swissprot) YIAK_ECOLI P37672 ESCHERICHIA COLI 562 -11535965 7000688010 hypothetical protein b3575:hypothetical protein o332 (db:pir2.dat) A65157 A65157 Escherichia coli 562 -11535965 7500937293 yia:b3575 putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:o332) (le:1770) (re:2768) (di:direct) AE000435 AE000435 g1790000 Escherichia coli 562 -11535965 5000693660 (de:(ecoli_3495) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3495 ECOLI_3495 Escherichia coli 562 10124046

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863505	12526	34682	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863510	12527	34683	387	128

Description

6500732108 yia:b3576 hypothetical 17.5 kd protein in avta-selb intergenic region:o155 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3576 b3576 Escherichia coli 562 -11535966 113131 yia:b3576 (de:hypothetical 17.5 kd protein in avta-selb intergenic region (o155)) (db:swissprot) YIAL_ECOLI P37673 ESCHERICHIA COLI 562 -11535966 163742 yial:b3576 hypothetical 17.5k protein avta-selb intergenic region:hypothetical protein o155 (cl:hypothetical protein hi0227) (db:pir2.dat) S47797 S47797 Escherichia coli 562 -11535966 7500937295 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:157995) (re:158462) (di:direct) ECOUW76 U00039 g466714 Escherichia coli 562 -11535966 236813 yial:b3576 putative lipase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:o155; 100 pct identical amino acid sequence and) (le:2780) (re:3247) (di:direct) AE000435 AE000435 g1790001 Escherichia coli 562 -11535966 5000693661 (de:(ecoli_3496) (pn:hypothetical 17) (gn:yial) (gtcfc:13.7:14.1) (ec:) (yial_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3496 ECOLI_3496 Escherichia coli 562 10054859

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863516	12528	34684	717	238

Description

6500732109 yiam:b3577 hypothetical 17.5 kd protein in avta-selb intergenic region:o157a (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3577 b3577 Escherichia coli 562 -11535967 113133 yiam (de:hypothetical 17.5 kd protein in avta-selb intergenic region (o157a)) (db:swissprot) YIAM_ECOLI P37674 ESCHERICHIA COLI 562 -11535967 163743 yiam hypothetical 17.5k protein avta-selb intergenic region:hypothetical protein o157a (db:pir2.dat) S47798 S47798 Escherichia coli 562 -11535967 7500937296 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:158580) (re:159053) (di:direct) ECOUW76 U00039 g466715 Escherichia coli 562 -11535967 236814 yiam orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:o157a; 100 pct identical amino acid sequence and) (le:3365) (re:3838) (di:direct) AE000435 AE000435 g1790002 Escherichia coli 562 -11535967 5000693662 (de:(ecoli_3497) (pn:hypothetical 17) (gn:yiam) (gtcfc:13.7:14.1) (ec:) (yiam_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3497 ECOLI_3497 Escherichia coli 562 10054861

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863522	12529	34685	561	186

Description

6500732110 yian:b3578 hypothetical 45.5 kd protein in avta-selb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3578 b3578 Escherichia coli 562 -11535968 113135 yian (de:hypothetical 45.5 kd protein in avta-selb intergenic region) (db:swissprot) YIAN_ECOLI P37675 ESCHERICHIA COLI 562 -11535968 163839 yian hypothetical 45.5k protein avta-selb intergenic region:hypothetical protein o424 (cl:conserved hypothetical protein hi1029) (db:pir2.dat) S47799 S47799 Escherichia coli 562 -11535968 7500937298 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:159056) (re:160330) (di:direct) ECOUW76 U00039 g466716 Escherichia coli 562 -11535968 236815 yian putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:o424; 100 pct identical amino acid sequence and) (le:3841) (re:5115) (di:direct) AE000435 AE000435 g1790003 Escherichia coli 562 -11535968 5000693663 (de:(ecoli_3498) (pn:hypothetical 45) (gn:yian) (gtcfc:13.7:14.1) (ec:) (yian_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3498 ECOLI_3498 Escherichia coli 562 10054863

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863527	12530	34686	1017	338

Description

6500732111 yiao:b3579 hypothetical 36.0 kd protein in avta-selb intergenic region:hypothetical 36.0 kd protein in avta-selb intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3579 b3579 Escherichia coli 562 -11535969 113137 yiao (de:hypothetical 36.0 kd protein in avta-selb intergenic region precursor) (db:swissprot) YIAO_ECOLI P37676 ESCHERICHIA COLI 562 -11535969 163811 yiao hypothetical 36k protein avta-selb intergenic region:hypothetical protein o328 (cl:conserved hypothetical protein hi1028) (db:pir2.dat) S47800 S47800 Escherichia coli 562 -11535969 7500937300 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:160347) (re:161333) (di:direct) ECOUW76 U00039 g466717 Escherichia coli 562 -11535969 236816 yiao putative solute-binding transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:o328; 100 pct identical amino acid sequence and) (le:5132) (re:6118) (di:direct) AE000435 AE000435 g1790004 Escherichia coli 562 -11535969 5000693664 (de:(ecoli_3499) (pn:hypothetical 36) (gn:yiao) (gtcfc:13.7:14.1) (ec:) (yiao_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3499 ECOLI_3499 Escherichia coli 562 10054865

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863538	12531	34687	969	322

Description

GTC ORF with score 227 to: (sr:aspergillus parasiticus (strain wild type) (tissue library) (db:genpept-pln2) (de:aspergillus parasiticus polyketide synthase (pksl1) gene, completedcs.) (le:421:773:1134:4909:5526) (re:707:1067:4856:5466:6938) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863548	12532	34688	840	280

Description

6500732112 yiar:sgbu:b3582 hypothetical 33.7 kd protein in avta-selb intergenic region:putative hexulose-6-phosphate isomerase:humpi (gtcfc:14.1) (ec:5.1.3.1) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3582 b3582 Escherichia coli 562 -11535970 113140 sgbu (ec:5.1.3.1) (de:putative hexulose-6-phosphate isomerase, (humpi)) (db:swissprot) SGBU_ECOLI P37679 ESCHERICHIA COLI 562 -11535970 163799 yiar hypothetical 33.7k protein avta-selb intergenic region:hypothetical protein o297 (cl:hypothetical protein hi1026) (db:pir2.dat) S47803 S47803 Escherichia coli 562 -11535970 7500891595 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:163452) (re:164345) (di:direct) ECOUW76 U00039 g466720 Escherichia coli 562 -11535970 236819 sgbu probable 3-hexulose-6-phosphate isomerase (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:o297; formerly designated yiar) (le:8237) (re:9130) (di:direct) AE000435 AE000435 g1790007 Escherichia coli 562 -11535970 5000693666 (de:(ecoli_3502) (pn:hypothetical 33) (gn:yiar) (gtcfc:13.7:14.1) (ec:) (yiar_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3502 ECOLI_3502 Escherichia coli 562 10054868

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863561	12533	34689	303	100

Description

6500732113 yias:sgbe:b3583 hypothetical 25.6 kd protein in avta-selb intergenic region:probable sugar isomerase sgbe (gtcfc:14.1) (ec:5.1.3.1) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3583 b3583 Escherichia coli 562 -11535971 113142 sgbe (ec:5.1.3.1) (de:probable sugar isomerase sgbe,) (db:swissprot) SGBE_ECOLI P37680 ESCHERICHIA COLI 562 -11535971 142080 yias l-ribulose-phosphate 4-epimerase homolog:yias:hypothetical protein o231 (cl:l-ribulose-phosphate 4-epimerase) (ec:5.1.3.1) (db:pir2.dat) S47804 S47804 Escherichia coli 562 -11535971 7500891591 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:164339) (re:165034) (di:direct) ECOUW76 U00039 g466721 Escherichia coli 562 -11535971 236820 sgbe putative epimerase/aldolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 325 of 400 of the completegenome.) (nt:o231; formerly designated yias) (le:9124) (re:9819) (di:direct) AE000435 AE000435 g1790008 Escherichia coli 562 -11535971 5000693667 (de:(ecoli_3503) (pn:hypothetical 25) (gn:yias) (gtcfc:13.7:14.1) (ec:) (yias_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3503 ECOLI_3503 Escherichia coli 562 10054870

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863568	12534	34690	513	170

Description

6500732114 yiat:b3584 hypothetical 27.4 kd protein in avta-selb intergenic region:hypothetical 27.4 kd protein in avta-selb intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3584 b3584 Escherichia coli 562 -11535972 113143 yiat (de:hypothetical 27.4 kd protein in avta-selb intergenic region precursor) (db:swissprot) YIAT_ECOLI P37681 ESCHERICHIA COLI 562 -11535972 163600 yiat hypothetical 27.4k protein avta-selb intergenic region (cl:hypothetical protein b1782) (db:pir2.dat) S47805 S47805 Escherichia coli 562 -11535972 7500937302 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:165381) (re:166121) (di:complement) ECOUW76 U00039 g466722 Escherichia coli 562 -11535972 236821 yiat putative outer membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 326 of 400 of the completengenome.) (nt:f246; 100 pct identical amino acid sequence and) (le:204) (re:944) (di:complement) AE000436 AE000436 g1790010 Escherichia coli 562 -11535972 5000693668 (de:(ecoli_3504) (pn:hypothetical 27) (gn:yiat) (gtcfc:13.7:14.1) (ec:) (yiat_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3504 ECOLI_3504 Escherichia coli 562 10054871

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863571	12535	34691	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863576	12536	34692	1875	624

Description

6500732115 yiau:b3585 hypothetical transcriptional regulator in avta-selb intergenic region:hypothetical transcriptional regulator in avta-selb intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3585 b3585 Escherichia coli 562 -11535973 113144 yiau (de:hypothetical transcriptional regulator in avta-selb intergenic region) (db:swissprot) YIAU_ECOLI P37682 ESCHERICHIA COLI 562 -11535973 163808 yiau hypothetical transcription regulator:avta-selb intergenic region:hypothetical protein o324 (db:pir2.dat) S47806 S47806 Escherichia coli 562 -11535973 7500937303 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:166245) (re:167219) (di:direct) ECOUW76 U00039 g466723 Escherichia coli 562 -11535973 236822 yiau putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 326 of 400 of the completegenome.) (nt:o324; 100 pct identical amino acid sequence and) (le:1068) (re:2042) (di:direct) AE000436 AE000436 g1790011 Escherichia coli 562 -11535973 5000693669 (de:(ecoli_3505) (pn:hypothetical transcriptional regulator in avta-selb intergenic region:o324) (gn:yiau) (gtcfc:13.7:14.1) (ec:) (yiau_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3505 ECOLI_3505 Escherichia coli 562 10054872

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863577	12537	34693	252	83

Description

6500732116 yia:b3586 hypothetical 41.8 kd protein in avta-selb intergenic region:hypothetical 41.8 kd protein in avta-selb intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3586 b3586 Escherichia coli 562 -11535974 113145 yia (de:hypothetical 41.8 kd protein in avta-selb intergenic region precursor) (db:swissprot) YIAV_ECOLI P37683 ESCHERICHIA COLI 562 -11535974 163647 yia hypothetical 41.8k protein avta-selb intergenic region:hypothetical protein f378a (cl:lipoyl/biotin-binding homology) (db:pir2.dat) S47807 S47807 Escherichia coli 562 -11535974 7500937304 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:167216) (re:168352) (di:complement) ECOUW76 U00039 g466724 Escherichia coli 562 -11535974 236823 yia putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 326 of 400 of the completegenome.) (nt:f378a; 100 pct identical amino acid sequence and) (le:2039) (re:3175) (di:complement) AE000436 AE000436 g1790012 Escherichia coli 562 -11535974 5000693670 (de:(ecoli_3506) (pn:hypothetical 41) (gn:yia) (gtcfc:13.7:14.1) (ec:) (yia_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3506 ECOLI_3506 Escherichia coli 562 10054873

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863587	12538	34694	771	256

Description

6500732117 yia:b3587 hypothetical 12.4 kd protein in avta-selb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3587 b3587 Escherichia coli 562 -11535975 113146 yia (de:hypothetical 12.4 kd protein in avta-selb intergenic region) (db:swissprot) YIAW_ECOLI P37684 ESCHERICHIA COLI 562 -11535975 163549 yia hypothetical 12.4k protein avta-selb intergenic region:hypothetical protein f107 (db:pir2.dat) S47808 S47808 Escherichia coli 562 -11535975 7500937305 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:168358) (re:168681) (di:complement) ECOUW76 U00039 g466725 Escherichia coli 562 -11535975 236824 yia orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 326 of 400 of the completegenome.) (nt:f107; 100 pct identical amino acid sequence and) (le:3181) (re:3504) (di:complement) AE000436 AE000436 g1790013 Escherichia coli 562 -11535975 5000693671 (de:(ecoli_3507) (pn:hypothetical 12) (gn:yia) (gtcfc:13.7:14.1) (ec:) (yia_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3507 ECOLI_3507 Escherichia coli 562 10054874

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863595	12539	34695	846	282

Description

GTC ORF with score 397 to: (sr:thale cress) (db:genpept-pln2)
 (de:arabidopsis thaliana dna chromosome 4, bac clone f28a23
 (essaiiproject).) (nt:strong similarity to phosphoglycerate)
 (le:14023:14850:15428:15872) (re:14578:15337:15523:16543) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863600	12540	34696	384	128

Description

6500732118 yibf:b3592 hypothetical protein:hypothetical 22.6 kd protein in sela-rhsa intergenic region:f202 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3592 b3592 Escherichia coli 562 -11535976 113160 yibf (de:hypothetical 22.6 kd protein in sela-rhsa intergenic region) (db:swissprot) YIBF_ECOLI P32105 ESCHERICHIA COLI 562 -11535976 163584 hypothetical protein b3592:hypothetical protein f202 (db:pir2.dat) S47813 S47813 Escherichia coli 562 -11535976 236829 (db:genpept-bct1) (de:escherichia coli core protein (rhsa), orf-a2 and orf-a3, plantstress protein homologue, apre protein homologue genes, completecds.) (nt:homology to plant; (potato, tobacco and soybean)) (le:116) (re:724) (di:complement) ECORHSA L19044 g664958 Escherichia coli 562 -11535976 238719 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yibf) (le:175599) (re:176207) (di:complement) ECUW76 U00039 g466730 Escherichia coli 562 -11535976 300025 unknown (db:genpept-bct1) (de:escherichia coli rhsa core extension protein, orf-b1, orf-a1, andunknown orf genes, complete cds.) (nt:similar to product encoded by genbank accession) (le:116) (re:724) (di:complement) ECU16247 U16247 g567055 Escherichia coli 562 -11535976 235798 yibf putative s-transferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 326 of 400 of the completegenome.) (nt:f202) (le:10420) (re:11028) (di:complement) AE000436 AE000436 g1790018 Escherichia coli 562 -11535976 5000693673 unknown (db:genpept) (de:escherichia coli core protein rhsa (rhsa) gene, complete cds; andunknown genes.) (nt:similar to plant (potato, tobacco and soybean)) (le:116) (re:724) (di:complement) ECORHSA L19044 g664958 Escherichia coli 562 -11535976

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863601	12541	34697	450	149

Description

6500732119 yiba:b3594 hypothetical 31.8 kd protein in rhsa-mtla intergenic region:orf-a2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3594 b3594 Escherichia coli 562 -11535977 113157 yiba (de:hypothetical 31.8 kd protein in rhsa-mtla intergenic region (orf-a2)) (db:swissprot) YIBA_ECOLI P24172 ESCHERICHIA COLI 562 -11535977 163791 yiba hypothetical 31.8k protein rhsa-mtla intergenic region:hypothetical protein o280b (db:pir2.dat) S47815 S47815 Escherichia coli 562 -11535977 236831 (db:genpept-bct1) (de:escherichia coli core protein (rhsa), orf-a2 and orf-a3, plantstress protein homologue, apre protein homologue genes, completecds.) (nt:orf-a2) (le:5106) (re:5948) (di:direct) ECORHSA L19044 g304935 Escherichia coli 562 -11535977 300027 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate name orf2 of rhsa locus; yiba) (le:180589) (re:181431) (di:direct) ECOUW76 U00039 g466732 Escherichia coli 562 -11535977 235800 yiba orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 327 of 400 of the completegenome.) (nt:o280b; 100 pct identical amino acid sequence and) (le:4318) (re:5160) (di:direct) AE000437 AE000437 g1790021 Escherichia coli 562 -11535977 5000693675 unknown (db:genpept) (de:escherichia coli core protein rhsa (rhsa) gene, complete cds; andunknown genes.) (nt:orf-a2) (le:5106) (re:5948) (di:direct) ECORHSA L19044 g304935 Escherichia coli 562 -11535977

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863608	12542	34698	522	173

Description

6500732120 yibj:b3595 hypothetical 26.4 kd protein in rhsa-mtla intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3595 b3595 Escherichia coli 562 -11535978 113164 yibj (de:hypothetical 26.4 kd protein in rhsa-mtla intergenic region) (db:swissprot) YIBJ_ECOLI P32109 ESCHERICHIA COLI 562 -11535978 7000688011 yibj hypothetical 26.4 kd protein in rhsa-mtla intergenic region:hypothetical protein o233 (db:pir2.dat) E65159 E65159 Escherichia coli 562 -11535978 7500937320 yibj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 327 of 400 of the completegenome.) (nt:o233; 96 pct identical amino acid sequence and) (le:5202) (re:5903) (di:direct) AE000437 AE000437 g2367250 Escherichia coli 562 -11535978

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863625	12543	34699	615	204
<u>Description</u>				
6500732121 yibg:b3596 hypothetical 18.1 kd protein in rhsa-mtla intergenic region:hypothetical 18.1 kd protein in rhsa-mtla intergenic region precursor:orf-a3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3596 b3596 Escherichia coli 562 -11535979 113161 yibg (de:(orf-a3)) (db:swissprot) YIBG_ECOLI P32106 ESCHERICHIA COLI 562 -11535979 163738 yibg hypothetical 18.1k protein rhsa-mtla intergenic region:hypothetical protein o153 (db:pir2.dat) S47817 S47817 Escherichia coli 562 -11535979 236833 (db:genpept-bct1) (de:escherichia coli core protein (rhsa), orf-a2 and orf-a3, plantstress protein homologue, apre protein homologue genes, completecds.) (nt:orf-a3) (le:6946) (re:7407) (di:direct) ECORHSA L19044 g304936 Escherichia coli 562 -11535979 300028 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate name orf3 of rhsa locus; yibg) (le:182429) (re:182890) (di:direct) ECOUW76 U00039 g466734 Escherichia coli 562 -11535979 235801 yibg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 327 of 400 of the completegenome.) (nt:o153; 100 pct identical amino acid sequence and) (le:6158) (re:6619) (di:direct) AE000437 AE000437 g1790023 Escherichia coli 562 -11535979 5000693677 unknown (db:genpept) (de:escherichia coli core protein rhsa (rhsa) gene, complete cds; andunknown genes.) (nt:orf-a3) (le:6946) (re:7407) (di:direct) ECORHSA L19044 g304936 Escherichia coli 562 -11535979				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863642	12544	34700	363	120
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863649	12545	34701	966	321

Description

6500732122 yibh:b3597 hypothetical 42.0 kd protein in rhsa-mtla intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3597 b3597 Escherichia coli 562 -11535980 7500937316 yibh (de:hypothetical 42.0 kd protein in rhsa-mtla intergenic region) (db:swissprot) YIBH_ECOLI P32107 ESCHERICHIA COLI 562 -11535980 163648 yibh hypothetical 42k protein rhsa-mtla intergenic region:hypothetical protein f378b (cl:lipoyl/biotin-binding homology) (db:pir2.dat) S47818 S47818 Escherichia coli 562 -11535980 7500937318 (db:genpept-bct1) (de:escherichia coli core protein (rhsa), orf-a2 and orf-a3, plantstress protein homologue, apre protein homologue genes, completecds.) (nt:possible homology to pseudomonas aeruginosa apre) (le:9012) (re:10148) (di:complement) ECORHSA L19044 g1857028 Escherichia coli 562 -11535980 236834 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yibh) (le:184495) (re:185631) (di:complement) ECOUW76 U00039 g466735 Escherichia coli 562 -11535980 300029 yibh putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 327 of 400 of the completegenome.) (nt:f378b; 99 pct identical amino acid sequence and) (le:8224) (re:9360) (di:complement) AE000437 AE000437 g1790024 Escherichia coli 562 -11535980 5000693678 unknown (db:genpept) (de:escherichia coli core protein rhsa (rhsa) gene, complete cds; andunknown genes.) (nt:similar to pseudomonas aeruginosa apre protein;) (le:9012) (re:10148) (di:complement) ECORHSA L19044 g1857028 Escherichia coli 562 -11535980

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863651	12546	34702	1044	347

Description

6500732123 yibi:b3598 hypothetical 13.9 kd protein in rhsa-mtla intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3598 b3598 Escherichia coli 562 -11535981 113163 yibi (de:hypothetical 13.9 kd protein in rhsa-mtla intergenic region) (db:swissprot) YIBI_ECOLI P32108 ESCHERICHIA COLI 562 -11535981 163554 yibi hypothetical 13.9k protein rhsa-mtla intergenic region:hypothetical protein f120 (db:pir2.dat) S47819 S47819 Escherichia coli 562 -11535981 236835 (db:genpept-bct1) (de:escherichia coli core protein (rhsa), orf-a2 and orf-a3, plantstress protein homologue, apre protein homologue genes, completecds.) (nt:orf) (le:10151) (re:10513) (di:complement) ECORHSA L19044 g304938 Escherichia coli 562 -11535981 300030 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yibi) (le:185634) (re:185996) (di:complement) ECOUW76 U00039 g466736 Escherichia coli 562 -11535981 235803 yibi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 327 of 400 of the completegenome.) (nt:f120; 100 pct identical amino acid sequence and) (le:9363) (re:9725) (di:complement) AE000437 AE000437 g1790025 Escherichia coli 562 -11535981 5000693679 unknown (db:genpept) (de:escherichia coli core protein rhsa (rhsa) gene, complete cds; andunknown genes.) (nt:orf) (le:10151) (re:10513) (di:complement) ECORHSA L19044 g304938 Escherichia coli 562 -11535981

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863653	12547	34703	384	127

Description

6500732124 yibl:b3602 hypothetical 13.7 kd protein in mtlr-lctp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3602 b3602 Escherichia coli 562 -11535982 113167 yibl (de:hypothetical 13.7 kd protein in mtlr-lctp intergenic region) (db:swissprot) YIBL_ECOLI P36564 ESCHERICHIA COLI 562 -11535982 163334 yibl hypothetical 13.7k protein mtlr-lctp intergenic region:hypothetical protein mtlr 3-region (db:pir2.dat) S47823 S47823 Escherichia coli 562 -11535982 7500937323 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yibl) (le:190915) (re:191277) (di:direct) ECOUW76 U00039 g466740 Escherichia coli 562 -11535982 236839 yibl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 328 of 400 of the completegenome.) (nt:ol20; 100 pct identical amino acid sequence and) (le:4461) (re:4823) (di:direct) AE000438 AE000438 g1790030 Escherichia coli 562 -11535982 5000693680 (de:(ecoli_3522) (pn:hypothetical 13) (gn:yibl) (gtcfc:13.7:14.1) (ec:) (yibl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3522 ECOLI_3522 Escherichia coli 562 10054895

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863665	12548	34704	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863666	12549	34705	1122	373

Description

6500732125 yibn:b3611 hypothetical 15.6 kd protein in secb-tdh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3611 b3611 Escherichia coli 562 -11535983 113168 yibn (de:hypothetical 15.6 kd protein in secb-tdh intergenic region) (db:swissprot) YIBN_ECOLI P37688 ESCHERICHIA COLI 562 -11535983 163565 yibn hypothetical 15.6k protein secb-tdh intergenic region:hypothetical protein f143 (cl:glpe protein) (db:pir2.dat) S47832 S47832 Escherichia coli 562 -11535983 7500937324 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:198834) (re:199265) (di:complement) ECOUW76 U00039 g466749 Escherichia coli 562 -11535983 236848 yibn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 329 of 400 of the completgenome.) (nt:f143; 100 pct identical amino acid sequence and) (le:2012) (re:2443) (di:complement) AE000439 AE000439 g1790040 Escherichia coli 562 -11535983 5000693683 (de:(ecoli_3531) (pn:hypothetical 15) (gn:yibn) (gtcfc:13.7:14.1) (ec:) (yibn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3531 ECOLI_3531 Escherichia coli 562 10054896

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863672	12550	34706	339	112

Description

6500732126 yibp:b3613 hypothetical 47.5 kd protein in secb-tdh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3613 b3613 Escherichia coli 562 -11535984 163841 yibp hypothetical 47.5k protein secb-tdh intergenic region:hypothetical protein o427 (db:pir2.dat) S47834 S47834 Escherichia coli 562 -11535984 7500937326 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:201064) (re:202347) (di:direct) ECOUW76 U00039 g466751 Escherichia coli 562 -11535984 236850 yibp putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 329 of 400 of the completgenome.) (nt:o427; 100 pct identical amino acid sequence and) (le:4242) (re:5525) (di:direct) AE000439 AE000439 g1790042 Escherichia coli 562 -11535984 113170 yibp (de:hypothetical 47.5 kd protein in secb-tdh intergenic region) (db:swissprot) YIBP_ECOLI P37690 ESCHERICHIA COLI 562 -11535984 5000693684 (de:(ecoli_3533) (pn:hypothetical 47) (gn:yibp) (gtcfc:13.7:14.1) (ec:) (yibp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3533 ECOLI_3533 Escherichia coli 562 10054898

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863675	12551	34707	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863678	12552	34708	810	269

Description

6500732127 yibq:b3614 hypothetical 30.7 kd protein in secb-tdh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3614 b3614 Escherichia coli 562 -11535985 113172 yibq (de:hypothetical 30.7 kd protein in secb-tdh intergenic region) (db:swissprot) YIBQ_ECOLI P37691 ESCHERICHIA COLI 562 -11535985 163400 yibq hypothetical 30.7k protein secb-tdh intergenic region (db:pir2.dat) S47835 S47835 Escherichia coli 562 -11535985 7500937328 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:202477) (re:203310) (di:direct) ECOUW76 U00039 g912478 Escherichia coli 562 -11535985 236851 yibq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 329 of 400 of the completegenome.) (nt:o277; 100 pct identical amino acid sequence and) (le:5655) (re:6488) (di:direct) AE000439 AE000439 g1790043 Escherichia coli 562 -11535985 5000693685 (de:(ecoli_3534) (pn:hypothetical 30) (gn:yibq) (gtcfc:13.7:14.1) (ec:)(yibq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3534 ECOLI_3534 Escherichia coli 562 10054900

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863684	12553	34709	294	97

Description

6500732128 yibd:b3615 hypothetical 40.5 kd protein in secb-tdh 5 region:hypothetical 40.5 kd protein in secb-tdh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3615 b3615 Escherichia coli 562 -11535986 113159 yibd (de:hypothetical 40.5 kd protein in secb-tdh intergenic region) (db:swissprot) YIBD_ECOLI P11290 ESCHERICHIA COLI 562 -11535986 157271 yibd hypothetical 40.5k protein secb-tdh 5 region:hypothetical protein f344 (db:pir1.dat) (mp:1 min) Q3ECTH S47836 Escherichia coli 562 -11535986 7500937315 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yibd) (le:203297) (re:204331) (di:complement) ECOUW76 U00039 g466753 Escherichia coli 562 -11535986 236852 yibd putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 329 of 400 of the completegenome.) (nt:f344; 100 pct identical amino acid sequence and) (le:6475) (re:7509) (di:complement) AE000439 AE000439 g1790044 Escherichia coli 562 -11535986 5000693686 (de:(ecoli_3535) (pn:hypothetical 40) (gn:yibd) (gtcfc:13.7:14.1) (ec:) (yibd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3535 ECOLI_3535 Escherichia coli 562 10054887

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863695	12554	34710	546	181

Description

6500732129 htrl:b3618 hypothetical protein:htrl protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3618 b3618 Escherichia coli 562 -11535987 113158 htrl (de:htrl protein) (db:swissprot) HTRL_ECOLI P25666 ESCHERICHIA COLI 562 -11535987 163624 hypothetical protein f290:hypothetical protein b3618 (db:pir2.dat) S47839 S47839 Escherichia coli 562 -11535987 236855 htrl (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e. coli htrl gene, complete cds.) (nt:33,991 dalton protein) (le:279) (re:1151) (di:direct) ECOHTRL M94888 g1209298 Escherichia coli 562 -11535987 7500883610 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yibb) (le:207076) (re:207948) (di:complement) ECOUW76 U00039 g466756 Escherichia coli 562 -11535987 234708 htrl involved in lipopolysaccharide biosynthesis (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 330 of 400 of the completegenome.) (nt:f290; alternate gene name yibb) (le:192) (re:1064) (di:complement) AE000440 AE000440 g1790048 Escherichia coli 562 -11535987 5000693687 (de:(ecoli_3538) (pn:hypothetical 34) (gtcfc:13.7:14.1) (ec:) (yibb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3538 ECOLI_3538 Escherichia coli 562 10054886

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863701	12555	34711	342	114

Description

6500732130 yicg:b3646 hypothetical 22.0 kd protein in rph-gmk intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3646 b3646 Escherichia coli 562 -11535988 7000690926 yicg hypothetical 22.0 kd protein in rph-gmk intergenic region (cl:hypothetical protein b1832) (db:pir2.dat) H65165 H65165 Escherichia coli 562 -11535988 7500959797 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:o223) (le:8212) (re:8883) (di:direct) ECOUW82 L10328 g290496 Escherichia coli 562 -11535988 236884 yicg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 332 of 400 of the completegenome.) (nt:o223; 100 pct identical to 205 amino acids of) (le:211) (re:882) (di:direct) AE000442 AE000442 g1790078 Escherichia coli 562 -11535988 5000693692 (de:(ecoli_3566) (pn:hypothetical 22) (gn:yicg) (gtcfc:13.7:14.1) (ec:) (yicg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3566 ECOLI_3566 Escherichia coli 562 10124052

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863702	12556	34712	810	269

Description

6500732131 yicf:b3647 hypothetical 63.2 kd protein in gmk 5region:hypothetical 63.2 kd protein in rph-gmk intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3647 b3647 Escherichia coli 562 -11535989 7000690966 yicf hypothetical 63.2k protein gmk 5region (db:pir2.dat) A65166 A65166 Escherichia coli 562 -11535989 7500959824 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:f562) (le:8880) (re:10568) (di:complement) ECOUW82 L10328 g290497 Escherichia coli 562 -11535989 236885 yicf putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 332 of 400 of the completegenome.) (nt:f562; 100 pct identical to 560 amino acids of) (le:879) (re:2567) (di:complement) AE000442 AE000442 g1790079 Escherichia coli 562 -11535989 5000693693 (de:(ecoli_3567) (pn:hypothetical 63) (gn:yicf) (gtcfc:13.7:14.1) (ec:) (yicf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3567 ECOLI_3567 Escherichia coli 562 10124053

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863703	12557	34713	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863713	12558	34714	222	73

Description

6500732132 yice:b3654 hypothetical 48.9 kd protein in glts
3region:hypothetical 48.9 kd protein in glts-selc intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3654
b3654 Escherichia coli 562 -11535990 113185 yice (de:hypothetical 48.9 kd
protein in glts-selc intergenic region) (db:swissprot) YICE_ECOLI P27432
ESCHERICHIA COLI 562 -11535990 7000688013 yice hypothetical 48.9 kd protein
in glts 3region (cl:hypothetical protein b2882) (db:pir2.dat) H65166 H65166
Escherichia coli 562 -11535990 7500937338 o463 (fn:unknown) (sr:escherichia
coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e.
coli; the region from 81.5 to 84.5 minutes.) (le:18337) (re:19728)
(di:direct) ECOUW82 L10328 g290504 Escherichia coli 562 -11535990 236892
yice putative transport protein (fn:putative transport; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 333 of 400 of the
completengenome.) (nt:o463; 100 pct identical amino acid sequence and)
(le:278) (re:1669) (di:direct) AE000443 AE000443 g1790087 Escherichia coli
562 -11535990 5000693694 (de:(ecoli_3574) (pn:hypothetical 48) (gn:yice)
(gtcfc:13.7:14.1) (ec:) (yice_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_3574 ECOLI_3574 Escherichia coli 562
10054913

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863714	12559	34715	456	151

Description

6500732133 yich:b3655 hypothetical 62.3 kd protein in glts-selc intergenic
region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)
b3655 b3655 Escherichia coli 562 -11535991 7500937340 yich (de:hypothetical
62.3 kd protein in glts-selc intergenic region) (db:swissprot) YICH_ECOLI
P31433 ESCHERICHIA COLI 562 -11535991 7000690964 yich hypothetical 62.3 kd
protein in glts-selc intergenic region (db:pir2.dat) A65167 A65167
Escherichia coli 562 -11535991 7500937342 yich orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
333 of 400 of the completengenome.) (nt:o569; 100 pct identical amino acid
sequence and) (le:1790) (re:3499) (di:direct) AE000443 AE000443 g1790088
Escherichia coli 562 -11535991 5000693695 (de:(ecoli_3575) (pn:hypothetical
62) (gn:yich) (gtcfc:13.7:14.1) (ec:) (yich_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3575 ECOLI_3575 Escherichia
coli 562 10124055

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863732	12560	34716	282	93

Description

6500732134 yici:b3656 hypothetical 88.1 kd protein in glts-selc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3656 b3656 Escherichia coli 562 -11535992 7500937343 yici (de:hypothetical 88.1 kd protein in glts-selc intergenic region) (db:swissprot) YICI_ECOLI P31434 ESCHERICHIA COLI 562 -11535992 7000690976 yici hypothetical 88.1 kd protein in glts-selc intergenic region (db:pir2.dat) B65167 B65167 Escherichia coli 562 -11535992 7500937345 yici orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 333 of 400 of the completegenome.) (nt:f772; 100 pct identical amino acid sequence and) (le:3552) (re:5870) (di:complement) AE000443 AE000443 g2367256 Escherichia coli 562 -11535992

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863737	12561	34717	555	184

Description

6500732135 yicj:b3657 hypothetical 51.0 kd protein in glts-selc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3657 b3657 Escherichia coli 562 -11535993 7000690954 yicj hypothetical 51.0 kd protein in glts-selc intergenic region (cl:melibiose carrier protein) (db:pir2.dat) C65167 C65167 Escherichia coli 562 -11535993 7500959818 yicj putative permease (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 333 of 400 of the completegenome.) (nt:f479; 100 pct identical to 460 amino acids of) (le:5880) (re:7319) (di:complement) AE000443 AE000443 g2367257 Escherichia coli 562 -11535993

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863740	12562	34718	570	189

Description

6500732136 yick:b3659 hypothetical 43.5 kd protein in selc-nlpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3659 b3659 Escherichia coli 562 -11535994 113192 yick (de:hypothetical 43.5 kd protein in selc-nlpa intergenic region) (db:swissprot) YICK_ECOLI P31436 ESCHERICHIA COLI 562 -11535994 7000688014 yick probable membrane protein yick (db:pir2.dat) D65167 D65167 Escherichia coli 562 -11535994 7500937347 o394 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to unidentified orf near 47 minutes) (le:26345) (re:27529) (di:direct) ECOUW82 L10328 g290508 Escherichia coli 562 -11535994 236896 yick two-module transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 333 of 400 of the completegenome.) (nt:o394; 100 pct identical to yick_ecoli sw:) (le:8286) (re:9470) (di:direct) AE000443 AE000443 g1790091 Escherichia coli 562 -11535994 5000693698 (de:(ecoli_3578) (pn:hypothetical 43) (gn:yick) (gtcfc:13.7:14.1) (ec:) (yick_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3578 ECOLI_3578 Escherichia coli 562 10054920

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863741	12563	34719	519	173

Description

6500732137 yicl:b3660 hypothetical 33.1 kd protein in nlpa 5 region:hypothetical 33.1 kd protein in selc-nlpa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3660 b3660 Escherichia coli 562 -11535995 113193 yicl (de:hypothetical 33.1 kd protein in selc-nlpa intergenic region) (db:swissprot) YICL_ECOLI P31437 ESCHERICHIA COLI 562 -11535995 7000688015 yicl hypothetical 33.1 kd protein in nlpa 5 region (cl:hypothetical protein yded) (db:pir2.dat) E65167 E65167 Escherichia coli 562 -11535995 7500937348 o307 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:27640) (re:28563) (di:direct) ECOUW82 L10328 g290509 Escherichia coli 562 -11535995 236897 yicl putative permease transporter (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 333 of 400 of the completegenome.) (nt:o307; 100 pct identical amino acid sequence and) (le:9581) (re:10504) (di:direct) AE000443 AE000443 g1790092 Escherichia coli 562 -11535995 5000693699 (de:(ecoli_3579) (pn:hypothetical 33) (gn:yicl) (gtcfc:13.7:14.1) (ec:) (yicl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3579 ECOLI_3579 Escherichia coli 562 10054921

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863742	12564	34720	1428	475

Description

6500732138 yicm:b3662 hypothetical 43.6 kd protein in nlpa 3 region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3662 b3662 Escherichia coli 562 -11535996 7000690941 yicm chloramphenicol resistance protein homolog nlpa 3 region (cl:streptomyces lividans chloramphenicol resistance protein) (db:pir2.dat) G65167 G65167 Escherichia coli 562 -11535996 7500959815 f451 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:29940) (re:31295) (di:complement) ECOUW82 L10328 g290511 Escherichia coli 562 -11535996 236899 yicm putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 334 of 400 of the completegenome.) (nt:f451; 100 pct identical to 412 amino acids of) (le:363) (re:1718) (di:complement) AE000444 AE000444 g1790095 Escherichia coli 562 -11535996 5000693700 (de:(ecoli_3581) (pn:hypothetical 43) (gn:yicm) (gtcfc:13.7:14.1) (ec:) (yicm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3581 ECOLI_3581 Escherichia coli 562 10124058

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863744	12565	34721	651	216

Description

6500732139 yicn:b3663 hypothetical 18.2 kd protein in nlpa-uhpt intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3663 b3663 Escherichia coli 562 -11535997 113195 yicn (de:hypothetical 18.2 kd protein in nlpa-uhpt intergenic region) (db:swissprot) YICN_ECOLI P31439 ESCHERICHIA COLI 562 -11535997 7000688016 yicn hypothetical 18.2 kd protein in nlpa-uhpt intergenic region (db:pir2.dat) H65167 H65167 Escherichia coli 562 -11535997 7500937351 f159 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:31341) (re:31820) (di:complement) ECOUW82 L10328 g290512 Escherichia coli 562 -11535997 236900 yicn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 334 of 400 of the completegenome.) (nt:f159; 100 pct identical amino acid sequence and) (le:1764) (re:2243) (di:complement) AE000444 AE000444 g1790096 Escherichia coli 562 -11535997 5000693701 (de:(ecoli_3582) (pn:hypothetical 18) (gn:yicn) (gtcfc:13.7:14.1) (ec:) (yicn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3582 ECOLI_3582 Escherichia coli 562 10054923

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863768	12566	34722	291	96

Description

6500732140 yico:b3664 hypothetical 49.9 kd protein in nlpa-uhpt intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3664 b3664 Escherichia coli 562 -11535998 113196 yico (de:hypothetical 49.9 kd protein in nlpa-uhpt intergenic region) (db:swissprot) YICO_ECOLI P31440 ESCHERICHIA COLI 562 -11535998 7000688017 yico hypothetical 49.9 kd protein in nlpa-uhpt intergenic region (cl:conserved hypothetical protein hi0125) (db:pir2.dat) A65168 A65168 Escherichia coli 562 -11535998 7500937352 yico orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 334 of 400 of the completegenome.) (nt:f470; 100 pct identical amino acid sequence and) (le:2269) (re:3681) (di:complement) AE000444 AE000444 g1790097 Escherichia coli 562 -11535998 5000693702 (de:(ecoli_3583) (pn:hypothetical 49) (gn:yico) (gtcfc:13.7:14.1) (ec:) (yico_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3583 ECOLI_3583 Escherichia coli 562 10124059

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863776	12567	34723	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863777	12568	34724	756	251

Description

6500732141 yidf:b3674 hypothetical 19.1 kd protein in ivbl-ibpb intergenic region:hypothetical 19.1 kd protein in emrd-glvg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3674 b3674 Escherichia coli 562 -11535999 113211 yidf (de:hypothetical 19.1 kd protein in emrd-glvg intergenic region) (db:swissprot) YIDF_ECOLI P31443 ESCHERICHIA COLI 562 -11535999 7000688020 yidf hypothetical 19.1 kd protein in ivbl-ibpb intergenic region (db:pir2.dat) C65169 C65169 Escherichia coli 562 -11535999 7500937365 yidf putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:f165; 100 pct identical amino acid sequence and) (le:2289) (re:2786) (di:complement) AE000445 AE000445 g1790108 Escherichia coli 562 -11535999 5000693704 (de:(ecoli_3593) (pn:hypothetical 19) (gn:yidf) (gtcfc:13.7:14.1) (ec:) (yidf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3593 ECOLI_3593 Escherichia coli 562 10124065

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863779	12569	34725	285	94

Description

GTC ORF with score 155 to: (sr:thale cress) (db:genpept-pln1) (ec:4.1.1.15) (de:arabidopsis thaliana columbia glutamate decarboxylase (gad) mrna,complete cds.) (nt:gad1 isoform; similar to the gad2 isoform of) (le:1) (re:1509) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863786	12570	34726	462	153

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863809	12571	34727	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863832	12572	34728	585	194

Description

6500732142 yidg:b3675 hypothetical 13.8 kd protein in ivbl-ibpb intergenic region:hypothetical 13.8 kd protein in emrd-glvg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3675 b3675 Escherichia coli 562 -11536000 113212 yidg (de:hypothetical 13.8 kd protein in emrd-glvg intergenic region) (db:swissprot) YIDG_ECOLI P31444 ESCHERICHIA COLI 562 -11536000 7000688021 yidg hypothetical 13.8 kd protein in ivbl-ibpb intergenic region (db:pir2.dat) D65169 D65169 Escherichia coli 562 -11536000 7500937366 f120 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:45002) (re:45364) (di:complement) ECOUW82 L10328 g290524 Escherichia coli 562 -11536000 236912 yidg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:f120; 100 pct identical amino acid sequence and) (le:2783) (re:3145) (di:complement) AE000445 AE000445 g1790109 Escherichia coli 562 -11536000 5000693705 (de:(ecoli_3594) (pn:hypothetical 13) (gn:yidg) (gtcfc:13.7:14.1) (ec:) (yidg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3594 ECOLI_3594 Escherichia coli 562 10054940

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863834	12573	34729	864	287
<u>Description</u>				

GTC ORF with score 243 to: (fn:glutamate-preferring neurocarboxypeptidase;) (sr:house mouse) (db:genpept-rod) (de:mus musculus prostate-specific membrane antigen homolog (mopsm)mrna, complete cds.) (nt:human prostate-specific membrane antigen ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863838	12574	34730	297	99
<u>Description</u>				

6500732143 yidh:b3676 hypothetical 12.8 kd protein in ivbl-ibpb intergenic region:hypothetical 12.8 kd protein in emrd-glvg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3676 b3676 Escherichia coli 562 -11536001 113213 yidh (de:hypothetical 12.8 kd protein in emrd-glvg intergenic region) (db:swissprot) YIDH_ECOLI P31445 ESCHERICHIA COLI 562 -11536001 7000688022 yidh hypothetical 12.8 kd protein in ivbl-ibpb intergenic region (db:pir2.dat) E65169 E65169 Escherichia coli 562 -11536001 7500937367 f115 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:45354) (re:45701) (di:complement) ECOUW82 L10328 g290525 Escherichia coli 562 -11536001 236913 yidh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:f115; 100 pct identical amino acid sequence and) (le:3135) (re:3482) (di:complement) AE000445 AE000445 g1790110 Escherichia coli 562 -11536001 5000693706 (de:(ecoli_3595) (pn:hypothetical 12) (gn:yidh) (gtcfc:13.7:14.1) (ec:) (yidh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3595 ECOLI_3595 Escherichia coli 562 10054941

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863859	12575	34731	2217	738

Description

6500732144 yidj:b3678 hypothetical 57.3 kd protein in ilvo-ibpb intergenic region:hypothetical 57.3 kd protein in emrd-glvg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3678 b3678 Escherichia coli 562 -11536002 113215 yidj (de:hypothetical 57.3 kd protein in emrd-glvg intergenic region) (db:swissprot) YIDJ_ECOLI P31447 ESCHERICHIA COLI 562 -11536002 7000688024 yidj hypothetical 57.3 kd protein in ilvo-ibpb intergenic region (db:pir2.dat) G65169 G65169 Escherichia coli 562 -11536002 7500937369 f497 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to arylsulfatases) (le:46305) (re:47798) (di:complement) ECOUW82 L10328 g290527 Escherichia coli 562 -11536002 236915 yidj putative sulfatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:f497; 100 pct identical to yidj_ecoli sw:) (le:4086) (re:5579) (di:complement) AE000445 AE000445 g1790112 Escherichia coli 562 -11536002 5000693708 (de:(ecoli_3597) (pn:hypothetical 57) (gn:yidj) (gtcfc:13.7:14.1) (ec:) (yidj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3597 ECOLI_3597 Escherichia coli 562 10054943

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863861	12576	34732	531	176

Description

6500732145 yidk:b3679 hypothetical 62.1 kd protein in ilvo-ibpb intergenic region:hypothetical 62.1 kd protein in emrd-glvg intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3679 b3679 Escherichia coli 562 -11536003 113216 yidk (de:hypothetical 62.1 kd protein in emrd-glvg intergenic region) (db:swissprot) YIDK_ECOLI P31448 ESCHERICHIA COLI 562 -11536003 7000688025 yidk hypothetical 62.1 kd protein in ilvo-ibpb intergenic region (db:pir2.dat) H65169 H65169 Escherichia coli 562 -11536003 7500937370 f571 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to glucose transport proteins) (le:47795) (re:49510) (di:complement) ECOUW82 L10328 g290528 Escherichia coli 562 -11536003 236916 yidk putative cotransporter (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:f571; 100 pct identical to yidk_ecoli sw:) (le:5576) (re:7291) (di:complement) AE000445 AE000445 g1790113 Escherichia coli 562 -11536003 5000693709 (de:(ecoli_3598) (pn:hypothetical 62) (gn:yidk) (gtcfc:13.7:14.1) (ec:) (yidk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3598 ECOLI_3598 Escherichia coli 562 10054944

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863872	12577	34733	765	254

Description

GTC ORF with score 793 to: (sr:thale cress) (db:genpept-pln1)
 (de:arabidopsis thaliana dna chromosome 4, bac clone t12h17
 (essaiiproject).) (nt:strong similarity to o-sialoglycoprotein)
 (le:30505:31148:31408) (re:31062:31303:31755) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863877	12578	34734	501	166

Description

6500732146 yidl:b3680 hypothetical protein:hypothetical transcriptional
 regulator in emrd-glvg intergenic region (gtcfc:10.2:14.1) (keggfc:14.2)
 (rileyfc:5.7.0) (db:gtc-escherichia coli) b3680 b3680 Escherichia coli 562
 -11536004 113217 yidl (de:hypothetical transcriptional regulator in
 emrd-glvg intergenic region) (db:swissprot) YIDL_ECOLI P31449 ESCHERICHIA
 COLI 562 -11536004 7000688026 hypothetical protein b3680 (db:pir2.dat)
 A65170 A65170 Escherichia coli 562 -11536004 7500937371 o307 (fn:unknown)
 (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52)
 (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.)
 (nt:similar to rhamnose operon regulatory protein) (le:49647) (re:50570)
 (di:direct) ECOUW82 L10328 g290529 Escherichia coli 562 -11536004 236917
 yidl putative arac-type regulatory protein (fn:putative regulator; not
 classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335
 of 400 of the completegenome.) (nt:o307; similar to rhamnose operon
 regulatory) (le:7428) (re:8351) (di:direct) AE000445 AE000445 g1790114
 Escherichia coli 562 -11536004 5000693710 (de:(ecoli_3599) (pn:hypothetical
 transcriptional regulator in ilvo-ibpb intergenic region) (gtcfc:13.7:14.1)
 (ec:) (yidl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
 ECOLI_3599 ECOLI_3599 Escherichia coli 562 10054945

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863878	12579	34735	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863888	12580	34736	678	226

Description

6500732147 yidp:b3684 hypothetical transcriptional regulator in ilvo-ibpb intergenic region:hypothetical transcriptional regulator in ilvo-ibpb intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3684 b3684 Escherichia coli 562 -11536005 113218 yidp (de:hypothetical transcriptional regulator in ilvo-ibpb intergenic region) (db:swissprot) YIDP_ECOLI P31453 ESCHERICHIA COLI 562 -11536005 7000688027 yidp hypothetical transcription regulator:ilvo-ibpb intergenic region (cl:transcription regulator gntr) (db:pir2.dat) E65170 E65170 Escherichia coli 562 -11536005 7500937372 o238 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to e. coli orf adjacent to suc operon;) (le:53293) (re:54009) (di:direct) ECOUW82 L10328 g290533 Escherichia coli 562 -11536005 236921 yidp putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:o238; 100 pct identical to yidp_ecoli sw:) (le:11074) (re:11790) (di:direct) AE000445 AE000445 g1790118 Escherichia coli 562 -11536005 5000693711 (de:(ecoli_3603) (pn:hypothetical transcriptional regulator in ilvo-ibpb intergenic region) (gn:yidp) (gtcfc:13.7:14.1) (ec:) (yidp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3603 ECOLI_3603 Escherichia coli 562 10054946

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863892	12581	34737	528	175

Description

6500732148 yide:b3685 hypothetical 58.9 kd protein in ibpb 3region:orfa (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3685 b3685 Escherichia coli 562 -11536006 7000690962 yide hypothetical 58.9 kd protein in ibpb 3region orfa (db:pir2.dat) F65170 F65170 Escherichia coli 562 -11536006 7500959821 f561 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:54006) (re:55691) (di:complement) ECOUW82 L10328 g290534 Escherichia coli 562 -11536006 236922 yide putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:f561; 100 pct identical to 553 amino acids of) (le:11787) (re:13472) (di:complement) AE000445 AE000445 g1790119 Escherichia coli 562 -11536006 5000693712 (de:(ecoli_3604) (pn:hypothetical 58) (gn:yide) (gtcfc:13.7:14.1) (ec:) (yide_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3604 ECOLI_3604 Escherichia coli 562 10124067

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863905	12582	34738	2193	731

Description

6500732149 yidr:b3689 hypothetical 46.4 kd protein in ibpa-gyrb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3689 b3689 Escherichia coli 562 -11536007 7500937374 yidr (de:hypothetical 46.4 kd protein in ibpa-gyrb intergenic region) (db:swissprot) YIDR_ECOLI P31455 ESCHERICHIA COLI 562 -11536007 7000690945 yidr hypothetical 46.4 kd protein in ibpa-gyrb intergenic region (db:pir2.dat) B65171 B65171 Escherichia coli 562 -11536007 7500937376 yidr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completegenome.) (nt:f416; 100 pct identical amino acid sequence and) (le:1136) (re:2386) (di:complement) AE000446 AE000446 g1790124 Escherichia coli 562 -11536007 5000693716 (de:(ecoli_3608) (pn:hypothetical 46) (gn:yidr) (gtcfc:13.7:14.1) (ec:) (yidr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3608 ECOLI_3608 Escherichia coli 562 10124069

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863909	12583	34739	1215	404

Description

6500732150 yids:b3690 hypothetical 41.0 kd protein in ibpa-gyrb intergenic region:hypothetical 41.0 kd protein in ibpa-gyrb intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3690 b3690 Escherichia coli 562 -11536008 113221 yids (de:hypothetical 41.0 kd protein in ibpa-gyrb intergenic region precursor) (db:swissprot) YIDS_ECOLI P31456 ESCHERICHIA COLI 562 -11536008 7000688029 yids hypothetical 41.0 kd protein in ibpa-gyrb intergenic region (db:pir2.dat) C65171 C65171 Escherichia coli 562 -11536008 7500937377 o361 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:58750) (re:59835) (di:direct) ECOUW82 L10328 g290539 Escherichia coli 562 -11536008 236927 yids orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completegenome.) (nt:o361; 100 pct identical amino acid sequence and) (le:2430) (re:3515) (di:direct) AE000446 AE000446 g1790125 Escherichia coli 562 -11536008 5000693717 (de:(ecoli_3609) (pn:hypothetical 41) (gn:yids) (gtcfc:13.7:14.1) (ec:) (yids_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3609 ECOLI_3609 Escherichia coli 562 10054949

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863910	12584	34740	231	76

Description

6500732151 yidt:b3691 hypothetical 48.8 kd protein in ibpa-gyrb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3691 b3691 Escherichia coli 562 -11536009 113222 dgot (de:d-galactonate transporter) (db:swissprot) DGOT_ECOLI P31457 ESCHERICHIA COLI 562 -11536009 7000688030 yidt hypothetical 48.8 kd protein in ibpa-gyrb intergenic region (cl:hexuronate transporter) (db:pir2.dat) D65171 D65171 Escherichia coli 562 -11536009 7500880220 f445 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:59832) (re:61169) (di:complement) ECOUW82 L10328 g290540 Escherichia coli 562 -11536009 236928 dgot d-galactonate transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completemgenome.) (nt:f445; formerly designated yidt) (le:3512) (re:4849) (di:complement) AE000446 AE000446 g1790126 Escherichia coli 562 -11536009 5000693718 (de:(ecoli_3610) (pn:hypothetical 48) (gn:yidt) (gtcfc:13.7:14.1) (ec: (yidt_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3610 ECOLI_3610 Escherichia coli 562 10054950

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863926	12585	34741	486	161

Description

6500732152 yidu:b3692 hypothetical 64.0 kd protein in ibpa-gyrb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3692 b3692 Escherichia coli 562 -11536010 7500880216 dgoa:dgod (ec:4.1.2.21:4.2.1.6) (de:phosphate aldolase) / galactonate dehydratase,) (db:swissprot) DGOA_ECOLI P31458 ESCHERICHIA COLI 562 -11536010 7000690968 yidu hypothetical 64.0 kd protein in ibpa-gyrb intergenic region (db:pir2.dat) E65171 E65171 Escherichia coli 562 -11536010 7500880218 dgoa 2-oxo-3-deoxygalactonate 6-phosphate aldolase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completemgenome.) (nt:f587; formerly designated yidu) (le:4924) (re:6687) (di:complement) AE000446 AE000446 g2367262 Escherichia coli 562 -11536010

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863930	12586	34742	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863953	12587	34743	1392	464

Description

6500732153 yidv:b3693 hypothetical 31.4 kd protein in ibpa-gyrb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3693 b3693 Escherichia coli 562 -11536011 113224 dgok (ec:2.7.1.58) (de:galactonokinase) (2-oxo-3-deoxygalactonate kinase)) (db:swissprot) DGOK_ECOLI P31459 ESCHERICHIA COLI 562 -11536011 7000688031 yidv hypothetical 31.4 kd protein in ibpa-gyrb intergenic region (db:pir2.dat) F65171 F65171 Escherichia coli 562 -11536011 7500880219 f292 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:62991) (re:63869) (di:complement) ECOUW82 L10328 g290542 Escherichia coli 562 -11536011 236930 dgok 2-oxo-3-deoxygalactonate kinase (fn:putative enzyme; degradation of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completegenome.) (nt:f292; formerly designated yidv) (le:6671) (re:7549) (di:complement) AE000446 AE000446 g1790128 Escherichia coli 562 -11536011 5000693720 (de:(ecoli_3612) (pn:hypothetical 31) (gn:yidv) (gtcfc:13.7:14.1) (ec:) (yidv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3612 ECOLI_3612 Escherichia coli 562 10054952

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501863962	12588	34744	1299	432

Description

6500732154 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3694 b3694 Escherichia coli 562 -11536012 7000691811 hypothetical protein b3694 (db:pir2.dat) G65171 G65171 Escherichia coli 562 -11536012 7500960318 b3694 putative fada-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completegenome.) (nt:f98; new orf adjacent to yidw) (le:7546) (re:7842) (di:complement) AE000446 AE000446 g2367263 Escherichia coli 562 -11536012

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863975	12589	34745	1800	599

Description

6500732155 yidw:b3695 hypothetical transcriptional regulator in ibpa-gyrb intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3695 b3695 Escherichia coli 562 -11536013
7000691848 yidw hypothetical transcription regulator ibpa-gyrb intergenic region (db:pir2.dat) H65171 H65171 Escherichia coli 562 -11536013
7500960365 yidw regulator protein for dgo operon (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completengenome.) (nt:f128; sequence change shortens and) (le:7848) (re:8234) (di:complement) AE000446 AE000446 g2367264 Escherichia coli 562 -11536013

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501863978	12590	34746	678	225

Description

6500732156 yidx:b3696 hypothetical 22.0 kd protein in ibpa-gyrb intergenic region: hypothetical 24.8 kd protein in ibpa-gyrb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3696 b3696 Escherichia coli 562 -11536014 113226 yidx (de:hypothetical 24.8 kd protein in ibpa-gyrb intergenic region) (db:swissprot) YIDX_ECOLI_P31461 ESCHERICHIA COLI 562 -11536014 7000688032 yidx hypothetical 22.0 kd protein in ibpa-gyrb intergenic region (db:pir2.dat) A65172 A65172 Escherichia coli 562 -11536014 7500937378 yidx putative replicase ec 2.7.- (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completengenome.) (nt:o223; ?? pct identical amino acid sequence and) (le:8569) (re:9240) (di:direct) AE000446 AE000446 g1790130 Escherichia coli 562 -11536014 5000693722 (de:(ecoli_3614) (pn:hypothetical 22) (gn:yidx) (gtcfc:13.7:14.1) (ec:) (yidx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3614 ECOLI_3614 Escherichia coli 562 10124071

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864001	12591	34747	321	106

Description

6500732157 yida:b3697 hypothetical 29.7 kd protein in ibpa-gyrb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3697 b3697 Escherichia coli 562 -11536015 113201 yida (de:hypothetical 29.7 kd protein in ibpa-gyrb intergenic region) (db:swissprot) YIDA_ECOLI P09997 ESCHERICHIA COLI 562 -11536015 7000688018 yida hypothetical 29.7k protein:ibpa-gyrb intergenic region (cl:methanobacterium thermoautotrophicum conserved hypothetical protein mth1071) (db:pir1.dat) (mp:83 min) QQECGB B65172 Escherichia coli 562 -11536015 7500937361 yida orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completegenome.) (nt:f270; 99 pct identical amino acid sequence and) (le:9215) (re:10027) (di:complement) AE000446 AE000446 g2367265 Escherichia coli 562 -11536015

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864002	12592	34748	1167	389

Description

6500732158 yidb:b3698 hypothetical protein:hypothetical 13.8 kd protein in ibpa-gyrb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3698 b3698 Escherichia coli 562 -11536016 7000688998 hypothetical 13.7k protein gyrb 3 region:hypothetical protein b3698 (db:pir1.dat) (mp:83 min) QQECG1 C65172 Escherichia coli 562 -11536016 7500953702 f135 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:66465) (re:66872) (di:complement) ECOUW82 L10328 g290546 Escherichia coli 562 -11536016 236934 yidb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 337 of 400 of the completegenome.) (nt:f135) (le:80) (re:487) (di:complement) AE000447 AE000447 g1790133 Escherichia coli 562 -11536016 5000693724 (de:(ecoli_3616) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3616 ECOLI_3616 Escherichia coli 562 10124073

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864019	12593	34749	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864023	12594	34750	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864029	12595	34751	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864046	12596	34752	2256	751

Description

6500732159 yidy:b3710 hypothetical 41.5 kd protein in tnab
3region:hypothetical 41.5 kd protein in tnab-bglb intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3710
b3710 Escherichia coli 562 -11536017 113227 yidy (de:hypothetical 41.5 kd
protein in tnab-bglb intergenic region) (db:swissprot) YIDY_ECOLI P31462
ESCHERICHIA COLI 562 -11536017 7000688033 yidy hypothetical 41.5 kd protein
in tnab 3region (cl:bicyclomycin resistance protein) (db:pir2.dat) G65173
G65173 Escherichia coli 562 -11536017 7500937379 yidy putative transport
protein (fn:putative transport; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 338 of 400 of the completegenome.)
(nt:o391; 100 pct identical amino acid sequence and) (le:3332) (re:4507)
(di:direct) AE000448 AE000448 g1790146 Escherichia coli 562 -11536017
5000693726 (de:(ecoli_3628) (pn:hypothetical 41) (gn:yidy)
(gtcfc:13.7:14.1) (ec:) (yidy_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_3628 ECOLI_3628 Escherichia coli 562
10124077

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864051	12597	34753	384	127

Description

6500732160 yidz:b3711 hypothetical transcriptional regulator in tnab-bglb intergenic region:hypothetical transcriptional regulator in tnab-bglb intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3711 b3711 Escherichia coli 562 -11536018 113228 yidz (de:hypothetical transcriptional regulator in tnab-bglb intergenic region) (db:swissprot) YIDZ_ECOLI P31463 ESCHERICHIA COLI 562 -11536018 7000688034 yidz hypothetical transcription regulator tnab-bglb intergenic region (db:pir2.dat) H65173 H65173 Escherichia coli 562 -11536018 7500937380 o319 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to r. meliloti nodulation protein d;) (le:82162) (re:83121) (di:direct) ECOUW82 L10328 g290559 Escherichia coli 562 -11536018 236947 yidz putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 338 of 400 of the completegenome.) (nt:o319; 100 pct identical to yidz_ecoli sw:) (le:4482) (re:5441) (di:direct) AE000448 AE000448 g1790147 Escherichia coli 562 -11536018 5000693727 (de:(ecoli_3629) (pn:hypothetical transcriptional regulator in tnab-bglb intergenic region) (gn:yidz) (gtcfc:13.7:14.1) (ec:) (yidz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3629 ECOLI_3629 Escherichia coli 562 10054956

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864058	12598	34754	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864062	12599	34755	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864064	12600	34756	693	230

Description

6500732161 yiee:b3712 hypothetical 28.0 kd protein in tnab-bglb intergenic region:hypothetical 28.2 kd protein in tnab-bglb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3712 b3712 Escherichia coli 562 -11536019 113240 yiee (de:hypothetical 28.2 kd protein in tnab-bglb intergenic region) (db:swissprot) YIEE_ECOLI P31464 ESCHERICHIA COLI 562 -11536019 7000688036 yiee hypothetical 28.0 kd protein in tnab-bglb intergenic region (db:pir2.dat) A65174 A65174 Escherichia coli 562 -11536019 7500937391 yiee orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 338 of 400 of the completengenome.) (nt:o253; ??? pct identical amino acid sequence and) (le:5586) (re:6347) (di:direct) AE000448 AE000448 g1790148 Escherichia coli 562 -11536019 5000693728 (de:(ecoli_3630) (pn:hypothetical 28) (gn:yiee) (gtcfc:13.7:14.1) (ec:) (yiee_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3630 ECOLI_3630 Escherichia coli 562 10124078

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864065	12601	34757	234	77

Description

6500732162 yief:b3713 hypothetical protein:hypothetical 20.4 kd protein in tnab-bglb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3713 b3713 Escherichia coli 562 -11536020 113241 yief (de:hypothetical 20.4 kd protein in tnab-bglb intergenic region) (db:swissprot) YIEF_ECOLI P31465 ESCHERICHIA COLI 562 -11536020 7000688037 hypothetical protein b3713 (db:pir2.dat) B65174 B65174 Escherichia coli 562 -11536020 7500937392 o188 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:84046) (re:84612) (di:direct) ECOUW82 L10328 g290561 Escherichia coli 562 -11536020 236949 yief orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 338 of 400 of the completengenome.) (nt:o188) (le:6369) (re:6935) (di:direct) AE000448 AE000448 g1790149 Escherichia coli 562 -11536020 5000693729 (de:(ecoli_3631) (pn:hypothetical 20) (gtcfc:13.7:14.1) (ec:) (yief_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3631 ECOLI_3631 Escherichia coli 562 10054969

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864086	12602	34758	960	320

Description

GTC ORF with score 204 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana chromosome i bac f14j9 genomic sequence contains phyta marker, complete sequence.) (nt:highly similar to cinnamyl alcohol dehydrogenase,) (le:50999:51232:51547:51833) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864094	12603	34759	1143	380

Description

GTC ORF with score 322 to: (fn:putative cytochrome p450 function) (db:genpept-bct2) (de:rhodococcus sp. x309 plasmid pslox putative repressor protein, putative replication protein (rep), and truncated putative replication protein (rep') genes, complete ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864096	12604	34760	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864110	12605	34761	333	110

Description

6500732163 yieg:b3714 hypothetical 46.9 kd protein in tnab-bglb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3714 b3714 Escherichia coli 562 -11536021 113242 yieg (de:hypothetical 46.9 kd protein in tnab-bglb intergenic region) (db:swissprot) YIEG_ECOLI P31466 ESCHERICHIA COLI 562 -11536021 7000688038 yieg hypothetical 46.9 kd protein in tnab-bglb intergenic region (cl:conserved hypothetical protein hi0125) (db:pir2.dat) C65174 C65174 Escherichia coli 562 -11536021 7500937393 yieg putative membrane / transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 338 of 400 of the complete genome.) (nt:f445; 100 pct identical amino acid sequence and) (le:6989) (re:8326) (di:complement) AE000448 AE000448 gl790150 Escherichia coli 562 -11536021 5000693730 (de:(ecoli_3632) (pn:hypothetical 46) (gn:yieg) (gtcfc:13.7:14.1) (ec: (yieg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3632 ECOLI_3632 Escherichia coli 562 10124079

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864111	12606	34762	978	325

Description

6500732164 yieh:b3715 hypothetical protein:hypothetical 24.7 kd protein in tnab-bglb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3715 b3715 Escherichia coli 562 -11536022 113243 yieh (de:hypothetical 24.7 kd protein in tnab-bglb intergenic region) (db:swissprot) YIEH_ECOLI P31467 ESCHERICHIA COLI 562 -11536022 7000688039 hypothetical protein b3715 (db:pir2.dat) D65174 D65174 Escherichia coli 562 -11536022 7500937394 o221 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:86168) (re:86833) (di:direct) ECOUW82 L10328 g290563 Escherichia coli 562 -11536022 236951 yieh putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 338 of 400 of the completegenome.) (nt:o221) (le:8491) (re:9156) (di:direct) AE000448 AE000448 g1790151 Escherichia coli 562 -11536022 5000693731 (de:(ecoli_3633) (pn:hypothetical 24) (gtcfc:13.7:14.1) (ec:) (yieh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3633 ECOLI_3633 Escherichia coli 562 10054971

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864114	12607	34763	240	80

Description

6500732165 yiei:b3716 hypothetical 16.7 kd protein in tnab-bglb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3716 b3716 Escherichia coli 562 -11536023 113244 yiei (de:hypothetical 16.7 kd protein in tnab-bglb intergenic region) (db:swissprot) YIEI_ECOLI P31468 ESCHERICHIA COLI 562 -11536023 7000688040 yiei hypothetical 16.7 kd protein in tnab-bglb intergenic region (db:pir2.dat) E65174 E65174 Escherichia coli 562 -11536023 7500937395 o155 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:86900) (re:87367) (di:direct) ECOUW82 L10328 g290564 Escherichia coli 562 -11536023 236952 yiei orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 338 of 400 of the completegenome.) (nt:o155; 100 pct identical amino acid sequence and) (le:9223) (re:9690) (di:direct) AE000448 AE000448 g1790152 Escherichia coli 562 -11536023 5000693732 (de:(ecoli_3634) (pn:hypothetical 16) (gn:yiei) (gtcfc:13.7:14.1) (ec:) (yiei_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3634 ECOLI_3634 Escherichia coli 562 10054972

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864115	12608	34764	240	79

Description

6500732166 yiej:b3717 hypothetical 22.5 kd protein in tna-bglb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3717 b3717 Escherichia coli 562 -11536024 113245 yiej (de:hypothetical 22.5 kd protein in tna-bglb intergenic region) (db:swissprot) YIEJ_ECOLI P31469 ESCHERICHIA COLI 562 -11536024 7000688041 yiej hypothetical 22.5 kd protein in tna-bglb intergenic region (db:pir2.dat) F65174 F65174 Escherichia coli 562 -11536024 7500937396 o195 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:87416) (re:88003) (di:direct) ECOUW82 L10328 g290565 Escherichia coli 562 -11536024 236953 yiej orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 338 of 400 of the completegenome.) (nt:o195; 100 pct identical amino acid sequence and) (le:9739) (re:10326) (di:direct) AE000448 AE000448 g1790153 Escherichia coli 562 -11536024 5000693733 (de:(ecoli_3635) (pn:hypothetical 22) (gn:yiej) (gtcfc:13.7:14.1) (ec:) (yiej_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3635 ECOLI_3635 Escherichia coli 562 10054973

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864121	12609	34765	1617	538

Description

6500732167 yiek:b3718 hypothetical 23.3 kd protein in tna-bglb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3718 b3718 Escherichia coli 562 -11536025 113246 yiek (de:hypothetical 23.3 kd protein in tna-bglb intergenic region) (db:swissprot) YIEK_ECOLI P31470 ESCHERICHIA COLI 562 -11536025 7000688042 yiek hypothetical 23.3 kd protein in tna-bglb intergenic region (db:pir2.dat) G65174 G65174 Escherichia coli 562 -11536025 7500937397 f213 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:88076) (re:88717) (di:complement) ECOUW82 L10328 g290566 Escherichia coli 562 -11536025 236954 yiek putative isomerase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 339 of 400 of the completegenome.) (nt:f213; 100 pct identical amino acid sequence and) (le:67) (re:708) (di:complement) AE000449 AE000449 g1790155 Escherichia coli 562 -11536025 5000693734 (de:(ecoli_3636) (pn:hypothetical 23) (gn:yiek) (gtcfc:13.7:14.1) (ec:) (yiek_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3636 ECOLI_3636 Escherichia coli 562 10054974

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864124	12610	34766	210	69
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864137	12611	34767	813	270
<u>Description</u>				

6500732168 yiel:b3719 hypothetical 44.7 kd protein in tnab-bglb intergenic region:hypothetical 44.1 kd protein in tnab-bglb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3719 b3719 Escherichia coli 562 -11536026 113247 yiel (de:hypothetical 44.1 kd protein in tnab-bglb intergenic region) (db:swissprot) YIEL_ECOLI P31471 ESCHERICHIA COLI 562 -11536026 7000688043 yiel hypothetical 44.7 kd protein in tnab-bglb intergenic region (db:pir2.dat) H65174 H65174 Escherichia coli 562 -11536026 7500937398 yiel putative xylanase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 339 of 400 of the completegenome.) (nt:f400; ??? pct identical amino acid sequence and) (le:792) (re:1994) (di:complement) AE000449 AE000449 g1790156 Escherichia coli 562 -11536026 5000693735 (de:(ecoli_3637) (pn:hypothetical 44) (gn:yeil) (gtcfc:13.7:14.1) (ec:) (yeil_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3637 ECOLI_3637 Escherichia coli 562 10124080

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864148	12612	34768	192	63
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864153	12613	34769	510	169

Description

6500732169 yiec:b3720 hypothetical 60.6 kd protein in bglb 5region:hypothetical 60.7 kd protein in tnab-bglb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3720 b3720 Escherichia coli 562 -11536027 113237 yiec (de:potential outer membrane protein yiec precursor) (db:swissprot) YIEC_ECOLI P26218 ESCHERICHIA COLI 562 -11536027 7000688035 yiec hypothetical 60.6 kd protein in bglb 5region (db:pir2.dat) A65175 A65175 Escherichia coli 562 -11536027 7500937390 yiec putative receptor protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 339 of 400 of the completegenome.) (nt:f538; ??? pct identical amino acid sequence and) (le:1988) (re:3604) (di:complement) AE000449 AE000449 g1790157 Escherichia coli 562 -11536027 5000693736 (de:(ecoli_3638) (pn:hypothetical 60) (gn:yiec) (gtcfc:13.7:14.1) (ec:) (yiec_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3638 ECOLI_3638 Escherichia coli 562 10124081

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864157	12614	34770	813	270

Description

6500732170 hypothetical 49.6 kd protein in asna 3 region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b3745 b3745 Escherichia coli 562 -11536028 7500937399 yiem (de:hypothetical 49.6 kd protein in asna-kup integenic region) (db:swissprot) YIEM_ECOLI P03818 ESCHERICHIA COLI 562 -11536028 7000689001 hypothetical 49.6 kd protein in asna 3 region (db:pir1.dat) (mp:84 min) QQECO3 B65178 Escherichia coli 562 -11536028 7500937401 yiem orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 341 of 400 of the completegenome.) (nt:f427; sequence change joins orfs yied and yiem from) (le:5249) (re:6532) (di:complement) AE000451 AE000451 g2367274 Escherichia coli 562 -11536028

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864176	12615	34771	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864203	12616	34772	498	165

Description

6500732171 yien:b3746 hypothetical 57.4 kd protein in asna-kup intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3746 b3746 Escherichia coli 562 -11536029 7000690960 yien hypothetical 57.4 kd protein in asna-kup intergenic region (db:pir2.dat) C65178 C65178 Escherichia coli 562 -11536029 7500959820 yien putative 2-component regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 341 of 400 of the completegenome.) (nt:f506; sequence change alters both ends of orf) (le:6693) (re:8213) (di:complement) AE000451 AE000451 g2367275 Escherichia coli 562 -11536029

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864207	12617	34773	894	297

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864209	12618	34774	606	201

Description

6500732172 yieo:b3754 hypothetical 51.5 kd protein in rbsr-rrsc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3754 b3754 Escherichia coli 562 -11536030 113250 yieo (de:hypothetical 51.5 kd protein in rbsr-rrsc intergenic region) (db:swissprot) YIEO_ECOLI P31474 ESCHERICHIA COLI 562 -11536030 7000688044 yieo hypothetical 51.5 kd protein in rbsr-rrsc intergenic region (cl:multidrug-efflux transporter) (db:pir2.dat) C65179 C65179 Escherichia coli 562 -11536030 7500937403 f475 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to drug resistance translocases) (le:128573) (re:130000) (di:complement) ECOUW82 L10328 g290604 Escherichia coli 562 -11536030 236992 yieo putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 342 of 400 of the completegenome.) (nt:f475; 100 pct identical to yieo_ecoli sw:) (le:6190) (re:7617) (di:complement) AE000452 AE000452 g1790195 Escherichia coli 562 -11536030 5000693740 (de:(ecoli_3673) (pn:hypothetical 51) (gn:yieo) (gtcfc:13.7:14.1) (ec:) (yieo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3673 ECOLI_3673 Escherichia coli 562 10054978

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864229	12619	34775	1113	370

Description

6500732173 yiep:b3755 hypothetical 20.8 kd protein in rbsr-rrsc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3755 b3755 Escherichia coli 562 -11536031 113252 yiep (de:hypothetical 20.8 kd protein in rbsr-rrsc intergenic region) (db:swissprot) YIEP_ECOLI P31475 ESCHERICHIA COLI 562 -11536031 7000688045 yiep hypothetical 20.8 kd protein in rbsr-rrsc intergenic region (db:pir2.dat) D65179 D65179 Escherichia coli 562 -11536031 7500937405 f181 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:130023) (re:130568) (di:complement) ECOUW82 L10328 g290605 Escherichia coli 562 -11536031 236993 yiep orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 342 of 400 of the completegenome.) (nt:f181; 100 pct identical to yiep_ecoli sw: p31475) (le:7640) (re:8185) (di:complement) AE000452 AE000452 g1790196 Escherichia coli 562 -11536031 5000693741 (de:(ecoli_3674) (pn:hypothetical 20) (gn:yiep) (gtcfc:13.7:14.1) (ec:) (yiep_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3674 ECOLI_3674 Escherichia coli 562 10054980

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864230	12620	34776	756	251

Description

6500732174 yifa:b3762 hypothetical 22.4 kd protein in trpt-pssr intergenic region:orf ii:f198 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3762 b3762 Escherichia coli 562 -11536032 113262 yifa (de:(f198)) (db:swissprot) YIFA_ECOLI P22788 ESCHERICHIA COLI 562 -11536032 7000688046 yifa hypothetical 22.4 kd protein in trpt-pssr intergenic region:hypothetical 20k protein ilvg-rrnc intergenic region (db:pir2.dat) (mp:82 min) E65179 E65179 Escherichia coli 562 -11536032 7500937420 f198 (fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:266) (re:862) (di:complement) ECOUW85 M87049 g148170 Escherichia coli 562 -11536032 236994 yifa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 343 of 400 of the completegenome.) (nt:f198; 100 pct identical to yifa_ecoli sw: p22788) (le:3489) (re:4085) (di:complement) AE000453 AE000453 g1790198 Escherichia coli 562 -11536032 5000693742 (de:(ecoli_3675) (pn:hypothetical 22) (gn:yifa) (gtcfc:13.7:14.1) (ec:) (yifa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3675 ECOLI_3675 Escherichia coli 562 10054990

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864235	12621	34777	1863	620

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864237	12622	34778	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864240	12623	34779	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864249	12624	34780	1632	543

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864257	12625	34781	1968	656

Description

6500732175 yife:b3764 hypothetical 13.1 kd protein in pssr-ilvl intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3764 b3764 Escherichia coli 562 -11536033 7000690912 yife hypothetical 13.1 kd protein in pssr-ilvl intergenic region (db:pir2.dat) G65179 G65179 Escherichia coli 562 -11536033 7500959776 yife orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 343 of 400 of the completegenome.) (nt:o112; sequence change shortens and) (le:4446) (re:4784) (di:direct) AE000453 AE000453 g2367277 Escherichia coli 562 -11536033

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864258	12626	34782	288	95

Description

6500732176 yifb:b3765 hypothetical 56.2 kd protein in pssr-ilvl intergenic region:orf iii:f516:contains:orf i (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3765 b3765 Escherichia coli 562 -11536034 113263 yifb (de:(f516) (contains: orf i)) (db:swissprot) YIFB_ECOLI P22787 ESCHERICHIA COLI 562 -11536034 163285 yifb hypothetical 56.2k protein ilvg-rrnc intergenic region:hypothetical 56.2k protein pssr-ilvl intergenic region:hypothetical protein f516:orfiii protein (cl:conserved hypothetical protein h1117) (db:pir2.dat) (mp:82 min) JQ0872 JQ0872 Escherichia coli 562 -11536034 7500937421 ilv-related (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli acetolactate synthase ii (ilvg) gene, 5' end;ribosomal protein (rrnc) gene, complete cds.) (nt:orf iii) (le:1767) (re:3317) (di:direct) ECORRNILV M37337 g147774 Escherichia coli 562 -11536034 235937 yifb putative 2-component regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 343 of 400 of the completegenome.) (nt:f516; 99 pct identical amino acid sequence and) (le:4809) (re:6359) (di:complement) AE000453 AE000453 g1790201 Escherichia coli 562 -11536034 5000693744 (de:(ecoli_3678) (pn:hypothetical 56) (gn:yifb) (gtcfc:13.7:14.1) (ec:) (yifb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3678 ECOLI_3678 Escherichia coli 562 10054991

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864271	12627	34783	546	181

Description

6500732177 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3776 b3776 Escherichia coli 562 -11536035 7000691812 hypothetical protein b3776 (db:pir2.dat) C65181 C65181 Escherichia coli 562 -11536035 7500960319 b3776 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 344 of 400 of the completegenome.) (nt:f91; residues 13-91 are 43 pct identical to) (le:2097) (re:2372) (di:complement) AE000454 AE000454 g2367279 Escherichia coli 562 -11536035

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864275	12628	34784	771	256

Description

6500732178 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3777 b3777 Escherichia coli 562 -11536036
7000691813 hypothetical protein b3777 (db:pir2.dat) D65181 D65181
Escherichia coli 562 -11536036 7500960320 yifn orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
344 of 400 of the completegenome.) (nt:f86; residues 21-80 are 51 pct
identical (2 gaps)) (le:2327) (re:2587) (di:complement) AE000454 AE000454
g2367280 Escherichia coli 562 -11536036

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864278	12629	34785	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864279	12630	34786	471	156

Description

GTC ORF with score 190 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe
chromosome iii cosmid c16c4.) (nt:spcc14g10.05, len:669, similarity:bos
taurus,) (le:10794:11045:11673:12455) (re:11000:11609:12413:12951)
(di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864281	12631	34787	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864299	12632	34788	249	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864300	12633	34789	1431	476

Description

GTC ORF with score 993 to: (db:genpept) (de:aureobasidium pullulans multidrug resistance protein 1 (mdr1) gene,promoter region and complete cds.) (nt:atp-binding cassette (abc) transporter protein) (le:542) (re:4450) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864308	12634	34790	276	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864324	12635	34791	729	242

Description

6500732179 yifc:b3785 hypothetical protein:hypothetical 39.6 kd protein in rfe-rffe intergenic region:o349 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3785 b3785 Escherichia coli 562 -11536037 113265 wzze:wzz (de:lipopolysaccharide biosynthesis protein wzze) (db:swissprot) WZZE_ECOLI P25905 ESCHERICHIA COLI 562 -11536037 7000688047 hypothetical 39.5k protein rfe 5 region (db:pir2.dat) (mp:85 min) D65182 D65182 Escherichia coli 562 -11536037 7500894425 wzze putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 344 of 400 of the completegenome.) (nt:o349) (le:11113) (re:12162) (di:direct) AE000454 AE000454 g2367281 Escherichia coli 562 -11536037

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864336	12636	34792	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864337	12637	34793	498	165

Description

6500732180 yifh:b3790 hypothetical 19.6 kd protein in rfpe-rfft intergenic region:ol81 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3790 b3790 Escherichia coli 562 -11536038 113268 rffc:wecd (de:lipopolysaccharide biosynthesis protein rffc) (db:swissprot) RFFC_ECOLI P27832 ESCHERICHIA COLI 562 -11536038 7000688048 yifh hypothetical 19.6 kd protein in rfpe-rfft intergenic region:hypothetical protein ol81 (db:pir2.dat) A65183 A65183 Escherichia coli 562 -11536038 7500889701 ol81 (fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:possibly rffa or rffc) (le:27716) (re:28261) (di:direct) ECOUW85 M87049 g148193 Escherichia coli 562 -11536038 237018 wecd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 345 of 400 of the completegenome.) (nt:ol81; formerly designated yifh) (le:4513) (re:5058) (di:direct) AE000455 AE000455 g1790225 Escherichia coli 562 -11536038 5000693747 (de:(ecoli_3700) (pn:hypothetical 19) (gn:yifh) (gtcfc:13.7:14.1) (ec:) (yifh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3700 ECOLI_3700 Escherichia coli 562 10054996

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864346	12638	34794	2325	775

Description

6500732181 yifi:b3791 hypothetical 41.9 kd protein in rfpe-rfft intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3791 b3791 Escherichia coli 562 -11536039 7500889698 rffa:wece (de:lipopolysaccharide biosynthesis protein rffa) (db:swissprot) RFFA_ECOLI P27833 ESCHERICHIA COLI 562 -11536039 7000689057 yifi hypothetical 41.9 kd protein in rfpe-rfft intergenic region (cl:erythromycin resistance protein) (db:pir2.dat) B65183 B65183 Escherichia coli 562 -11536039 7500889700 wece putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 345 of 400 of the completegenome.) (nt:o376; formerly designated yifi) (le:5063) (re:6193) (di:direct) AE000455 AE000455 g2367285 Escherichia coli 562 -11536039

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864363	12639	34795	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864371	12640	34796	474	157

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864375	12641	34797	210	69

Description

6500732182 yifj:b3792 hypothetical 45.0 kd protein in rfef-rfft intergenic region:o416 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3792 b3792 Escherichia coli 562 -11536040 113270 wzxe:wzx (de:lipopolysaccharide biosynthesis protein wzxe) (db:swissprot) WZXE_ECOLI P27834 ESCHERICHIA COLI 562 -11536040 7000688049 yifj hypothetical 45.0 kd protein in rfef-rfft intergenic region:hypothetical protein o416 (db:pir2.dat) C65183 C65183 Escherichia coli 562 -11536040 7500894422 o416 (fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:possibly rffa or rffc) (le:29394) (re:30644) (di:direct) ECOUW85 M87049 g148195 Escherichia coli 562 -11536040 237020 wzxe putative cytochrome (fn:putative carrier; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 345 of 400 of the completengenome.) (nt:o416; formerly designated yifj) (le:6195) (re:7445) (di:direct) AE000455 AE000455 g1790227 Escherichia coli 562 -11536040 5000693749 (de:(ecoli_3702) (pn:hypothetical 45) (gn:yifj) (gtcfc:13.7:14.1) (ec:) (yifj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3702 ECOLI_3702 Escherichia coli 562 10054998

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864383	12642	34798	777	258

Description

6500732183 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4404 b4404 Escherichia coli 562 -11536041 7000691822 hypothetical protein b4404 (db:pir2.dat) D65183 D65183 Escherichia coli 562 -11536041 7500960329 yifm_1 orf:conceptual translation in swissprot is (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 345 of 400 of the completengenome.) (nt:o74; sequence changes disrupt a larger orf that was) (le:7442) (re:7666) (di:direct) AE000455 AE000455 g2367286 Escherichia coli 562 -11536041

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864395	12643	34799	2286	761
<u>Description</u>				
6500732184 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4405 b4405 Escherichia coli 562 -11536042				
7000691823 hypothetical protein b4405 (db:pir2.dat) E65183 E65183				
Escherichia coli 562 -11536042 7500960330 yifm_2 orf:conceptual translation in swissprot is (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 345 of 400 of the completegenome.) (nt:o204; sequence changes disrupt a larger orf that) (le:7908) (re:8522) (di:direct) AE000455 AE000455 g2367287 Escherichia coli 562 -11536042				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864398	12644	34800	1554	517
<u>Description</u>				
6500732185 o161:b3808 very hypothetical 17.3 kd protein in cyaa region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3808 b3808 Escherichia coli 562 -11536043 116996 (de:very hypothetical 17.3 kd protein in cyaa region (cyax) (o161)) (db:swissprot) YZCX_ECOLI P11291				
ESCHERICHIA COLI 562 -11536043 162882 cyax cyax protein cya operon:hypothetical 17.3k protein cyaa region (db:pir2.dat) (mp:85 min) S30698 S30698 Escherichia coli 562 -11536043 7500953075 o161 (fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:called cyax in x01653) (le:46962) (re:47447) (di:direct) ECUW85 M87049 g148207 Escherichia coli 562 -11536043 237032 b3808 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 346 of 400 of the completegenome.) (nt:o161; 100 pct identical to yzcx_ecoli sw: p11291) (le:10992) (re:11477) (di:direct) AE000456 AE000456 g1790240 Escherichia coli 562 -11536043 5000693753 (de:(ecoli_3714) (pn:very hypothetical 17) (gn:o161) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3714 ECOLI_3714 Escherichia coli 562 10058721				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501864415	12645	34801	1002	333

Description

6500732186 yiga:b3810 hypothetical 26.7 kd protein in dapf-xerc intergenic region:orf 235 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3810 b3810 Escherichia coli 562 -11536044 113281 yiga (de:hypothetical 26.7 kd protein in dapf-xerc intergenic region (orf 235)) (db:swissprot) YIGA_ECOLI P23305 ESCHERICHIA COLI 562 -11536044 163474 yiga hypothetical 26.7k protein dapf-xerc intergenic region (db:pir2.dat) B37841 B37841 Escherichia coli 562 -11536044 237640 o235 (fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:48695) (re:49402) (di:direct) ECOUW85 M87049 g148209 Escherichia coli 562 -11536044 7500937440 orf::235 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lambda-integrase (xerc) gene, complete cds,diaminopimelate (dapf), 3' end, and helicase ii (uvrd) gene, 5'end.) (le:48) (re:755) (di:direct) ECOXERC M38257 g148269 Escherichia coli 562 -11536044 237034 yiga orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 347 of 400 of the completegenome.) (nt:o235; 100 pct identical to yiga_ecoli sw: p23305) (le:1215) (re:1922) (di:direct) AE000457 AE000457 g1790243 Escherichia coli 562 -11536044 5000693754 (de:(ecoli_3716) (pn:hypothetical 26) (gn:yiga) (gtcfc:13.7:14.1) (ec:) (yiga_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3716 ECOLI_3716 Escherichia coli 562 10055009

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501864438	12646	34802	183	60

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501864440	12647	34803	282	93

Description

GTC ORF with score 119 to: (fn:probable transporter of sugars across plasma) (sr:saccharomyces cerevisiae dna) (db:genpept-pln1) (de:saccharomyces cerevisiae sugar transporter (stl1) gene, completedcds.) (nt:stl1p) (le:208) (re:1818) (di:direct)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501864443	12648	34804	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864444	12649	34805	972	323

Description

6500732187 yigb:b3812 hypothetical 27.1 kd protein in xerc-uvrd intergenic region:orf 238 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3812 b3812 Escherichia coli 562 -11536045
 7500937441 yigb (de:hypothetical 27.1 kd protein in xerc-uvrd intergenic region (orf 238)) (db:swissprot) YIGB_ECOLI P23306 ESCHERICHIA COLI 562 -11536045 163475 yigb hypothetical 27.1k protein xerc-uvrd intergenic region:hypothetical protein o238 (db:pir2.dat) D37841 D37841 Escherichia coli 562 -11536045 7500937443 yigb putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 347 of 400 of the completegenome.) (nt:o238; 99 pct identical amino acid sequence and) (le:2815) (re:3531) (di:direct) AE000457 AE000457 g2367295 Escherichia coli 562 -11536045

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864445	12650	34806	345	114

Description

5000693756 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3814 b3814 Escherichia coli 562 -11536046
 7000691814 hypothetical protein b3814 (db:pir2.dat) G65185 G65185 Escherichia coli 562 -11536046 7500960321 b3814 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 347 of 400 of the completegenome.) (nt:f99) (le:5924) (re:6223) (di:complement) AE000457 AE000457 g1790247 Escherichia coli 562 -11536046
 6500732188 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3814 b3814 Escherichia coli 562 -11536046

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864472	12651	34807	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864478	12652	34808	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864481	12653	34809	813	271

Description

6500732189 yigf:b3817 hypothetical 14.5 kd protein in cora 3 region:hypothetical 14.5 kd protein in cora-rard intergenic region:f126 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3817 b3817 Escherichia coli 562 -11536047 113285 yigf (de:hypothetical 14.5 kd protein in cora-rard intergenic region (f126)) (db:swissprot) YIGF_ECOLI P27842 ESCHERICHIA COLI 562 -11536047 162590 yigf hypothetical 14.5k protein cora 3 region (db:pir2.dat) (mp:86 min) S30707 S30707 Escherichia coli 562 -11536047 237041 (sr:escherichia coli (individual_isolate pbd434, strain k-12) dna) (db:genpept-bct1) (de:e. coli dna helicase ii (uvrd) gene, 3' end, mg-transport system i(cora) gene, complete cds, chloamphenicol sensitive (rard) gene,complete cds, detergent-resistant... ECOCORAX L02122 g145578 Escherichia coli 562 -11536047 7500937444 f126 (fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:55529) (re:55909) (di:complement) ECOUW85 M87049 g148216 Escherichia coli 562 -11536047 234035 yigf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 347 of 400 of the completegenome.) (nt:f126; 100 pct identical to yigf_ecoli sw: p27842) (le:8050) (re:8430) (di:complement) AE000457 AE000457 g1790250 Escherichia coli 562 -11536047 5000693758 (de:(ecoli_3723) (pn:hypothetical 14) (gn:yigf) (gtcfc:13.7:14.1) (ec:) (yigf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3723 ECOLI_3723 Escherichia coli 562 10055013

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501864484	12654	34810	1770	589

Description

6500732190 yigg:b3818 hypothetical 15.8 kd protein in cora-rard intergenic region:f138 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3818 b3818 Escherichia coli 562 -11536048 113287 yigg (de:hypothetical 15.8 kd protein in cora-rard intergenic region) (db:swissprot) YIGG_ECOLI P27843 ESCHERICHIA COLI 562 -11536048 162593 yigg hypothetical 15.8k protein cora-rard intergenic region (db:pir2.dat) (mp:86 min) S30708 S30708 Escherichia coli 562 -11536048 237042 (sr:escherichia coli (individual_isolate pbd434, strain k-12) dna) (db:genpept-bct1) (de:e. coli dna helicase ii (uvrd) gene, 3' end, mg-transport system i(cora) gene, complete cds, chloamphenicol sensitive (rard) gene,complete cds, detergent-resistant... ECOCORAX L02122 g145579 Escherichia coli 562 -11536048 7500937445 f138 (fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:55923) (re:56339) (di:complement) ECOUW85 M87049 g148217 Escherichia coli 562 -11536048 234036 yigg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 347 of 400 of the completegenome.) (nt:f138; 100 pct identical to yigg_ecoli sw: p27843) (le:8444) (re:8860) (di:complement) AE000457 AE000457 g1790251 Escherichia coli 562 -11536048 5000693759 (de:(ecoli_3724) (pn:hypothetical 15) (gn:yigg) (gtcfc:13.7:14.1) (ec:) (yigg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3724 ECOLI_3724 Escherichia coli 562 10055015

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501864495	12655	34811	2478	825

Description

6500732191 yigi:b3820 hypothetical 17.1 kd protein in rard-plda intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3820 b3820 Escherichia coli 562 -11536049 163497 yigi hypothetical 17.1k protein rard-plda intergenic region:hypothetical protein f161 (db:pir2.dat) S30747 S30747 Escherichia coli 562 -11536049 7500959787 (sr:escherichia coli (individual_isolate pbd434, strain k-12) dna) (db:genpept-bct1) (de:e. coli dna helicase ii (uvrd) gene, 3' end, mg-transport system i(cora) gene, complete cds, chloamphenicol sensitive (rard) gene,complete cds, detergent-resistant... ECOCORAX L02122 g145581 Escherichia coli 562 -11536049 234038 yigi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 347 of 400 of the completegenome.) (nt:f161; 99 pct identical to 155 amino acids of) (le:9860) (re:10345) (di:complement) AE000457 AE000457 g2367298 Escherichia coli 562 -11536049

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864501	12656	34812	252	84

Description

6500732192 yigj:b3823 hypothetical 13.3 kd protein in recq 3 region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3823 b3823 Escherichia coli 562 -11536050 7000690913 yigj hypothetical 13.3 kd protein in recq 3 region:hypothetical protein o128 (db:pir2.dat) H65186 H65186 Escherichia coli 562 -11536050 7500959779 yigj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 348 of 400 of the completegenome.) (nt:o122; sequence change shortens and) (le:3224) (re:3592) (di:direct) AE000458 AE000458 g2367302 Escherichia coli 562 -11536050

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864509	12657	34813	1461	486

Description

6500732193 yigk:b3824 hypothetical 15.4 kd protein in recq-pldb intergenic region:f138 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3824 b3824 Escherichia coli 562 -11536051 113291 yigk (de:hypothetical 15.4 kd protein in recq-pldb intergenic region (f138)) (db:swissprot) YIGK_ECOLI P27847 ESCHERICHIA COLI 562 -11536051 7000688050 yigk hypothetical 15.4 kd protein in recq-pldb intergenic region:hypothetical protein f138 (db:pir2.dat) A65187 A65187 Escherichia coli 562 -11536051 7500937448 f138 (fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:61543) (re:61959) (di:complement) ECOUW85 M87049 g148223 Escherichia coli 562 -11536051 237048 yigk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 348 of 400 of the completegenome.) (nt:f138; 100 pct identical to yigk_ecoli sw: p27847) (le:3654) (re:4070) (di:complement) AE000458 AE000458 g1790258 Escherichia coli 562 -11536051 5000693763 (de:(ecoli_3730) (pn:hypothetical 15) (gn:yigk) (gtcfc:13.7:14.1) (ec:) (yigk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3730 ECOLI_3730 Escherichia coli 562 10055019

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864542	12658	34814	1566	521

Description

6500732194 yigm:b3827 hypothetical 33.7 kd protein in pldb-metr intergenic region:o299 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3827 b3827 Escherichia coli 562 -11536052 7000688051 yigm hypothetical 33.7 kd protein in pldb-metr intergenic region:hypothetical protein o299 (db:pir2.dat) D65187 D65187 Escherichia coli 562 -11536052 7500937450 o299 (fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:overlaps metr) (le:64162) (re:65061) (di:direct) ECOUW85 M87049 g148226 Escherichia coli 562 -11536052 237051 yigm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 348 of 400 of the completegenome.) (nt:o299; 100 pct identical to yigm_ecoli sw: p27849) (le:6274) (re:7173) (di:direct) AE000458 AE000458 g1790261 Escherichia coli 562 -11536052 113294 yigm (de:hypothetical 33.7 kd protein in pldb-metr intergenic region (o299)) (db:swissprot) YIGM_ECOLI P27849 ESCHERICHIA COLI 562 -11536052 5000693765 (de:(ecoli_3733) (pn:hypothetical 33) (gn:yigm) (gtcfc:13.7:14.1) (ec:) (yigm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3733 ECOLI_3733 Escherichia coli 562 10055022

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864543	12659	34815	237	78

Description

6500732195 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3830 b3830 Escherichia coli 562 -11536053 7000691815 hypothetical protein b3830 (db:pir2.dat) G65187 G65187 Escherichia coli 562 -11536053 7500960322 ysga putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 348 of 400 of the completegenome.) (nt:f332; revealed by sequence change relative) (le:10329) (re:11327) (di:complement) AE000458 AE000458 g2367305 Escherichia coli 562 -11536053

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864554	12660	34816	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864563	12661	34817	900	300

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501864575	12662	34818	420	139

Description

6500732196 yign:b3832 hypothetical 54.7 kd protein in udp 3 region precursor:hypothetical 54.7 kd protein in udp-rfah intergenic region precursor:o475 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3832 b3832 Escherichia coli 562 -11536054 113295 yign (de:hypothetical 54.7 kd protein in udp-ubie intergenic region precursor) (db:swissprot) YIGN_ECOLI P27850 ESCHERICHIA COLI 562 -11536054 7000688052 yign hypothetical 54.7 kd protein in udp 3 region precursor o475:hypothetical protein o475 (db:pir2.dat) A65188 A65188 Escherichia coli 562 -11536054 7500937451 yign putative alpha helix chain (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 349 of 400 of the completegenome.) (nt:o475; 99 pct identical amino acid sequence and) (le:1070) (re:2497) (di:direct) AE000459 AE000459 g1790266 Escherichia coli 562 -11536054 5000693766 (de:(ecoli_3737) (pn:hypothetical 54) (gn:yign) (gtcfc:13.7:14.1) (ec:) (yign_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3737 ECOLI_3737 Escherichia coli 562 10055023

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501864588	12663	34819	1128	375

Description

GTC ORF with score 124 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid r144.) (nt:weak similarity to adenylyl cyclase-associated) (le:20801:20959:21377:21537) (re:20911:21181:21442:21688) ...

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501864598	12664	34820	1191	396

Description

6500732197 yigp:b3834 hypothetical 22.3 kd protein in udp-rfah intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3834 b3834 Escherichia coli 562 -11536055 7500937453 yigp (de:hypothetical 22.2 kd protein in ubie-rfah intergenic region) (db:swissprot) YIGP_ECOLI P27852 ESCHERICHIA COLI 562 -11536055 7000690928 yigp hypothetical 22.3 kd protein in udp-rfah intergenic region (db:pir2.dat) C65188 C65188 Escherichia coli 562 -11536055 7500937455 yigp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 349 of 400 of the completegenome.) (nt:o201; sequence changes cause internal changes to) (le:3361) (re:3966) (di:direct) AE000459 AE000459 g2367308 Escherichia coli 562 -11536055

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864600	12665	34821	309	102
<u>Description</u>				
6500732198 hypothetical 63.2 kd protein in udp-rfah intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b3835 b3835 Escherichia coli 562 -11536056 7500937456 aarf (de:ubiquinone biosynthesis protein aarf) (db:swissprot) AARF_ECOLI P27854 ESCHERICHIA COLI 562 -11536056 7000690965 hypothetical 63.2 kd protein in udp-rfah intergenic region (cl:synechocystis abc-type transport protein slr1919) (db:pir2.dat) D65188 D65188 Escherichia coli 562 -11536056 7500937458 yigr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 349 of 400 of the completegenome.) (nt:o546; sequence change joins orfs yigq, yigr, and) (le:3963) (re:5603) (di:direct) AE000459 AE000459 g2367309 Escherichia coli 562 -11536056				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864608	12666	34822	264	87
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864609	12667	34823	534	177
<u>Description</u>				
6500732199 hypothetical 11.3 kd protein in udp-rfah intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3836 b3836 Escherichia coli 562 -11536057 7000690908 hypothetical 11.3 kd protein in udp-rfah intergenic region (cl:conserved hypothetical secreted protein hp0320) (db:pir2.dat) E65188 E65188 Escherichia coli 562 -11536057 7500959767 mttal mttal (fn:involved in folded protein translocation and) (db:genpept-bct1) (de:escherichia coli mttal (mttal), mttal2 (mttal2), mttb (mttb), andmttc (mttc) genes, complete cds.) (nt:tata; yigt) (le:642) (re:953) (di:direct) AF067848 AF067848 g3193217 Escherichia coli 562 -11536057 7500959768 b3836 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 349 of 400 of the completegenome.) (nt:o103; sequence change split orf of earlier) (le:5640) (re:5951) (di:direct) AE000459 AE000459 g2367310 Escherichia coli 562 -11536057				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864626	12668	34824	198	65
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864646	12669	34825	1449	482

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864647	12670	34826	402	133

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864653	12671	34827	882	293

Description

6500732200 hypothetical 12.1 kd protein in udp-rfah intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3837 b3837 Escherichia coli 562 -11536058 7000690909 hypothetical 12.1 kd protein in udp-rfah intergenic region (db:pir2.dat) F65188 F65188 Escherichia coli 562 -11536058 7500959771 b3837 putative histone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 349 of 400 of the completegenome.) (nt:ol13; sequence change split orf of earlier) (le:5815) (re:6156) (di:direct) AE000459 AE000459 g2367311 Escherichia coli 562 -11536058

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864677	12672	34828	801	266

Description

6500732201 hypothetical 15.6 kd protein in udp-rfah intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3838 b3838 Escherichia coli 562 -11536059 7000690920 hypothetical 15.6 kd protein in udp-rfah intergenic region (db:pir2.dat) G65188 G65188 Escherichia coli 562 -11536059 7500959785 b3838 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 349 of 400 of the completegenome.) (nt:ol45; sequence change split orf of earlier) (le:6035) (re:6472) (di:direct) AE000459 AE000459 g2367312 Escherichia coli 562 -11536059

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864680	12673	34829	291	96
<u>Description</u>				
5000693775 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3841 b3841 Escherichia coli 562 -11536060				
7000691964 yigw yigw protein:hypothetical protein o113 (db:pir2.dat) B65189 B65189 Escherichia coli 562 -11536060 7500960522 o113 (fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (le:77062) (re:77403) (di:direct) ECOUW85 M87049 g148240 Escherichia coli 562 -11536060 237065 yigw_2 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 349 of 400 of the completegenome.) (nt:o113; 100 pct identical to 80 residues of a 264 aa) (le:7735) (re:8076) (di:direct) AE000459 AE000459 g1790275 Escherichia coli 562 -11536060 6500732202 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3841 b3841 Escherichia coli 562 -11536060				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864681	12674	34830	651	217
<u>Description</u>				
6500732203 yigz:b3848 hypothetical 21.9 kd protein in pepq-trkh intergenic region:o205 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3848 b3848 Escherichia coli 562 -11536061 113307 yigz (de:hypothetical 21.9 kd protein in pepq-trkh intergenic region (o205)) (db:swissprot) YIGZ_ECOLI P27862 ESCHERICHIA COLI 562 -11536061 163336 yigz hypothetical protein pepq 5 region:hypothetical 21.9k protein pepq-trkh intergenic region:hypothetical protein o205 (cl:hypothetical protein hi0722) (db:pir2.dat) (mp:86 min) S30739 S30739 Escherichia coli 562 -11536061 7500937466 o205 (db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to 86.5 minutes.) (nt:similar to product of an uncharacterized orf of b.) (le:85553) (re:86170) (di:direct) ECOUW85 M87049 g148248 Escherichia coli 562 -11536061 237073 yigz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 350 of 400 of the completegenome.) (nt:o205; 100 pct identical amino acid sequence and) (le:5230) (re:5847) (di:direct) AE000460 AE000460 g1790283 Escherichia coli 562 -11536061 5000693777 (de:(ecoli_3753) (pn:hypothetical 21) (gn:yigz) (gtcfc:13.7:14.1) (ec:) (yigz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3753 ECOLI_3753 Escherichia coli 562 10055035				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864689	12675	34831	1161	386

Description

5000693778 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3856 b3856 Escherichia coli 562 -11536062 163574 hypothetical protein f170:hypothetical protein b3856 (db:pir2.dat) S40802 S40802 Escherichia coli 562 -11536062 7500960333 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:matches ps00017: atp_gtp_a) (le:2546) (re:3058) (di:complement) ECOUW87 L19201 g304962 Escherichia coli 562 -11536062 237076 mobb molybdopterin-guanine dinucleotide biosynthesis (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 351 of 400 of the completegenome.) (nt:f170; matches ps00017: atp_gtp_a) (le:3505) (re:4017) (di:complement) AE000461 AE000461 g1790287 Escherichia coli 562 -11536062 6500732204 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3856 b3856 Escherichia coli 562 -11536062

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864692	12676	34832	636	211

Description

6500732205 yihd:b3858 hypothetical 10.3 kd protein in moba 3region:hypothetical 10.3 kd protein in moba-dsba intergenic region:o89 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3858 b3858 Escherichia coli 562 -11536063 113317 yihd (de:hypothetical 10.3 kd protein in moba-dsba intergenic region (o89)) (db:swissprot) YIHD_ECOLI P32126 ESCHERICHIA COLI 562 -11536063 163875 yihd hypothetical 10.3k protein moba 3region o89 (db:pir2.dat) S40804 S40804 Escherichia coli 562 -11536063 7500937480 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:3709) (re:3978) (di:direct) ECOUW87 L19201 g304964 Escherichia coli 562 -11536063 237078 yihd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 351 of 400 of the completegenome.) (nt:o89; 100 pct identical amino acid sequence and) (le:4668) (re:4937) (di:direct) AE000461 AE000461 g1790289 Escherichia coli 562 -11536063 5000693779 (de:(ecoli_3758) (pn:hypothetical 10) (gn:yihd) (gtcfc:13.7:14.1) (ec:) (yihd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3758 ECOLI_3758 Escherichia coli 562 10055045

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864712	12677	34833	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864742	12678	34834	423	140

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864747	12679	34835	582	193

Description

6500732206 yihe:b3859 hypothetical 38.1 kd protein in dsba
5region:hypothetical 38.1 kd protein in moba-dsba intergenic region:o328
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3859
b3859 Escherichia coli 562 -11536064 237079 yihe (de:hypothetical 38.1 kd
protein in moba-dsba intergenic region) (db:swissprot) YIHE_ECOLI P32127
ESCHERICHIA COLI 562 -11536064 163810 yihe hypothetical 38.1k protein dsba
5region o328 (db:pir2.dat) S40805 S40805 Escherichia coli 562 -11536064
5000693780 (db:genpept-bct1) (de:e.coli dsba gene, orfa and orfb.)
(nt:orfa) (le:1091) (re:2077) (di:direct) ECDSBAAB X80762 g762927
Escherichia coli 562 -11536064 304557 (sr:escherichia coli (sub_strain
mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli
chromosomal region from 87.2 to 89.2 minutes.) (le:4056) (re:5042)
(di:direct) ECOUW87 L19201 g304965 Escherichia coli 562 -11536064 232705
yihe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 351 of 400 of the completegenome.)
(nt:o328; 100 pct identical amino acid sequence and) (le:5015) (re:6001)
(di:direct) AE000461 AE000461 g1790290 Escherichia coli 562 -11536064
113319 yihe (de:hypothetical 38.1 kd protein in moba-dsba intergenic
region) (db:swissprot) YIHE_ECOLI P32127 ESCHERICHIA COLI 562 -11536064

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864752	12680	34836	1386	461

Description

6500732207 yihf:b3861 hypothetical 54.1 kd protein in dsba
3region:hypothetical 54.1 kd protein in dsba-pola intergenic region:o490
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3861
b3861 Escherichia coli 562 -11536065 7500937482 yihf (de:hypothetical 54.2
kd protein in dsba-pola intergenic region) (db:swissprot) YIHF_ECOLI P32128
ESCHERICHIA COLI 562 -11536065 7000690959 yihf hypothetical 54.1 kd protein
in dsba 3region o490:hypothetical protein o490 (cl:hypothetical protein
b1614) (db:pir2.dat) A65191 A65191 Escherichia coli 562 -11536065
7500937484 yihf putative gtp-binding protein (fn:orf; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 351 of 400 of the
completegenome.) (nt:o490; 99 pct identical to yihf_ecoli sw: p32128)
(le:6756) (re:8228) (di:direct) AE000461 AE000461 g2367319 Escherichia coli
562 -11536065

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864753	12681	34837	1125	374

Description

6500732208 yihg:b3862 hypothetical 36.3 kd protein in pola
5region:hypothetical 36.3 kd protein in dsba-pola intergenic region:f310
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3862
b3862 Escherichia coli 562 -11536066 113321 yihg (de:hypothetical 36.3 kd
protein in dsba-pola intergenic region) (db:swissprot) YIHG_ECOLI P32129
ESCHERICHIA COLI 562 -11536066 163631 yihg atp:polyribonucleotide
adenylyltransferase (ec:2.7.7.-) (db:pir2.dat) S40808 S40808 Escherichia
coli 562 -11536066 7500937485 (sr:escherichia coli (sub_strain mg1655,
strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal
region from 87.2 to 89.2 minutes.) (le:7310) (re:8242) (di:complement)
ECOUW87 L19201 g304968 Escherichia coli 562 -11536066 237082 yihg putative
endonuclease (fn:putative enzyme; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 351 of 400 of the completegenome.)
(nt:f310; 100 pct identical amino acid sequence and) (le:8269) (re:9201)
(di:complement) AE000461 AE000461 g1790293 Escherichia coli 562 -11536066
5000693782 (de:(ecoli_3762) (pn:hypothetical 36) (gn:yihg)
(gtcfc:13.7:14.1) (ec:) (yihg_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_3762 ECOLI_3762 Escherichia coli 562
10055049

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864770	12682	34838	1005	334

Description

6500732209 yiha:b3865 hypothetical protein:hypothetical gtp-binding protein
in pola-hemm intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b3865 b3865 Escherichia coli 562 -11536067 163580
hypothetical protein f199:hypothetical protein b3865 (cl:translation
elongation factor tu homology) (db:pir2.dat) S40810 S40810 Escherichia coli
562 -11536067 237084 (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli
k12 pola gene coding for dna polymerase i, complete cds.) (nt:unidentified
protein) (le:3468) (re:4067) (di:complement) ECOPLA J01663 g147313
Escherichia coli 562 -11536067 7500960334 (sr:escherichia coli (sub_strain
mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli
chromosomal region from 87.2 to 89.2 minutes.) (nt:matches ps00017:
atp_gtp_a) (le:11773) (re:12372) (di:complement) ECUW87 L19201 g304970
Escherichia coli 562 -11536067 235514 yiha orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
352 of 400 of the completegenome.) (nt:f199; matches ps00017: atp_gtp_a)
(le:66) (re:665) (di:complement) AE000462 AE000462 g1790296 Escherichia coli
562 -11536067 5000693783 (de:(ecoli_3764) (pn:function not assigned)
(gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia
coli)) ECOLI_3764 ECOLI_3764 Escherichia coli 562 10087009

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501864773	12683	34839	204	68

Description

6500732210 yihi:b3866 hypothetical 19.1 kd protein in pola-hemn intergenic region:o169 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3866 b3866 Escherichia coli 562 -11536068 113322 yihi (de:hypothetical 19.1 kd protein in pola-hemn intergenic region (o169)) (db:swissprot) YIHI_ECOLI P32130 ESCHERICHIA COLI 562 -11536068 163749 yihi hypothetical 19.1k protein pola-hemn intergenic region:hypothetical protein o169 (db:pir2.dat) S40811 S40811 Escherichia coli 562 -11536068 237085 orfa (sr:escherichia coli (strain:k-12, sub_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli orfa, hemn and glng genes, complete and partialcds.) (le:561) (re:1070) (di:direct) ECOORFGLNG D16509 g1220105 Escherichia coli 562 -11536068 7500937486 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:12987) (re:13496) (di:direct) ECOUW87 L19201 g304971 Escherichia coli 562 -11536068 235302 yihi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 352 of 400 of the completegenome.) (nt:o169; 100 pct identical amino acid sequence and) (le:1280) (re:1789) (di:direct) AE000462 AE000462 g1790297 Escherichia coli 562 -11536068 5000693784 (de:(ecoli_3765) (pn:hypothetical 19) (gn:yihi) (gtcfc:13.7:14.1) (ec:) (yihi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3765 ECOLI_3765 Escherichia coli 562 10055050

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501864775	12684	34840	1629	542

Description

6500732211 yihl:b3872 hypothetical protein:hypothetical transcriptional regulator in glna-rbn intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3872 b3872 Escherichia coli 562 -11536069 113327 yihl (de:hypothetical transcriptional regulator in glna-rbn intergenic region) (db:swissprot) YIHL_ECOLI P32133 ESCHERICHIA COLI 562 -11536069 163779 hypothetical protein b3872:hypothetical protein o236 (db:pir2.dat) S40817 S40817 Escherichia coli 562 -11536069 7500937488 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:close match to ps00043: hth_gntr_family; similar to) (le:22087) (re:22797) (di:direct) ECOUW87 L19201 g304977 Escherichia coli 562 -11536069 237091 yihl putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 353 of 400 of the completegenome.) (nt:o236; close match to ps00043:) (le:106) (re:816) (di:direct) AE000463 AE000463 g1790304 Escherichia coli 562 -11536069 5000693787 (de:(ecoli_3771) (pn:hypothetical transcriptional regulator in glna-fdhe intergenic region:o236) (gtcfc:13.7:14.1) (ec:)(yihl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3771 ECOLI_3771 Escherichia coli 562 10055055

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501865805	12685	34841	561	186

Description

GTC ORF with score 820 to: (db:genpept-pln2) (de:emerella nidulans alternatively spliced cyclin-dependent proteinkinase phoa(m1) and phoa(m47) isoforms (phoa) gene, complete cds.) (nt:contains pstaire motif; non-essential) (le:843:1088:1194) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501865807	12686	34842	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501865815	12687	34843	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865827	12688	34844	840	279

Description

6500732212 yihm:b3873 hypothetical 36.9 kd protein in glna-fdhe intergenic region:hypothetical 36.9 kd protein in glna-rbn intergenic region:o326 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3873 b3873 Escherichia coli 562 -11536070 113328 yihm (de:hypothetical 36.9 kd protein in glna-rbn intergenic region (o326)) (db:swissprot) YIHM_ECOLI P32134 ESCHERICHIA COLI 562 -11536070 163809 yihm hypothetical 36.9k protein glna-fdhe intergenic region:hypothetical protein o326 (db:pir2.dat) S40818 S40818 Escherichia coli 562 -11536070 7500937489 (sr:escherichia coli (sub_strain mgl655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:22805) (re:23785) (di:direct) ECOUW87 L19201 g304978 Escherichia coli 562 -11536070 237092 yihm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 353 of 400 of the completegenome.) (nt:o326; 100 pct identical amino acid sequence and) (le:824) (re:1804) (di:direct) AE000463 AE000463 g1790305 Escherichia coli 562 -11536070 5000693788 (de:(ecoli_3772) (pn:hypothetical 36) (gn:yihm) (gtcfc:13.7:14.1) (ec:) (yihm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3772 ECOLI_3772 Escherichia coli 562 10055056

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865831	12689	34845	570	189

Description

6500732213 yihn:b3874 hypothetical 46.3 kd protein in glna-fdhe intergenic region:hypothetical 46.3 kd protein in glna-rbn intergenic region:o421 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3874 b3874 Escherichia coli 562 -11536071 113329 yihn (de:hypothetical 46.3 kd protein in glna-rbn intergenic region (o421)) (db:swissprot) YIHN_ECOLI P32135 ESCHERICHIA COLI 562 -11536071 163837 yihn hypothetical 46.3k protein glna-fdhe intergenic region:hypothetical protein o421 (cl:escherichia coli hypothetical protein (glna-fdhe intergenic region)) (db:pir2.dat) S40819 S40819 Escherichia coli 562 -11536071 7500937490 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:23887) (re:25152) (di:direct) ECOUW87 L19201 g304979 Escherichia coli 562 -11536071 237093 yihn putative resistance protein transport (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 353 of 400 of the completegenome.) (nt:o421; 100 pct identical to yihn_ecoli sw: p32135) (le:1906) (re:3171) (di:direct) AE000463 AE000463 g1790306 Escherichia coli 562 -11536071 5000693789 (de:(ecoli_3773) (pn:hypothetical 46) (gn:yihn) (gtcfc:13.7:14.1) (ec:) (yihn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3773 ECOLI_3773 Escherichia coli 562 10055057

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865891	12690	34846	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865894	12691	34847	2475	824

Description

5000693790 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3875 b3875 Escherichia coli 562 -11536072 7500952718 ysha (de:hypothetical 27.2 kd protein in glna-rbn intergenic region precursor) (db:swissprot) YSHA_ECOLI P76773 ESCHERICHIA COLI 562 -11536072 7000691816 hypothetical protein b3875 (db:pir2.dat) F65192 F65192 Escherichia coli 562 -11536072 7500952720 ysha orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 353 of 400 of the completegenome.) (nt:f230; sequence change split yiho (yiho_ecoli) (le:3262) (re:3954) (di:complement) AE000463 AE000463 g1790307 Escherichia coli 562 -11536072 6500732214 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3875 b3875 Escherichia coli 562 -11536072

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865910	12692	34848	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865913	12693	34849	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865935	12694	34850	420	139

Description

6500732215 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3876 b3876 Escherichia coli 562 -11536073
7500937491 yiho (de:hypothetical symporter in glna-rbn intergenic region) (db:swissprot) YIHO_ECOLI P32136 ESCHERICHIA COLI 562 -11536073 7000691817 hypothetical protein b3876 (cl:melibiose carrier protein) (db:pir2.dat) G65192 G65192 Escherichia coli 562 -11536073 7500937493 yiho putative permease (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 353 of 400 of the completegenome.) (nt:f487; sequence change split yiho (yiho_ecoli) (le:3969) (re:5432) (di:complement) AE000463 AE000463 g2367321 Escherichia coli 562 -11536073

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865942	12695	34851	909	302

Description

6500732216 yihp:b3877 hypothetical 51.7 kd protein in glna-fdhe intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3877 b3877 Escherichia coli 562 -11536074 7000690955 yihp hypothetical 51.7 kd protein in glna-fdhe intergenic region:hypothetical protein f481 (cl:melibiose carrier protein) (db:pir2.dat) H65192 H65192 Escherichia coli 562 -11536074 7500937496 yihp putative permease (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 353 of 400 of the completegenome.) (nt:f468; sequence change shortens and) (le:5469) (re:6875) (di:complement) AE000463 AE000463 g2367322 Escherichia coli 562 -11536074 7500937494 yihp (de:hypothetical 51.7 kd protein in glna-rbn intergenic region) (db:swissprot) YIHP_ECOLI P32137 ESCHERICHIA COLI 562 -11536074

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865951	12696	34852	390	129

Description

6500732217 yihq:b3878 hypothetical 77.2 kd protein in glna-fdhe intergenic region:hypothetical 77.2 kd protein in glna-rbn intergenic region:f678 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3878 b3878 Escherichia coli 562 -11536075 7500937497 yihq (de:hypothetical 77.3 kd protein in glna-rbn intergenic region) (db:swissprot) YIHQ_ECOLI P32138 ESCHERICHIA COLI 562 -11536075 7000690973 yihq hypothetical 77.2 kd protein in glna-fdhe intergenic region:hypothetical protein f678 (db:pir2.dat) A65193 A65193 Escherichia coli 562 -11536075 7500937499 yihq putative glycosidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 353 of 400 of the completegenome.) (nt:f678; 100 pct identical amino acid sequence and) (le:6900) (re:8936) (di:complement) AE000463 AE000463 g2367323 Escherichia coli 562 -11536075

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865962	12697	34853	861	286

Description

6500732218 yihr:b3879 hypothetical 34 kd protein in glna-fdhe intergenic region:f3:hypothetical 34 kd protein in glna-rbn intergenic region:f308 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3879 b3879 Escherichia coli 562 -11536076 113333 yihr (de:hypothetical 34.0 kd protein in glna-rbn intergenic region) (db:swissprot) YIHR_ECOLI P32139 ESCHERICHIA COLI 562 -11536076 163629 yihr hypothetical 34k protein glna-fdhe intergenic region (db:pir2.dat) S40823 S40823 Escherichia coli 562 -11536076 7500937500 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:31114) (re:32040) (di:complement) ECOUW87 L19201 g304983 Escherichia coli 562 -11536076 237097 yihr putative aldose-1-epimerase ec 5.1.3.3 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 353 of 400 of the completegenome.) (nt:f308; 100 pct identical amino acid sequence and) (le:9135) (re:10061) (di:complement) AE000463 AE000463 g1790311 Escherichia coli 562 -11536076 5000693794 (de:(ecoli_3778) (pn:hypothetical 34 kd protein in glna-fdhe intergenic region:f308) (gn:yihr) (gtcfc:13.7:14.1) (ec:) (yihr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3778 ECOLI_3778 Escherichia coli 562 10055061

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501865963	12698	34854	750	249

Description

6500732219 yihs:b3880 hypothetical 48 kd protein in glna-fdhe intergenic region:f4:hypothetical 48 kd protein in glna-rbn intergenic region:f418 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3880 b3880 Escherichia coli 562 -11536077 163659 yihs hypothetical 48k protein glna-fdhe intergenic region:hypothetical protein f418 (db:pir2.dat) S40824 S40824 Escherichia coli 562 -11536077 7500937501 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:32154) (re:33410) (di:complement) ECOUW87 L19201 g304984 Escherichia coli 562 -11536077 237098 yihs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f418; 100 pct identical amino acid sequence and) (le:74) (re:1330) (di:complement) AE000464 AE000464 g1790313 Escherichia coli 562 -11536077 5000693795 yihs orf:hypothetical protein (fn:orf; unknown) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f418; 100 pct identical amino acid sequence and) (le:74) (re:1330) (di:complement) AE000464 AE000464 g1790313 Escherichia coli 562 -11536077 113334 yihs (de:hypothetical 48 kd protein in glna-rbn intergenic region (f418)) (db:swissprot) YIHS_ECOLI P32140 ESCHERICHIA COLI 562 -11536077

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501865965	12699	34855	402	133

Description

6500732220 yiht:b3881 hypothetical 32 kd protein in glna-fdhe intergenic region:f2:hypothetical 32 kd protein in glna-rbn intergenic region:f292 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3881 b3881 Escherichia coli 562 -11536078 113335 yiht (de:hypothetical 32 kd protein in glna-rbn intergenic region (f292)) (db:swissprot) YIHT_ECOLI P32141 ESCHERICHIA COLI 562 -11536078 163625 yiht hypothetical 32k protein glna-fdhe intergenic region:hypothetical protein f292 (db:pir2.dat) S40825 S40825 Escherichia coli 562 -11536078 7500937502 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:33412) (re:34290) (di:complement) ECOUW87 L19201 g304985 Escherichia coli 562 -11536078 237099 yiht putative aldolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f292; 100 pct identical amino acid sequence and) (le:1332) (re:2210) (di:complement) AE000464 AE000464 g1790314 Escherichia coli 562 -11536078 5000693796 yiht putative aldolase (fn:putative enzyme; not classified) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f292; 100 pct identical amino acid sequence and) (le:1332) (re:2210) (di:complement) AE000464 AE000464 g1790314 Escherichia coli 562 -11536078

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865971	12700	34856	399	132

Description

6500732221 yihu:b3882 hypothetical 31.2 kd protein in glna-fdhe intergenic region:hypothetical 31.2 kd protein in glna-rbn intergenic region:f298 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3882 b3882 Escherichia coli 562 -11536079 113336 yihu (de:hypothetical 31.2 kd protein in glna-rbn intergenic region) (db:swissprot) YIHU_ECOLI P32142 ESCHERICHIA COLI 562 -11536079 163626 yihu hypothetical 31.2k protein glna-fdhe intergenic region:hypothetical protein f298 (cl:3-hydroxyisobutyrate dehydrogenase homology) (db:pir2.dat) S40826 S40826 Escherichia coli 562 -11536079 7500937503 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:similar to 3-hydroxyisobutyrate dehydrogenases;) (le:34314) (re:35210) (di:complement) ECOUW87 L19201 g304986 Escherichia coli 562 -11536079 237100 yihu putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f298; 100 pct identical to yihu_ecoli sw:) (le:2234) (re:3130) (di:complement) AE000464 AE000464 g1790315 Escherichia coli 562 -11536079 5000693797 yihu putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:f298; 100 pct identical to yihu_ecoli sw:) (le:2234) (re:3130) (di:complement) AE000464 AE000464 g1790315 Escherichia coli 562 -11536079

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865972	12701	34857	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501865997	12702	34858	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866004	12703	34859	348	115

Description

6500732222 yihv:b3883 hypothetical 31.9 kd protein in glna-fdhe intergenic region:hypothetical 31.9 kd protein in glna-rbn intergenic region:o300 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3883 b3883 Escherichia coli 562 -11536080 163802 yihv hypothetical 31.9k protein glna-fdhe intergenic region:hypothetical protein o300 (cl:ribokinase) (db:pir2.dat) S40827 S40827 Escherichia coli 562 -11536080 7500937504 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:matches ps00584: pfkb_kinases_2; similar to members) (le:35372) (re:36274) (di:direct) ECOUW87 L19201 g304987 Escherichia coli 562 -11536080 237101 yihv putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o300; 100 pct identical to yihv_ecoli sw:) (le:3292) (re:4194) (di:direct) AE000464 AE000464 g1790316 Escherichia coli 562 -11536080 5000693798 yihv putative kinase (fn:putative enzyme; not classified) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o300; 100 pct identical to yihv_ecoli sw:) (le:3292) (re:4194) (di:direct) AE000464 AE000464 g1790316 Escherichia coli 562 -11536080 113337 yihv (de:hypothetical 31.9 kd protein in glna-rbn intergenic region (o300)) (db:swissprot) YIHV_ECOLI P32143 ESCHERICHIA COLI 562 -11536080

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866005	12704	34860	486	162

Description

6500732223 yihw:b3884 hypothetical transcriptional regulator in glna-fdhe intergenic region:hypothetical transcriptional regulator in glna-rbn intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3884 b3884 Escherichia coli 562 -11536081 113338 yihw (de:hypothetical transcriptional regulator in glna-rbn intergenic region) (db:swissprot) YIHW_ECOLI P32144 ESCHERICHIA COLI 562 -11536081 163789 yihw hypothetical transcription regulator:glna-fdhe intergenic region:hypothetical protein o269 (db:pir2.dat) S40828 S40828 Escherichia coli 562 -11536081 7500937505 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:similar to e. coli glpr repressor) (le:36284) (re:37093) (di:direct) ECOUW87 L19201 g304988 Escherichia coli 562 -11536081 237102 yihw putative deor-type transcriptional regulator (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o269; similar to e. coli glpr repressor; 100 pct) (le:4204) (re:5013) (di:direct) AE000464 AE000464 g1790317 Escherichia coli 562 -11536081 5000693799 yihw putative deor-type transcriptional regulator (fn:putative enzyme; not classified) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o269; similar to e. coli glpr repressor; 100 pct) (le:4204) (re:5013) (di:direct) AE000464 AE000464 g1790317 Escherichia coli 562 -11536081

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866013	12705	34861	2058	686

Description

6500732224 yihx:b3885 hypothetical 23.5 kd protein in glna-fdhe intergenic region:hypothetical 23.5 kd protein in glna-rbn intergenic region:o206 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3885 b3885 Escherichia coli 562 -11536082 163763 yihx hypothetical 23.5k protein glna-fdhe intergenic region:hypothetical protein o206 (db:pir2.dat) S40829 S40829 Escherichia coli 562 -11536082 7500937506 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:37171) (re:37791) (di:direct) ECOUW87 L19201 g304989 Escherichia coli 562 -11536082 237103 yihx putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o206; 100 pct identical amino acid sequence and) (le:5091) (re:5711) (di:direct) AE000464 AE000464 g1790318 Escherichia coli 562 -11536082 5000693800 yihx putative phosphatase (fn:putative enzyme; not classified) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o206; 100 pct identical amino acid sequence and) (le:5091) (re:5711) (di:direct) AE000464 AE000464 g1790318 Escherichia coli 562 -11536082 113339 yihx (de:hypothetical 23.5 kd protein in glna-rbn intergenic region (o206)) (db:swissprot) YIHX_ECOLI P32145 ESCHERICHIA COLI 562 -11536082

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866018	12706	34862	921	306
<u>Description</u>				
6500732225 yihy:rbn:b3886 hypothetical 32.8 kd protein in glna-fdhe intergenic region:ribonuclease bn:rnase bn (gtcfc:14.1) (ec:3.1.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3886 b3886 Escherichia coli 562 -11536083 113340 rbn (ec:3.1.-.-) (de:ribonuclease bn, (rnase bn)) (db:swissprot) RBN_ECOLI P32146 ESCHERICHIA COLI 562 -11536083 163795 yihy hypothetical 32.8k protein glna-fdhe intergenic region:hypothetical protein o290 (db:pir2.dat) S40830 S40830 Escherichia coli 562 -11536083 7500889461 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:37785) (re:38657) (di:direct) ECOUW87 L19201 g304990 Escherichia coli 562 -11536083 237104 rbn trna processing exoribonuclease bn (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completengenome.) (nt:o290; formerly designated yihy) (le:5705) (re:6577) (di:direct) AE000464 AE000464 g1790319 Escherichia coli 562 -11536083 5000693801 rbn trna processing exoribonuclease bn (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completengenome.) (nt:o290; formerly designated yihy) (le:5705) (re:6577) (di:direct) AE000464 AE000464 g1790319 Escherichia coli 562 -11536083				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866030	12707	34863	1206	401

Description

6500732226 yihz:b3887 hypothetical 15.9 kd protein in glna-fdhe intergenic region:hypothetical 15.9 kd protein in rbn-fdhe intergenic region:o145 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3887 b3887 Escherichia coli 562 -11536084 113342 yihz (de:hypothetical 15.9 kd protein in rbn-fdhe intergenic region (o145)) (db:swissprot) YIHZ_ECOLI P32147 ESCHERICHIA COLI 562 -11536084 163735 yihz hypothetical 15.9k protein glna-fdhe intergenic region:hypothetical protein o145 (cl:conserved hypothetical protein hi0670) (db:pir2.dat) S40831 S40831 Escherichia coli 562 -11536084 7500937507 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:38654) (re:39091) (di:direct) ECOUW87 L19201 g304991 Escherichia coli 562 -11536084 237105 yihz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o145; 100 pct identical amino acid sequence and) (le:6574) (re:7011) (di:direct) AE000464 AE000464 g1790320 Escherichia coli 562 -11536084 5000693802 yihz orf:hypothetical protein (fn:orf; unknown) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o145; 100 pct identical amino acid sequence and) (le:6574) (re:7011) (di:direct) AE000464 AE000464 g1790320 Escherichia coli 562 -11536084

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866032	12708	34864	579	192

Description

6500732227 yyid:b3888 hypothetical 37.1 kd protein in glna-fdhe intergenic region:hypothetical 37.1 kd protein in rbn-fdhe intergenic region:o329 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3888 b3888 Escherichia coli 562 -11536085 113350 yyid (de:hypothetical 37.1 kd protein in rbn-fdhe intergenic region (o329)) (db:swissprot) YIID_ECOLI P32148 ESCHERICHIA COLI 562 -11536085 163812 yyid hypothetical 37.1k protein glna-fdhe intergenic region:hypothetical protein o329 (db:pir2.dat) S40832 S40832 Escherichia coli 562 -11536085 7500937518 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:39088) (re:40077) (di:direct) ECOUW87 L19201 g304992 Escherichia coli 562 -11536085 237106 yyid putative acetyltransferase ec 2.3.1.18 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o329; 100 pct identical amino acid sequence and) (le:7008) (re:7997) (di:direct) AE000464 AE000464 g1790321 Escherichia coli 562 -11536085 5000693803 yyid putative acetyltransferase ec 2.3.1.18 (fn:putative enzyme; not classified) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o329; 100 pct identical amino acid sequence and) (le:7008) (re:7997) (di:direct) AE000464 AE000464 g1790321 Escherichia coli 562 -11536085

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866035	12709	34865	657	218

Description

6500732228 yiie:b3889 hypothetical 9.4 kd protein in glna-fdhe intergenic region:hypothetical 9.4 kd protein in rbn-fdhe intergenic region:o81 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3889 b3889 Escherichia coli 562 -11536086 113351 yiie (de:hypothetical 9.4 kd protein in rbn-fdhe intergenic region (o81)) (db:swissprot) YIIE_ECOLI P32149 ESCHERICHIA COLI 562 -11536086 163872 yiie hypothetical 9.4k protein glna-fdhe intergenic region:hypothetical protein o81 (db:pir2.dat) S40833 S40833 Escherichia coli 562 -11536086 7500937519 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:40903) (re:41148) (di:direct) ECOUW87 L19201 g304993 Escherichia coli 562 -11536086 237107 yiie orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o81; 100 pct identical amino acid sequence and) (le:8823) (re:9068) (di:direct) AE000464 AE000464 g1790322 Escherichia coli 562 -11536086 5000693804 yiie orf:hypothetical protein (fn:orf; unknown) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o81; 100 pct identical amino acid sequence and) (le:8823) (re:9068) (di:direct) AE000464 AE000464 g1790322 Escherichia coli 562 -11536086

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866038	12710	34866	1047	348

Description

6500732229 yiif:b3890 hypothetical 9.2 kd protein in fdhe 5 region:hypothetical 9.2 kd protein in rbn-fdhe intergenic region:o80 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3890 b3890 Escherichia coli 562 -11536087 113352 yiif (de:hypothetical 9.2 kd protein in rbn-fdhe intergenic region (o80)) (db:swissprot) YIIF_ECOLI P32150 ESCHERICHIA COLI 562 -11536087 163871 yiif hypothetical 9.2k protein fdhe 5 region o80 (db:pir2.dat) S40834 S40834 Escherichia coli 562 -11536087 7500937520 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:matches ps00659: glycosyl_hydrol_f5) (le:41366) (re:41608) (di:direct) ECOUW87 L19201 g304994 Escherichia coli 562 -11536087 237108 yiif orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o80; 100 pct identical to yiif_ecoli sw:) (le:9286) (re:9528) (di:direct) AE000464 AE000464 g1790323 Escherichia coli 562 -11536087 5000693805 yiif orf:hypothetical protein (fn:orf; unknown) (db:genpept) (de:escherichia coli k-12 mg1655 section 354 of 400 of the completegenome.) (nt:o80; 100 pct identical to yiif_ecoli sw:) (le:9286) (re:9528) (di:direct) AE000464 AE000464 g1790323 Escherichia coli 562 -11536087

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866041	12711	34867	696	231

Description

6500732230 yiig:b3896 hypothetical 39.3 kd protein in fdhd 3region:hypothetical 39.3 kd protein in fdhd-frvr intergenic region:o351 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3896 b3896 Escherichia coli 562 -11536088 113353 yiig (de:hypothetical 39.3 kd protein in fdhd-frvr intergenic region (o351)) (db:swissprot) YIIG_ECOLI P32151 ESCHERICHIA COLI 562 -11536088 163820 yiig hypothetical 39.3k protein fdhd 3region:hypothetical protein o351 (db:pir2.dat) S40840 S40840 Escherichia coli 562 -11536088 7500937521 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:48641) (re:49696) (di:direct) ECOUW87 L19201 g305000 Escherichia coli 562 -11536088 237114 yiig orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:o351; 100 pct identical amino acid sequence and) (le:1179) (re:2234) (di:direct) AE000465 AE000465 g1790330 Escherichia coli 562 -11536088 5000693806 (de:(ecoli_3795) (pn:hypothetical 39) (gn:yiig) (gtcfc:13.7:14.1) (ec:) (yiig_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3795 ECOLI_3795 Escherichia coli 562 10055081

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866042	12712	34868	303	100

Description

6500732231 yiil:b3901 hypothetical 12.3 kd protein in rhad 3region:hypothetical 12.3 kd protein in frva-rhad intergenic region:f104 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3901 b3901 Escherichia coli 562 -11536089 113354 yiil (de:hypothetical 12.3 kd protein in frva-rhad intergenic region (f104)) (db:swissprot) YIIL_ECOLI P32156 ESCHERICHIA COLI 562 -11536089 163548 yiil hypothetical 12.3k protein rhad 3region:hypothetical protein f104 (db:pir2.dat) S40845 S40845 Escherichia coli 562 -11536089 7500937522 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:54761) (re:55075) (di:complement) ECOUW87 L19201 g305005 Escherichia coli 562 -11536089 237119 yiil orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completegenome.) (nt:f104; 100 pct identical amino acid sequence and) (le:7302) (re:7616) (di:complement) AE000465 AE000465 g1790335 Escherichia coli 562 -11536089 5000693808 (de:(ecoli_3800) (pn:hypothetical 12) (gn:yiil) (gtcfc:13.7:14.1) (ec:) (yiil_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3800 ECOLI_3800 Escherichia coli 562 10055082

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866043	12713	34869	1230	409

Description

6500732232 yiim:b3910 hypothetical 26.6 kd protein in kdgt-cpxa intergenic region:o234 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3910 b3910 Escherichia coli 562 -11536090 113355 yiim (de:hypothetical 26.6 kd protein in kdgt-cpxa intergenic region (o234)) (db:swissprot) YIIM_ECOLI P32157 ESCHERICHIA COLI 562 -11536090 163778 yiim hypothetical 26.6k protein kdgt-cpxa intergenic region:hypothetical protein o234 (cl:hypothetical protein hi0278) (db:pir2.dat) S40854 S40854 Escherichia coli 562 -11536090 7500937523 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:64425) (re:65129) (di:direct) ECOUW87 L19201 g305014 Escherichia coli 562 -11536090 237128 yiim orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 356 of 400 of the completegenome.) (nt:o234; 100 pct identical amino acid sequence and) (le:69) (re:773) (di:direct) AE000466 AE000466 g1790345 Escherichia coli 562 -11536090 5000693809 (de:(ecoli_3809) (pn:hypothetical 26) (gn:yiim) (gtcfc:13.7:14.1) (ec:) (yiim_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3809 ECOLI_3809 Escherichia coli 562 10055083

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866045	12714	34870	408	135

Description

6500732233 hypothetical 5.2 kd protein in cpxa-pfka intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3913 b3913 Escherichia coli 562 -11536091 7000690953 hypothetical 5.2 kd protein in cpxa-pfka intergenic region (db:pir2.dat) D65197 D65197 Escherichia coli 562 -11536091 7500959817 b3913 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 356 of 400 of the completegenome.) (nt:o49; sequence change split orf relative to) (le:3094) (re:3243) (di:direct) AE000466 AE000466 g2367330 Escherichia coli 562 -11536091

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866047	12715	34871	531	176

Description

6500732234 hypothetical 14.4 kd protein in cpxa-pfka intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3914 b3914 Escherichia coli 562 -11536092 7000690916 hypothetical 14.4 kd protein in cpxa-pfka intergenic region (db:pir2.dat) E65197 E65197 Escherichia coli 562 -11536092 7500959783 b3914 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 356 of 400 of the completegenome.) (nt:o122; sequence change split orf relative to) (le:3228) (re:3596) (di:direct) AE000466 AE000466 g2367331 Escherichia coli 562 -11536092

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866048	12716	34872	1173	390

Description

6500732235 yiip:b3915 hypothetical 32.9 kd protein in cpxa-pfka intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3915 b3915 Escherichia coli 562 -11536093 113358 yiip (de:hypothetical 32.9 kd protein in cpxa-pfka intergenic region) (db:swissprot) YIIP_ECOLI P32159 ESCHERICHIA COLI 562 -11536093 163803 yiip hypothetical 32.9k protein cpxa-pfka intergenic region:hypothetical protein o300 (db:pir2.dat) S40858 S40858 Escherichia coli 562 -11536093 7500937524 (sr:escherichia coli (sub_strain mgl655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:similar to rickettsia rickettsii protein p34) (le:68102) (re:69004) (di:direct) ECOUW87 L19201 g305018 Escherichia coli 562 -11536093 237132 yiip putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 356 of 400 of the completegenome.) (nt:o300; 100 pct identical to yiip_ecoli sw:) (le:3745) (re:4647) (di:direct) AE000466 AE000466 g1790349 Escherichia coli 562 -11536093 5000693812 (de:(ecoli_3813) (pn:hypothetical 32) (gn:yiip) (gtcfc:13.7:14.1) (ec:) (yiip_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3813 ECOLI_3813 Escherichia coli 562 10055086

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866050	12717	34873	513	170

Description

6500732236 yiiq:b3920 hypothetical 21.8 kd protein in tpia 3region precursor:hypothetical 21.8 kd protein in tpia-fpr intergenic region precursor:f199 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3920 b3920 Escherichia coli 562 -11536094 113359 yiiq (de:hypothetical 21.8 kd protein in tpia-fpr intergenic region precursor) (db:swissprot) YIIQ_ECOLI P32160 ESCHERICHIA COLI 562 -11536094 163581 yiiq hypothetical 21.8k protein tpia 3region precursor:hypothetical protein f199 (db:pir2.dat) S40863 S40863 Escherichia coli 562 -11536094 7500937525 (sr:escherichia coli (sub_strain mgl655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:73248) (re:73847) (di:complement) ECOUW87 L19201 g305023 Escherichia coli 562 -11536094 237137 yiiq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 356 of 400 of the completegenome.) (nt:f199; 100 pct identical amino acid sequence and) (le:8891) (re:9490) (di:complement) AE000466 AE000466 g1790354 Escherichia coli 562 -11536094 5000693813 (de:(ecoli_3818) (pn:hypothetical 21) (gn:yiiq) (gtcfc:13.7:14.1) (ec:) (yiiq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3818 ECOLI_3818 Escherichia coli 562 10055087

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866052	12718	34874	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866053	12719	34875	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866056	12720	34876	420	139

Description

6500732237 yvir:b3921 hypothetical 16.5 kd protein in tpia-fpr intergenic region:ol46 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3921 b3921 Escherichia coli 562 -11536095 113360 yvir (de:hypothetical 16.5 kd protein in tpia-fpr intergenic region (ol46)) (db:swissprot) YVIR_ECOLI P32161 ESCHERICHIA COLI 562 -11536095 163736 yvir hypothetical 16.5k protein tpia-fpr intergenic region:hypothetical protein ol46 (db:pir2.dat) S40864 S40864 Escherichia coli 562 -11536095 7500937526 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:73948) (re:74388) (di:direct) ECOLU87 L19201 g305024 Escherichia coli 562 -11536095 237138 yvir orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 356 of 400 of the completegenome.) (nt:ol46; 100 pct identical amino acid sequence and) (le:9591) (re:10031) (di:direct) AE000466 AE000466 g1790355 Escherichia coli 562 -11536095 5000693814 (de:(ecoli_3819) (pn:hypothetical 16) (gn:yvir) (gtcfc:13.7:14.1) (ec:) (yvir_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3819 ECOLI_3819 Escherichia coli 562 10055088

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866059	12721	34877	363	120

Description

6500732238 yiis:b3922 hypothetical 10.8 kd protein in tpia-fpr intergenic region:o99 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3922 b3922 Escherichia coli 562 -11536096 113361 yiis (de:hypothetical 10.8 kd protein in tpia-fpr intergenic region) (db:swissprot) YIIS_ECOLI P32162 ESCHERICHIA COLI 562 -11536096 163880 yiis c4-dicarboxylate transport protein homolog tpia-fpr intergenic region:hypothetical protein o99 (cl:c4-dicarboxylate carrier protein) (db:pir2.dat) S40865 S40865 Escherichia coli 562 -11536096 7500937527 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:74600) (re:74899) (di:direct) ECOUW87 L19201 g305025 Escherichia coli 562 -11536096 237139 yiis orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of 400 of the completegenome.) (nt:o99; 100 pct identical amino acid sequence and) (le:93) (re:392) (di:direct) AE000467 AE000467 g1790357 Escherichia coli 562 -11536096 5000693815 (de:(ecoli_3820) (pn:hypothetical 10) (gn:yiis) (gtcfc:13.7:14.1) (ec:) (yiis_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3820 ECOLI_3820 Escherichia coli 562 10055089

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866080	12722	34878	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866120	12723	34879	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866125	12724	34880	969	322

Description

6500732239 yiit:b3923 hypothetical 16.3 kd protein in fpr
3region:o142:hypothetical 16.3 kd protein in tpia-fpr intergenic region
(gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3923
b3923 Escherichia coli 562 -11536097 113363 yiit (de:hypothetical 16.3 kd
protein in tpia-fpr intergenic region) (db:swissprot) YIIT_ECOLI P32163
ESCHERICHIA COLI 562 -11536097 163734 yiit hypothetical 16.3k protein fpr
3region o142 (cl:universal stress protein a) (db:pir2.dat) S40866 S40866
Escherichia coli 562 -11536097 7500937528 (sr:escherichia coli (sub_strain
mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli
chromosomal region from 87.2 to 89.2 minutes.) (le:74926) (re:75354)
(di:direct) ECOUW87 L19201 g305026 Escherichia coli 562 -11536097 237140
yiit putative regulator (fn:putative regulator; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of 400 of the
completegenome.) (nt:o142; 100 pct identical amino acid sequence and)
(le:419) (re:847) (di:direct) AE000467 AE000467 g1790358 Escherichia coli
562 -11536097 5000693816 (de:(ecoli_3821) (pn:hypothetical 16) (gn:yiit)
(gtcfc:13.7:14.1) (ec:) (yiit_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_3821 ECOLI_3821 Escherichia coli 562
10055091

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866127	12725	34881	525	174

Description

6500732240 yiiu:b3928 hypothetical 9.6 kd protein in glpf-hslu intergenic
region:o81 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia
coli) b3928 b3928 Escherichia coli 562 -11536098 113364 yiiu
(de:hypothetical 9.6 kd protein in glpf-hslu intergenic region (o81))
(db:swissprot) YIIU_ECOLI P32164 ESCHERICHIA COLI 562 -11536098 163873 yiiu
hypothetical 9.6k protein glpf-hslu intergenic region:hypothetical protein
o81 (db:pir2.dat) S40871 S40871 Escherichia coli 562 -11536098 7500937529
(sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda)
(db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.)
(le:80148) (re:80393) (di:direct) ECOUW87 L19201 g305031 Escherichia coli
562 -11536098 237145 yiiu orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of 400 of the
completegenome.) (nt:o81; 100 pct identical amino acid sequence and)
(le:5641) (re:5886) (di:direct) AE000467 AE000467 g1790363 Escherichia coli
562 -11536098 5000693818 (de:(ecoli_3826) (pn:hypothetical 9) (gn:yiiu)
(gtcfc:13.7:14.1) (ec:) (yiiu_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_3826 ECOLI_3826 Escherichia coli 562
10055092

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866128	12726	34882	678	225

Description

6500732241 ylix:b3937 hypothetical 23.1 kd protein in rpme-metj intergenic region:hypothetical 23.1 kd protein in rpme-metj intergenic region precursor:f202 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3937 b3937 Escherichia coli 562 -11536099 113366 ylix (de:(f202)) (db:swissprot) YIIX_ECOLI P32167 ESCHERICHIA COLI 562 -11536099 163583 ylix hypothetical 23.1k protein rpme-metj intergenic region:hypothetical protein f202 (db:pir2.dat) S40880 S40880 Escherichia coli 562 -11536099 7500937531 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:similar to e. coli hypoth. 26.8 kda protein,) (le:88919) (re:89527) (di:complement) ECOUW87 L19201 g305040 Escherichia coli 562 -11536099 237154 ylix orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of 400 of the completegenome.) (nt:f202; 100 pct identical amino acid sequence and) (le:14412) (re:15020) (di:complement) AE000467 AE000467 g1790372 Escherichia coli 562 -11536099 5000693822 (de:(ecoli_3835) (pn:hypothetical 23) (gn:ylix) (gtcfc:13.7:14.1) (ec:) (ylix_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3835 ECOLI_3835 Escherichia coli 562 10055094

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866148	12727	34883	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866158	12728	34884	441	146

Description

6500732242 yije:b3943 hypothetical 34.1 kd protein in katg-glda intergenic region:o312 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3943 b3943 Escherichia coli 562 -11536100 162607 yije hypothetical 34.1k protein katg-glda intergenic region (db:pir2.dat) I78664 I78664 Escherichia coli 562 -11536100 237161 yije orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 358 of 400 of the completegenome.) (nt:o312; 100 pct identical to yije_ecoli sw:) (le:7626) (re:8564) (di:direct) AE000468 AE000468 g1790379 Escherichia coli 562 -11536100 7500937550 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to desulfurolobus ambivalens hypoth. 28.3) (le:1317) (re:2255) (di:direct) ECOUW89 U00006 g409786 Escherichia coli 562 -11536100 113380 yije (de:hypothetical 34.1 kd protein in katg-glda intergenic region (o312)) (db:swissprot) YIJE_ECOLI P32667 ESCHERICHIA COLI 562 -11536100 5000693823 (de:(ecoli_3841) (pn:hypothetical 34) (gn:yije) (gtcfc:13.7:14.1) (ec:) (yije_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3841 ECOLI_3841 Escherichia coli 562 10055108

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866190	12729	34885	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866197	12730	34886	1233	410

Description

6500732243 yijf:b3944 hypothetical 23.0 kd protein in katg-glda intergenic region:hypothetical 23.0 kd protein in katg-glda intergenic region precursor:f205 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3944 b3944 Escherichia coli 562 -11536101 113381 yijf (de:(f205)) (db:swissprot) YIJF_ECOLI P32668 ESCHERICHIA COLI 562 -11536101 163586 yijf hypothetical 23.0k protein katg-glda intergenic region:hypothetical protein f205 (db:pir2.dat) I78665 I78665 Escherichia coli 562 -11536101 237162 yijf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 358 of 400 of the completegenome.) (nt:f205; 100 pct identical amino acid sequence and) (le:8591) (re:9208) (di:complement) AE000468 AE000468 g1790380 Escherichia coli 562 -11536101 7500937551 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:2282) (re:2899) (di:complement) ECOUW89 U00006 g396291 Escherichia coli 562 -11536101 5000693824 (de:(ecoli_3842) (pn:hypothetical 23) (gn:yijf) (gtcfc:13.7:14.1) (ec:) (yijf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3842 ECOLI_3842 Escherichia coli 562 10055109

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866211	12731	34887	360	119

Description

6500732244 yiji:b3948 hypothetical 11.8 kd protein in ptsa-frwc intergenic region:o109 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3948 b3948 Escherichia coli 562 -11536102 7000688055 yiji hypothetical 11.8 kd protein in ptsa-frwc intergenic region (db:pir2.dat) G65201 G65201 Escherichia coli 562 -11536102 7500959770 yiji orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 358 of 400 of the completegenome.) (nt:o109; 100 pct identical amino acid sequence and) (le:13408) (re:13737) (di:direct) AE000468 AE000468 g1790384 Escherichia coli 562 -11536102 237166 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:7099) (re:7428) (di:direct) ECOUW89 U00006 g409788 Escherichia coli 562 -11536102 113382 yiji_ecoli (de:hypothetical 11.8 kd protein in ptsa-frwc intergenic region (o109).) P32671 P32671 Escherichia coli 562 -11536102 5000693827 (de:(ecoli_3846) (pn:hypothetical 11) (gn:yiji) (gtcfc:13.7:14.1) (ec:) (yiji_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3846 ECOLI_3846 Escherichia coli 562 10055110

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866214	12732	34888	294	98

Description

6500732245 yijo:b3954 hypothetical transcriptional regulator in glda-ppc intergenic:hypothetical transcriptional regulator in glda-ppc intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3954 b3954 Escherichia coli 562 -11536103 113383 yijo (de:hypothetical transcriptional regulator in glda-ppc intergenic region) (db:swissprot) YIJO_ECOLI P32677 ESCHERICHIA COLI 562 -11536103 7000688056 yijo hypothetical transcription regulator glda-ppc intergenic (cl:hypothetical protein b2382) (db:pir2.dat) E65202 E65202 Escherichia coli 562 -11536103 237172 yijo putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 359 of 400 of the completegenome.) (nt:f283; 100 pct identical to yijo_ecoli sw:) (le:5234) (re:6085) (di:complement) AE000469 AE000469 g1790391 Escherichia coli 562 -11536103 7500937552 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:matches ps00041: bacterial regulatory proteins,) (le:12707) (re:13558) (di:complement) ECOUW89 U00006 g396301 Escherichia coli 562 -11536103 5000693829 (de:(ecoli_3852) (pn:hypothetical transcriptional regulator in glda-ppc intergenic region:f283) (gn:yijo) (gtcfc:13.7:14.1) (ec:) (yijo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3852 ECOLI_3852 Escherichia coli 562 10055111

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866217	12733	34889	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866218	12734	34890	447	148

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866221	12735	34891	597	198

Description

GTC ORF with score 134 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmid 9747, 8198, 9781, andlambda clones 3612 and 6052.) (nt:similar to x-pro aminopeptidase ii from escherichia) (le:6790)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866224	12736	34892	276	91

Description

6500732246 yijp:b3955 hypothetical 66.6 kd protein in frwd-ppc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3955 b3955 Escherichia coli 562 -11536104 113384 yijp (de:hypothetical 66.6 kd protein in frwd-ppc intergenic region) (db:swissprot) YIJP_ECOLI P32678 ESCHERICHIA COLI 562 -11536104 7000688057 yijp hypothetical 66.6 kd protein in frwd-ppc intergenic region (db:pir2.dat) F65202 F65202 Escherichia coli 562 -11536104 237173 yijp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 359 of 400 of the completegenome.) (nt:f577; 100 pct identical amino acid sequence and) (le:6300) (re:8033) (di:complement) AE000469 AE000469 g1790392 Escherichia coli 562 -11536104 7500937553 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:13773) (re:15506) (di:complement) ECOUW89 U00006 g396302 Escherichia coli 562 -11536104 5000693830 (de:(ecoli_3853) (pn:hypothetical 66) (gn:yijp) (gtcfc:13.7:14.1) (ec:) (yijp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3853 ECOLI_3853 Escherichia coli 562 10055112

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866226	12737	34893	420	139

Description

GTC ORF with score 209 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmid 9747, 8198, 9781, andlambda clones 3612 and 6052.) (nt:similar to x-pro aminopeptidase ii from escherichia) (le:6790)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866227	12738	34894	429	142

Description

GTC ORF with score 196 to: (sr:baker's yeast strain=s288c (ab972)) (db:genpept-pln1) (de:saccharomyces cerevisiae chromosome v cosmid 9747, 8198, 9781, andlambda clones 3612 and 6052.) (nt:similar to x-pro aminopeptidase ii from escherichia) (le:6790)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866238	12739	34895	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866246	12740	34896	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866249	12741	34897	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866252	12742	34898	465	155

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866259	12743	34899	786	262

Description

6500732247 yijc:b3963 hypothetical 26.6 kd protein in udha-trma intergenic region:orfa (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3963 b3963 Escherichia coli 562 -11536105 113377 yijc (de:hypothetical 26.6 kd protein in udha-trma intergenic region (orfa)) (db:swissprot) YIJC_ECOLI P27307 ESCHERICHIA COLI 562 -11536105 7000688053 yijc hypothetical 26.6 kd protein in udha-trma intergenic region (db:pir2.dat) F65203 F65203 Escherichia coli 562 -11536105 237181 yijc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 360 of 400 of the completegenome.) (nt:o234a; 100 pct identical amino acid sequence and) (le:7953) (re:8657) (di:direct) AE000470 AE000470 g1790401 Escherichia coli 562 -11536105 7500937547 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:alternate name yijc) (le:26309) (re:27013) (di:direct) ECOUW89 U00006 g396310 Escherichia coli 562 -11536105 5000693832 (de:(ecoli_3861) (pn:hypothetical 26) (gn:yijc) (gtcfc:13.7:14.1) (ec:) (yijc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3861 ECOLI_3861 Escherichia coli 562 10055105

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866268	12744	34900	390	129

Description

5000693834 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3975 b3975 Escherichia coli 562 -11536106
7000691818 hypothetical protein b3975 (db:pir2.dat) F65204 F65204
Escherichia coli 562 -11536106 237189 b3975 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 362 of 400 of the completegenome.) (nt:f51; this 51 aa orf is 33 pct identical (1 gap)) (le:177) (re:332) (di:complement) AE000472 AE000472 g1790411 Escherichia coli 562 -11536106 7500960323 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:40455) (re:40610) (di:complement) ECOUW89 U00006 g396318 Escherichia coli 562 -11536106
6500732248 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3975 b3975 Escherichia coli 562 -11536106

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866275	12745	34901	768	255

Description

6500732249 yjae:b3995 hypothetical protein:hypothetical 18.2 kd protein in thic-heme intergenic region:f158 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3995 b3995 Escherichia coli 562 -11536107 113598 rsd (de:regulator of sigma d) (db:swissprot) RSD_ECOLI P31690 ESCHERICHIA COLI 562 -11536107 7000688061 hypothetical protein b3995 (db:pir2.dat) F65206 F65206 Escherichia coli 562 -11536107 237205 yjae putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:f158; similar to pseudomonas aeruginosa alginate) (le:6694) (re:7170) (di:complement) AE000473 AE000473 g1790428 Escherichia coli 562 -11536107 7500891143 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to pseudomonas aeruginosa alginate) (le:61573) (re:62049) (di:complement) ECOUW89 U00006 g396334 Escherichia coli 562 -11536107 5000693836 (de:(ecoli_3885) (pn:hypothetical 18) (gtcfc:13.7:14.1) (ec:)) (yjae_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3885 ECOLI_3885 Escherichia coli 562 10055326

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866294	12746	34902	270	89

Description

6500732250 yjad:b3996 hypothetical 29.8 kd protein in thic-heme intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3996 b3996 Escherichia coli 562 -11536108 113596 yjad (de:hypothetical 29.8 kd protein in thic-heme intergenic region) (db:swissprot) YJAD_ECOLI P32664 ESCHERICHIA COLI 562 -11536108 7000688060 yjad hypothetical 29.8 kd protein in thic-heme intergenic region (cl:hypothetical protein hi0432:mutt domain homology) (db:pir2.dat) G65206 G65206 Escherichia coli 562 -11536108 237206 yjad orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:o257; 100 pct identical amino acid sequence and) (le:7265) (re:8038) (di:direct) AE000473 AE000473 g1790429 Escherichia coli 562 -11536108 7500937845 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:62144) (re:62917) (di:direct) ECOUW89 U00006 g396335 Escherichia coli 562 -11536108 5000693837 (de:(ecoli_3886) (pn:hypothetical 29) (gn:yjad) (gtcfc:13.7:14.1) (ec:) (yjad_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3886 ECOLI_3886 Escherichia coli 562 10055324

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866295	12747	34903	303	100

Description

6500732251 yjaf:nfi:b3998 hypothetical 24.9 kd protein in heme-hupa intergenic region:endonuclease v:deoxyinosine 3endonuclease (gtcfc:14.1) (ec:3.1.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3998 b3998 Escherichia coli 562 -11536109 7000690930 yjaf hypothetical 24.9 kd protein in heme-hupa intergenic region (cl:conserved hypothetical protein af0129) (db:pir2.dat) A65207 A65207 Escherichia coli 562 -11536109 237208 nfi endonuclease v deoxyinosine 3endonuclease (fn:enzyme; degradation of dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:o225; formerly designated yjaf) (le:9146) (re:9823) (di:direct) AE000473 AE000473 g1790431 Escherichia coli 562 -11536109 7500959800 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to o.berteriana mitochon. protein involved) (le:64025) (re:64702) (di:direct) ECOUW89 U00006 g409792 Escherichia coli 562 -11536109 5000693838 (de:(ecoli_3888) (pn:hypothetical 24) (gn:yjaf) (gtcfc:13.7:14.1) (ec:) (yjaf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3888 ECOLI_3888 Escherichia coli 562 10055327

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866299	12748	34904	789	262

Description

6500732252 yjag:b3999 hypothetical 22.6 kd protein in heme-hupa intergenic region:hypothetical 22.6 kd protein in nfi-hupa intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b3999 b3999 Escherichia coli 562 -11536110 113600 yjag (de:hypothetical 22.6 kd protein in nfi-hupa intergenic region) (db:swissprot) YJAG_ECOLI P32680 ESCHERICHIA COLI 562 -11536110 7000688062 yjag hypothetical 22.6 kd protein in heme-hupa intergenic region (db:pir2.dat) B65207 B65207 Escherichia coli 562 -11536110 237209 yjag orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:o196; 100 pct identical amino acid sequence and) (le:9866) (re:10456) (di:direct) AE000473 AE000473 g1790432 Escherichia coli 562 -11536110 7500937847 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:64745) (re:65335) (di:direct) ECOUW89 U00006 g396338 Escherichia coli 562 -11536110 5000693839 (de:(ecoli_3889) (pn:hypothetical 22) (gn:yjag) (gtcfc:13.7:14.1) (ec:) (yjag_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3889 ECOLI_3889 Escherichia coli 562 10055328

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866301	12749	34905	429	142

Description

6500732253 yjah:b4001 hypothetical 26.3 kd protein in hupa-hydh intergenic region:o231 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4001 b4001 Escherichia coli 562 -11536111 113602 yjah (de:hypothetical 26.3 kd protein in hupa-hydh intergenic region (o231)) (db:swissprot) YJAH_ECOLI P32681 ESCHERICHIA COLI 562 -11536111 7000688063 yjah hypothetical 26.3 kd protein in hupa-hydh intergenic region (db:pir2.dat) D65207 D65207 Escherichia coli 562 -11536111 237211 yjah orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:o231; 100 pct identical amino acid sequence and) (le:10928) (re:11623) (di:direct) AE000473 AE000473 g1790434 Escherichia coli 562 -11536111 7500937849 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:65807) (re:66502) (di:direct) ECOUW89 U00006 g409793 Escherichia coli 562 -11536111 5000693840 (de:(ecoli_3891) (pn:hypothetical 26) (gn:yjah) (gtcfc:13.7:14.1) (ec:) (yjah_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3891 ECOLI_3891 Escherichia coli 562 10055330

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866304	12750	34906	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866327	12751	34907	432	143

Description

6500732254 yjai:b4002 hypothetical 20.4 kd protein in hupa-hydh intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4002 b4002 Escherichia coli 562 -11536112 113603 yjai (de:hypothetical 20.4 kd protein in hupa-hydh intergenic region) (db:swissprot) YJAI_ECOLI P32682 ESCHERICHIA COLI 562 -11536112 7000688064 yjai hypothetical 20.4 kd protein in hupa-hydh intergenic region (db:pir2.dat) E65207 E65207 Escherichia coli 562 -11536112 237212 yjai orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completegenome.) (nt:f188; 100 pct identical amino acid sequence and) (le:11625) (re:12191) (di:complement) AE000473 AE000473 g1790435 Escherichia coli 562 -11536112 7500937850 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:66504) (re:67070) (di:complement) ECOUW89 U00006 g396341 Escherichia coli 562 -11536112 5000693841 (de:(ecoli_3892) (pn:hypothetical 20) (gn:yjai) (gtcfc:13.7:14.1) (ec:) (yjai_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3892 ECOLI_3892 Escherichia coli 562 10055331

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866328	12752	34908	204	67

Description

6500732255 yjaa:b4011 hypothetical 14.4 kd protein in rrfe-meta intergenic region:ol27 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4011 b4011 Escherichia coli 562 -11536113 238183 yjaa (de:hypothetical 14.4 kd protein in rrfe-meta intergenic region (ol27)) (db:swissprot) YJAA_ECOLI P09162 ESCHERICHIA COLI 562 -11536113 135220 yjaa hypothetical 14.4 kd protein rrfe-meta intergenic region (db:pir1.dat) (mp:90 min) Q3ECE4 A24340 Escherichia coli 562 -11536113 5000693842 (db:genpept-bct1) (de:e. coli 5' end of rrne operon for 5s rrna and downstream region.) (nt:unidentified reading frame (pot. aa 1-127)) (le:195) (re:578) (di:direct) ECCRNE1 X02800 g42883 Escherichia coli 562 -11536113 237217 yjaa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl1655 section 364 of 400 of the completegenome.) (nt:ol27b; 100 pct identical amino acid sequence and) (le:5365) (re:5748) (di:direct) AE000474 AE000474 g1790441 Escherichia coli 562 -11536113 7500937843 (sr:escherichia coli (sub_strain mgl1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:alternate name yjaa) (le:78476) (re:78859) (di:direct) ECOUW89 U00006 g396346 Escherichia coli 562 -11536113 113593 yjaa (de:hypothetical 14.4 kd protein in rrfe-meta intergenic region (ol27)) (db:swissprot) YJAA_ECOLI P09162 ESCHERICHIA COLI 562 -11536113

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866336	12753	34909	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866338	12754	34910	1263	420

Description

6500732256 yjab:b4012 hypothetical 16.4 kd protein in rrfe-meta intergenic region:f147 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4012 b4012 Escherichia coli 562 -11536114 238184 yjab (de:hypothetical 16.4 kd protein in rrfe-meta intergenic region (f147)) (db:swissprot) YJAB_ECOLI P09163 ESCHERICHIA COLI 562 -11536114 135221 yjab hypothetical 16.4k protein rrfe-meta intergenic region (db:pir1.dat) (mp:90 min) Q3ECE6 B24340 Escherichia coli 562 -11536114 5000693843 (db:genpept-bct1) (de:e. coli 5' end of rrne operon for 5s rrna and downstream region.) (nt:unidentified reading frame (pot. aa 1-147)) (le:641) (re:1084) (di:complement) ECRRNE1 X02800 g42884 Escherichia coli 562 -11536114 237218 yjab orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 364 of 400 of the completengenome.) (nt:f147; 100 pct identical amino acid sequence and) (le:5811) (re:6254) (di:complement) AE000474 AE000474 g1790442 Escherichia coli 562 -11536114 7500937844 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:alternate name yjab) (le:78922) (re:79365) (di:complement) ECOUW89 U00006 g396347 Escherichia coli 562 -11536114 113594 yjab (de:hypothetical 16.4 kd protein in rrfe-meta intergenic region (f147)) (db:swissprot) YJAB_ECOLI P09163 ESCHERICHIA COLI 562 -11536114

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866341	12755	34911	420	139

Description

6500732257 arp:b4017 hypothetical 82.6 kd protein in acek-iclr intergenic region:ankyrin-like regulatory protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4017 b4017 Escherichia coli 562 -11536115 7000690974 arp hypothetical 82.6 kd protein acek-iclr intergenic region (db:pir2.dat) H65208 H65208 Escherichia coli 562 -11536115 7500959834 arp regulator of acetyl coa synthetase (fn:regulator; fatty acid and phosphatidic acid) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 364 of 400 of the completengenome.) (nt:f728; 99 pct identical amino acid sequence and) (le:12432) (re:14618) (di:complement) AE000474 AE000474 g1790447 Escherichia coli 562 -11536115 5000693844 (de:(ecoli_3903) (pn:ankyrin-like regulatory protein) (gn:arp) (gtcfc:13.7:14.1) (ec:) (arp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3903 ECOLI_3903 Escherichia coli 562 10124132

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866350	12756	34912	783	260

Description

6500732258 yjbb:b4020 hypothetical 59.5 kd protein in meth-pepe intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4020 b4020 Escherichia coli 562 -11536116 113614 yjbb (de:hypothetical 59.5 kd protein in meth-pepe intergenic region) (db:swissprot) YJBB_ECOLI P32683 ESCHERICHIA COLI 562 -11536116 7000688066 yjbb hypothetical 59.5 kd protein in meth-pepe intergenic region (db:pir2.dat) C65209 C65209 Escherichia coli 562 -11536116 237226 yjbb putative alpha helix protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 365 of 400 of the completegenome.) (nt:o543; 100 pct identical amino acid sequence and) (le:5087) (re:6718) (di:direct) AE000475 AE000475 g1790451 Escherichia coli 562 -11536116 7500937869 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:92973) (re:94604) (di:direct) ECOUW89 U00006 g409795 Escherichia coli 562 -11536116 5000693845 (de:(ecoli_3906) (pn:hypothetical 59) (gn:yjbb) (gtcfc:13.7:14.1) (ec:) (yjbb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3906 ECOLI_3906 Escherichia coli 562 10055342

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866359	12757	34913	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866384	12758	34914	483	160

Description

6500732259 yjbc:b4022 hypothetical 32.5 kd protein in pepe-lysc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4022 b4022 Escherichia coli 562 -11536117 113616 yjbc (de:hypothetical 32.5 kd protein in pepe-lysc intergenic region) (db:swissprot) YJBC_ECOLI P32684 ESCHERICHIA COLI 562 -11536117 7000688067 yjbc hypothetical 32.5 kd protein in pepe-lysc intergenic region (db:pir2.dat) E65209 E65209 Escherichia coli 562 -11536117 237228 yjbc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 365 of 400 of the completegenome.) (nt:o290a; 100 pct identical amino acid sequence and) (le:7710) (re:8582) (di:direct) AE000475 AE000475 g1790453 Escherichia coli 562 -11536117 7500937870 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:95596) (re:96468) (di:direct) ECOUW89 U00006 g396357 Escherichia coli 562 -11536117 5000693846 (de:(ecoli_3908) (pn:hypothetical 32) (gn:yjbc) (gtcfc:13.7:14.1) (ec:) (yjbc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3908 ECOLI_3908 Escherichia coli 562 10055344

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866385	12759	34915	1383	460

Description

6500732260 yjbd:b4023 hypothetical 10.5 kd protein in pepe-lysc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4023 b4023 Escherichia coli 562 -11536118 113617 yjbd (de:hypothetical 10.5 kd protein in pepe-lysc intergenic region) (db:swissprot) YJBD_ECOLI P32685 ESCHERICHIA COLI 562 -11536118 7000688068 yjbd hypothetical 10.5 kd protein in pepe-lysc intergenic region (db:pir2.dat) F65209 F65209 Escherichia coli 562 -11536118 237229 yjbd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 365 of 400 of the completegenome.) (nt:f90; 100 pct identical amino acid sequence and) (le:8715) (re:8987) (di:complement) AE000475 AE000475 g1790454 Escherichia coli 562 -11536118 7500937871 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:96601) (re:96873) (di:complement) ECOUW89 U00006 g396358 Escherichia coli 562 -11536118 5000693847 (de:(ecoli_3909) (pn:hypothetical 10) (gn:yjbd) (gtcfc:13.7:14.1) (ec:) (yjbd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3909 ECOLI_3909 Escherichia coli 562 10055345

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866389	12760	34916	639	212

Description

6500732261 yjbe:b4026 hypothetical 7.4 kd protein in pgi-xyle intergenic region:hypothetical 7.4 kd protein in pgi-xyle intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4026 b4026 Escherichia coli 562 -11536119 7000688069 yjbe hypothetical 7.4 kd protein in pgi-xyle intergenic region (db:pir2.dat) A65210 A65210 Escherichia coli 562 -11536119 7500959830 yjbe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 366 of 400 of the completegenome.) (nt:o80; 100 pct identical amino acid sequence and) (le:2617) (re:2859) (di:direct) AE000476 AE000476 g1790458 Escherichia coli 562 -11536119 237232 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:101148) (re:101390) (di:direct) ECOUW89 U00006 g396361 Escherichia coli 562 -11536119 113618 yjbe_ecoli (de:hypothetical 7.4 kd protein in pgi-xyle intergenic region precursor (o80).) P32686 P32686 Escherichia coli 562 -11536119 5000693848 (de:(ecoli_3912) (pn:hypothetical 7) (gn:yjbe) (gtcfc:13.7:14.1) (ec:) (yjbe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3912 ECOLI_3912 Escherichia coli 562 10055346

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866397	12761	34917	186	61

Description

6500732262 yjbf:b4027 hypothetical 25.0 kd lipoprotein in pgi-xyle intergenic region:hypothetical 25.0 kd lipoprotein in pgi-xyle intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4027 b4027 Escherichia coli 562 -11536120 113619 yjbf (de:precursor) (db:swissprot) YJBF_ECOLI P32687 ESCHERICHIA COLI 562 -11536120 7000688070 yjbf hypothetical 25.0 kd lipoprotein in pgi-xyle intergenic region (db:pir2.dat) B65210 B65210 Escherichia coli 562 -11536120 237233 yjbf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 366 of 400 of the completegenome.) (nt:o222; 100 pct identical amino acid sequence and) (le:2943) (re:3611) (di:direct) AE000476 AE000476 g1790459 Escherichia coli 562 -11536120 7500937872 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:101474) (re:102142) (di:direct) ECOUW89 U00006 g409796 Escherichia coli 562 -11536120 5000693849 (de:(ecoli_3913) (pn:hypothetical 25) (gn:yjbf) (gtcfc:13.7:14.1) (ec:) (yjbf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3913 ECOLI_3913 Escherichia coli 562 10055347

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866415	12762	34918	1221	406

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866420	12763	34919	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866422	12764	34920	999	332

Description

6500732263 yjbg:b4028 hypothetical 26.3 kd protein in pgi-xyle intergenic region:hypothetical 26.3 kd protein in pgi-xyle intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4028 b4028 Escherichia coli 562 -11536121 113620 yjbg (de:hypothetical 26.3 kd protein in pgi-xyle intergenic region precursor) (db:swissprot) YJBG_ECOLI P32688 ESCHERICHIA COLI 562 -11536121 7000688071 yjbg hypothetical 26.3 kd protein in pgi-xyle intergenic region (cl:hypothetical protein b0985) (db:pir2.dat) C65210 C65210 Escherichia coli 562 -11536121 237234 yjbg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 366 of 400 of the completegenome.) (nt:o245; 100 pct identical amino acid sequence and) (le:3608) (re:4345) (di:direct) AE000476 AE000476 g1790460 Escherichia coli 562 -11536121 7500937873 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:102139) (re:102876) (di:direct) ECOUW89 U00006 g396363 Escherichia coli 562 -11536121 5000693850 (de:(ecoli_3914) (pn:hypothetical 26) (gn:yjbg) (gtcfc:13.7:14.1) (ec:) (yjbg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3914 ECOLI_3914 Escherichia coli 562 10055348

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866433	12765	34921	492	163

Description

6500732264 yjbh:b4029 hypothetical 78.5 kd protein in pgi-xyle intergenic region:hypothetical 78.5 kd lipoprotein in pgi-xyle intergenic region precursor (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4029 b4029 Escherichia coli 562 -11536122 113621 yjbh (de:precursor) (db:swissprot) YJBH_ECOLI P32689 ESCHERICHIA COLI 562 -11536122 7000688072 yjbh yjbh protein precursor (cl:vibrio cholerae otng protein) (db:pir2.dat) D65210 D65210 Escherichia coli 562 -11536122 237235 yjbh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 366 of 400 of the completegenome.) (nt:o698; 100 pct identical amino acid sequence and) (le:4345) (re:6441) (di:direct) AE000476 AE000476 g1790461 Escherichia coli 562 -11536122 7500937874 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:matches ps00107: protein kinases atp-binding region) (le:102876) (re:104972) (di:direct) ECOUW89 U00006 g396364 Escherichia coli 562 -11536122 5000693851 (de:(ecoli_3915) (pn:hypothetical 78) (gn:yjbh) (gtcfc:13.7:14.1) (ec:)) (yjbh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3915 ECOLI_3915 Escherichia coli 562 10055349

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866434	12766	34922	183	60

Description

GTC ORF with score 167 to: -reductase) (fn:possibly involved in mitochondrial fatty acid) (db:genpept-pln1) (de:neurospora crassa 3-oxoacyl-(acyl-carrier-protein)-reductase(oar-1) mrna, nuclear gene encoding mitochondrial protein, completedcds.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866435	12767	34923	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866437	12768	34924	639	212

Description

6500732265 yjbi:b4038 hypothetical 51.7 kd protein in malm-ubic intergenic region:o442 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4038 b4038 Escherichia coli 562 -11536123 113622 yjbi (de:hypothetical 51.7 kd protein in malm-ubic intergenic region (o442)) (db:swissprot) YJBI_ECOLI P32690 ESCHERICHIA COLI 562 -11536123 7000688073 yjbi chorismate lyase ubic (db:pir2.dat) E65211 E65211 Escherichia coli 562 -11536123 237244 yjbi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 367 of 400 of the completegenome.) (nt:o442; 100 pct identical amino acid sequence and) (le:3050) (re:4378) (di:direct) AE000477 AE000477 g1790471 Escherichia coli 562 -11536123 7500937875 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:116197) (re:117525) (di:direct) ECOUW89 U00006 g396373 Escherichia coli 562 -11536123 5000693853 (de:(ecoli_3924) (pn:hypothetical 51) (gn:yjbi) (gtcfc:13.7:14.1) (ec:) (yjbi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3924 ECOLI_3924 Escherichia coli 562 10055350

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866453	12769	34925	582	193

Description

6500732266 ybjb:b4045 hypothetical protein:8.3 kd protein in dinf-qor intergenic region:o69 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4045 b4045 Escherichia coli 562 -11536124 113623 ybjb (de:8.3 kd protein in dinf-qor intergenic region (o69)) (db:swissprot) YJBJ_ECOLI P32691 ESCHERICHIA COLI 562 -11536124 7000688074 hypothetical protein b4045 (db:pir2.dat) D65212 D65212 Escherichia coli 562 -11536124 237251 ybjb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 368 of 400 of the completegenome.) (nt:o69) (le:76) (re:285) (di:direct) AE000478 AE000478 g1790479 Escherichia coli 562 -11536124 7500937876 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:124479) (re:124688) (di:direct) ECOUW89 U00006 g396380 Escherichia coli 562 -11536124 5000693855 (de:(ecoli_3931) (pn:8) (gtcfc:13.7:14.1) (ec:) (ybjb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3931 ECOLI_3931 Escherichia coli 562 10055351

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866461	12770	34926	951	317

Description

6500732267 yjbk:b4046 hypothetical 21.7 kd protein in dinf-qor intergenic region:f191 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4046 b4046 Escherichia coli 562 -11536125 7000688075 yjbk hypothetical 21.7 kd protein in dinf-qor intergenic region (db:pir2.dat) E65212 E65212 Escherichia coli 562 -11536125 7500937877 yjbk putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 368 of 400 of the completegenome.) (nt:f191; 100 pct identical to yjbk_ecoli sw:) (le:327) (re:902) (di:complement) AE000478 AE000478 g1790480 Escherichia coli 562 -11536125 113624 yjbk (de:hypothetical 21.7 kd protein in dinf-qor intergenic region (f191)) (db:swissprot) YJBK_ECOLI P32692 ESCHERICHIA COLI 562 -11536125 5000693856 (de:(ecoli_3932) (pn:hypothetical 21) (gn:yjbk) (gtcfc:13.7:14.1) (ec:) (yjbk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3932 ECOLI_3932 Escherichia coli 562 10124137

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866462	12771	34927	429	142

Description

6500732268 yjbl:b4047 o8:hypothetical 9.7 kd protein in dinf-qor intergenic region:o84 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4047 b4047 Escherichia coli 562 -11536126 113625 yjbl (de:hypothetical 9.7 kd protein in dinf-qor intergenic region (o84)) (db:swissprot) YJBL_ECOLI P32693 ESCHERICHIA COLI 562 -11536126 7000688076 yjbl hypothetical 9.7 kd protein in dinf-qor intergenic region (db:pir2.dat) F65212 F65212 Escherichia coli 562 -11536126 237253 yjbl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 368 of 400 of the completegenome.) (nt:o84; 100 pct identical amino acid sequence and) (le:1160) (re:1414) (di:direct) AE000478 AE000478 g1790481 Escherichia coli 562 -11536126 7500937878 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:125565) (re:125819) (di:direct) ECOUW89 U00006 g396382 Escherichia coli 562 -11536126 5000693857 (de:(ecoli_3933) (pn:hypothetical 9) (gn:yjbl) (gtcfc:13.7:14.1) (ec:) (yjbl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3933 ECOLI_3933 Escherichia coli 562 10055353

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866464	12772	34928	510	169

Description

6500732269 yjbm:b4048 hypothetical 26.7 kd protein in dinf-qor intergenic region:o235 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4048 b4048 Escherichia coli 562 -11536127 113626 yjbm (de:hypothetical 26.7 kd protein in dinf-qor intergenic region (o235)) (db:swissprot) YJBM_ECOLI P32694 ESCHERICHIA COLI 562 -11536127 7000688077 yjbm hypothetical 26.7 kd protein in dinf-qor intergenic region (db:pir2.dat) G65212 G65212 Escherichia coli 562 -11536127 7500937879 yjbm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 368 of 400 of the completegenome.) (nt:o235; 100 pct identical amino acid sequence and) (le:1438) (re:2145) (di:direct) AE000478 AE000478 g1790482 Escherichia coli 562 -11536127 5000693858 (de:(ecoli_3934) (pn:hypothetical 26) (gn:yjbm) (gtcfc:13.7:14.1) (ec:) (yjbm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3934 ECOLI_3934 Escherichia coli 562 10124138

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866488	12773	34929	1455	484

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866492	12774	34930	405	134

Description

6500732270 yjbn:b4049 hypothetical 38.4 kd protein in dinf-qor intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4049 b4049 Escherichia coli 562 -11536128 7000688078 yjbn hypothetical 38.4 kd protein in dinf-qor intergenic region (cl:haemophilus influenzae conserved hypothetical protein hi0634) (db:pir2.dat) H65212 H65212 Escherichia coli 562 -11536128 7500959809 yjbn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 368 of 400 of the completegenome.) (nt:o345 100 pct identical to yjbn_ecoli sw: p32695) (le:2508) (re:3545) (di:direct) AE000478 AE000478 g1790483 Escherichia coli 562 -11536128 113627 yjbn_ecoli (de:hypothetical 38.4 kd protein in dinf-qor intergenic region (o345).) P32695 P32695 Escherichia coli 562 -11536128 5000693859 (de:(ecoli_3935) (pn:hypothetical 38) (gn:yjbn) (gtcfc:13.7:14.1) (ec:) (yjbn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3935 ECOLI_3935 Escherichia coli 562 10124139

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866512	12775	34931	225	74

Description

6500732271 yjbo:b4050 hypothetical 17.4 kd protein in dinf-qor intergenic region:ol50 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4050 b4050 Escherichia coli 562 -11536129 7000688079 yjbo hypothetical 17.4 kd protein in dinf-qor intergenic region (db:pir2.dat) A65213 A65213 Escherichia coli 562 -11536129 7500959791 yjbo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 368 of 400 of the completegenome.) (nt:ol50; 100 pct identical to yjbo_ecoli sw: p32696) (le:3469) (re:3921) (di:direct) AE000478 AE000478 g1790484 Escherichia coli 562 -11536129 237256 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:127874) (re:128326) (di:direct) ECOUW89 U00006 g409799 Escherichia coli 562 -11536129 113629 yjbo_ecoli (de:hypothetical 17.4 kd protein in dinf-qor intergenic region (ol50).) P32696 P32696 Escherichia coli 562 -11536129 5000693860 (de:(ecoli_3936) (pn:hypothetical 17) (gn:yjbo) (gtcfc:13.7:14.1) (ec:) (yjbo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3936 ECOLI_3936 Escherichia coli 562 10055357

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866520	12776	34932	843	280

Description

6500732272 yjbq:b4056 hypothetical 15.7 kd protein in tyrb-uvra intergenic region:hypothetical 15.7 kd protein in apha-uvra intergenic region:ol38 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4056 b4056 Escherichia coli 562 -11536130 113632 yjbq (de:hypothetical 15.7 kd protein in apha-uvra intergenic region (ol38)) (db:swissprot) YJBQ_ECOLI P32698 ESCHERICHIA COLI 562 -11536130 7000688080 yjbq hypothetical 15.7 kd protein in tyrb-uvra intergenic region (cl:hypothetical protein mj1081) (db:pir2.dat) G65213 G65213 Escherichia coli 562 -11536130 237262 yjbq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 369 of 400 of the completegenome.) (nt:ol38; 100 pct identical amino acid sequence and) (le:1217) (re:1633) (di:direct) AE000479 AE000479 g1790491 Escherichia coli 562 -11536130 7500937883 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:135478) (re:135894) (di:direct) ECOUW89 U00006 g396391 Escherichia coli 562 -11536130 5000693862 (de:(ecoli_3942) (pn:hypothetical 15) (gn:yjbq) (gtcfc:13.7:14.1) (ec:) (yjbq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3942 ECOLI_3942 Escherichia coli 562 10055360

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866524	12777	34933	933	310

Description

6500732273 yjbr:b4057 hypothetical 13.4 kd protein in tyrb-uvra intergenic region:hypothetical 13.4 kd protein in apha-uvra intergenic region:ol18 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4057 b4057 Escherichia coli 562 -11536131 7500937884 yjbr (de:hypothetical 13.5 kd protein in apha-uvra intergenic region) (db:swissprot) YJBR_ECOLI P32699 ESCHERICHIA COLI 562 -11536131 7000690914 yjbr hypothetical 13.4 kd protein in tyrb-uvra intergenic region (db:pir2.dat) H65213 H65213 Escherichia coli 562 -11536131 7500937886 yjbr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 369 of 400 of the completegenome.) (nt:ol18; 100 pct identical amino acid sequence and) (le:1637) (re:1993) (di:direct) AE000479 AE000479 g2367342 Escherichia coli 562 -11536131

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866527	12778	34934	666	221

Description

6500732274 yjcb:b4060 hypothetical 13.0 kd protein in ssb-soxs intergenic region:f116 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4060 b4060 Escherichia coli 562 -11536132 7000688081 yjcb hypothetical 13.0 kd protein in ssb-soxs intergenic region (db:pir2.dat) C65214 C65214 Escherichia coli 562 -11536132 7500959775 yjcb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 369 of 400 of the completegenome.) (nt:f116; 100 pct identical amino acid sequence and) (le:5739) (re:6089) (di:complement) AE000479 AE000479 g1790495 Escherichia coli 562 -11536132 237266 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:140000) (re:140350) (di:complement) ECOUW89 U00006 g409801 Escherichia coli 562 -11536132 113640 yjcb_ecoli (de:hypothetical 13.0 kd protein in ssb-soxs intergenic region (f116).) P32700 P32700 Escherichia coli 562 -11536132 5000693864 (de:(ecoli_3946) (pn:hypothetical 13) (gn:yjcb) (gtcfc:13.7:14.1) (ec:) (yjcb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3946 ECOLI_3946 Escherichia coli 562 10055368

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866528	12779	34935	591	196

Description

6500732275 yjcc:b4061 hypothetical 60.8 kd protein in ssb-soxs intergenic region:o528 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4061 b4061 Escherichia coli 562 -11536133 113641 yjcc (de:hypothetical 60.8 kd protein in ssb-soxs intergenic region (o528)) (db:swissprot) YJCC_ECOLI P32701 ESCHERICHIA COLI 562 -11536133 7000688082 yjcc hypothetical 60.8 kd protein in ssb-soxs intergenic region (cl:probable membrane protein ylab) (db:pir2.dat) D65214 D65214 Escherichia coli 562 -11536133 7500937900 yjcc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 369 of 400 of the completengenome.) (nt:o528; 100 pct identical to yjcc_ecoli sw:) (le:6450) (re:8036) (di:direct) AE000479 AE000479 g1790496 Escherichia coli 562 -11536133 5000693865 (de:(ecoli_3947) (pn:hypothetical 60) (gn:yjcc) (gtcfc:13.7:14.1) (ec:) (yjcc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3947 ECOLI_3947 Escherichia coli 562 10124144

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866534	12780	34936	501	166

Description

6500732276 yjcd:b4064 hypothetical 45.7 kd protein in soxr-acs intergenic region:o449 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4064 b4064 Escherichia coli 562 -11536134 113642 yjcd (de:hypothetical 45.7 kd protein in soxr-acs intergenic region (o449)) (db:swissprot) YJCD_ECOLI P32702 ESCHERICHIA COLI 562 -11536134 7000688083 yjcd hypothetical 45.7 kd protein in soxr-acs intergenic region (cl:conserved hypothetical protein hi0125) (db:pir2.dat) G65214 G65214 Escherichia coli 562 -11536134 237270 yjcd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 369 of 400 of the completengenome.) (nt:o449; 100 pct identical to yjcd_ecoli sw:) (le:9458) (re:10807) (di:direct) AE000479 AE000479 g1790499 Escherichia coli 562 -11536134 7500937901 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:matches ps00017: atp/gtp-binding site motif a;) (le:143719) (re:145068) (di:direct) ECOUW89 U00006 g396399 Escherichia coli 562 -11536134 5000693866 (de:(ecoli_3950) (pn:hypothetical 45) (gn:yjcd) (gtcfc:13.7:14.1) (ec:) (yjcd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3950 ECOLI_3950 Escherichia coli 562 10055370

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866537	12781	34937	825	275

Description

6500732277 yjce:b4065 hypothetical 60.5 kd protein in soxr-acs intergenic region:o549 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4065 b4065 Escherichia coli 562 -11536135 113644 yjce (de:hypothetical 60.5 kd protein in soxr-acs intergenic region (o549)) (db:swissprot) YJCE_ECOLI P32703 ESCHERICHIA COLI 562 -11536135 7000688084 yjce hypothetical 60.5 kd protein in soxr-acs intergenic region (cl:hypothetical protein yvgp) (db:pir2.dat) H65214 H65214 Escherichia coli 562 -11536135 237271 yjce orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 370 of 400 of the completgenome.) (nt:o549b; 100 pct identical to yjce_ecoli sw:) (le:83) (re:1732) (di:direct) AE000480 AE000480 g1790501 Escherichia coli 562 -11536135 7500937903 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to eukaryotic na+/h+ exchangers) (le:145220) (re:146869) (di:direct) ECOUW89 U00006 g396400 Escherichia coli 562 -11536135 5000693867 (de:(ecoli_3951) (pn:hypothetical 60) (gn:yjce) (gtcfc:13.7:14.1) (ec:) (yjce_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3951 ECOLI_3951 Escherichia coli 562 10055372

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866557	12782	34938	441	146

Description

6500732278 yjcf:b4066 hypothetical 49.4 kd protein in soxr-acs intergenic region:f430 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4066 b4066 Escherichia coli 562 -11536136 113645 yjcf (de:hypothetical 49.4 kd protein in soxr-acs intergenic region (f430)) (db:swissprot) YJCF_ECOLI P32704 ESCHERICHIA COLI 562 -11536136 7000688085 yjcf hypothetical 49.4 kd protein in soxr-acs intergenic region (db:pir2.dat) A65215 A65215 Escherichia coli 562 -11536136 237272 yjcf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 370 of 400 of the completgenome.) (nt:f430; 100 pct identical amino acid sequence and) (le:1886) (re:3178) (di:complement) AE000480 AE000480 g1790502 Escherichia coli 562 -11536136 7500937904 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:147023) (re:148315) (di:complement) ECOUW89 U00006 g396401 Escherichia coli 562 -11536136 5000693868 (de:(ecoli_3952) (pn:hypothetical 49) (gn:yjcf) (gtcfc:13.7:14.1) (ec:) (yjcf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3952 ECOLI_3952 Escherichia coli 562 10055373

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866560	12783	34939	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866562	12784	34940	1443	480

Description

GTC ORF with score 239 to: (sr:caenorhabditis elegans strain-bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f53h8.) (nt:similar to clathrin coat assembly protein.) (le:17230:17324:17461:17633) (re:17264:17402:17566:17745) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866564	12785	34941	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866582	12786	34942	2034	677

Description

6500732279 yjcg:b4067 hypothetical 59.2 kd protein in soxr-acs intergenic region:f549 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4067 b4067 Escherichia coli 562 -11536137 113646 yjcg (de:hypothetical 59.2 kd protein in soxr-acs intergenic region (f549)) (db:swissprot) YJCG_ECOLI P32705 ESCHERICHIA COLI 562 -11536137 7000688086 yjcg hypothetical 59.2 kd protein in soxr-acs intergenic region (cl:proline carrier protein) (db:pir2.dat) B65215 B65215 Escherichia coli 562 -11536137 237273 yjcg putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 370 of 400 of the completegenome.) (nt:f549; 100 pct identical to yjcg_ecoli sw:) (le:3356) (re:5005) (di:complement) AE000480 AE000480 g1790503 Escherichia coli 562 -11536137 7500937905 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to salmonella proline permease; (putp) 5') (le:148493) (re:150142) (di:complement) ECOUW89 U00006 g396402 Escherichia coli 562 -11536137 5000693869 (de:(ecoli_3953) (pn:hypothetical 59) (gn:yjcg) (gtcfc:13.7:14.1) (ec:) (yjcg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3953 ECOLI_3953 Escherichia coli 562 10055374

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866583	12787	34943	495	164

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866615	12788	34944	1887	628

Description

6500732280 yjch:b4068 hypothetical 11.7 kd protein in soxr-acis intergenic region:f104 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4068 b4068 Escherichia coli 562 -11536138 113647 yjch (de:hypothetical 11.7 kd protein in soxr-acis intergenic region (f104)) (db:swissprot) YJCH_ECOLI P32706 ESCHERICHIA COLI 562 -11536138 7000688087 yjch hypothetical 11.7 kd protein in soxr-acis intergenic region (db:pir2.dat) C65215 C65215 Escherichia coli 562 -11536138 237274 yjch orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 370 of 400 of the completegenome.) (nt:f104; 100 pct identical amino acid sequence and) (le:5002) (re:5316) (di:complement) AE000480 AE000480 g1790504 Escherichia coli 562 -11536138 7500937906 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:150139) (re:150453) (di:complement) ECOUW89 U00006 g396403 Escherichia coli 562 -11536138 5000693870 (de:(ecoli_3954) (pn:hypothetical 11) (gn:yjch) (gtcfc:13.7:14.1) (ec:) (yjch_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3954 ECOLI_3954 Escherichia coli 562 10055375

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866621	12789	34945	528	175

Description

6500732281 yjco:b4078 hypothetical 25.1 kd protein in gltp-fdhf intergenic region:hypothetical 25.1 kd protein in gltp-fdhf intergenic region
precursor:f229 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b4078 b4078 Escherichia coli 562 -11536139 113648
yjco (de:(f229)) (db:swissprot) YJCO_ECOLI P32713 ESCHERICHIA COLI 562
-11536139 7000688088 yjco hypothetical 25.1 kd protein in gltp-fdhf
intergenic region (db:pir2.dat) E65216 E65216 Escherichia coli 562 -11536139
237284 yjco orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.)
(nt:f229b; 100 pct identical amino acid sequence and) (le:4994) (re:5683)
(di:complement) AE000481 AE000481 g1790515 Escherichia coli 562 -11536139
7500937907 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library:
lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8
minutes.) (le:161676) (re:162365) (di:complement) ECOUW89 U00006 g396413
Escherichia coli 562 -11536139 5000693871 yjco orf:hypothetical protein
(fn:orf; unknown) (db:genpept) (de:escherichia coli k-12 mg1655 section 371
of 400 of the completegenome.) (nt:f229b; 100 pct identical amino acid
sequence and) (le:4994) (re:5683) (di:complement) AE000481 AE000481 g1790515
Escherichia coli 562 -11536139

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866622	12790	34946	330	109

Description

6500732282 yjcp:b4080 hypothetical 53.4 kd protein in fdhf-phnp intergenic
region:f488 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia
coli) b4080 b4080 Escherichia coli 562 -11536140 7500937908 yjcp
(de:hypothetical 53.4 kd protein in fdhf-phnp intergenic region)
(db:swissprot) YJCP_ECOLI P32714 ESCHERICHIA COLI 562 -11536140 7000690958
yjcp hypothetical 53.4 kd protein in fdhf-phnp intergenic region
(db:pir2.dat) G65216 G65216 Escherichia coli 562 -11536140 7500937910 yjcp
putative enzyme (fn:orf; not classified) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:f488; 99 pct
identical to yjcp_ecoli sw:) (le:8122) (re:9588) (di:complement) AE000481
AE000481 g2367348 Escherichia coli 562 -11536140 7502852279 yjcp putative
enzyme (fn:orf; not classified) (db:genpept) (de:escherichia coli k-12
mg1655 section 371 of 400 of the completegenome.) (nt:f488; 99 pct identical
to yjcp_ecoli sw:) (le:8122) (re:9588) (di:complement) AE000481 AE000481
g2367348 Escherichia coli 562 -11536140

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866624	12791	34947	876	291

Description

6500732283 yjcq:b4081 hypothetical 70.9 kd protein in fdhf-phnp intergenic region:f636 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4081 b4081 Escherichia coli 562 -11536141 7000688089 yjcq hypothetical 70.9 kd protein in fdhf-phnp intergenic region (db:pir2.dat) H65216 H65216 Escherichia coli 562 -11536141 7500959832 yjcq putative enzyme (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:f636; 100 pct identical to yjcq_ecoli sw:) (le:9585) (re:11495) (di:complement) AE000481 AE000481 g1790518 Escherichia coli 562 -11536141 237287 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to neurospora crassa phosphate-repressible) (le:166267) (re:168177) (di:complement) ECOUW89 U00006 g396416 Escherichia coli 562 -11536141 5000693873 yjcq putative enzyme (fn:orf; not classified) (db:genpept) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:f636; 100 pct identical to yjcq_ecoli sw:) (le:9585) (re:11495) (di:complement) AE000481 AE000481 g1790518 Escherichia coli 562 -11536141 113650 yjcq_ecoli (de:hypothetical 70.9 kd protein in fdhf-phnp intergenic region (f636).) P32715 P32715 Escherichia coli 562 -11536141

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866647	12792	34948	492	163

Description

6500732284 yjcr:b4082 hypothetical 36.9 kd protein in fdhf-phnp intergenic region:f343 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4082 b4082 Escherichia coli 562 -11536142 113651 yjcr (de:hypothetical 36.9 kd protein in fdhf-phnp intergenic region (f343)) (db:swissprot) YJCR_ECOLI P32716 ESCHERICHIA COLI 562 -11536142 7000688090 yjcr hypothetical 36.9 kd protein in fdhf-phnp intergenic region (cl:escherichia coli hypothetical protein b1644) (db:pir2.dat) A65217 A65217 Escherichia coli 562 -11536142 237288 yjcr putative membrane protein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:f343; 100 pct identical to yjcr_ecoli sw:) (le:11636) (re:12667) (di:complement) AE000481 AE000481 g1790519 Escherichia coli 562 -11536142 7500937912 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to e. coli multidrug resistance protein a) (le:168317) (re:169348) (di:complement) ECOUW89 U00006 g396417 Escherichia coli 562 -11536142 5000693874 yjcr putative membrane protein (fn:putative membrane; not classified) (db:genpept) (de:escherichia coli k-12 mg1655 section 371 of 400 of the completegenome.) (nt:f343; 100 pct identical to yjcr_ecoli sw:) (le:11636) (re:12667) (di:complement) AE000481 AE000481 g1790519 Escherichia coli 562 -11536142

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866653	12793	34949	261	86

Description

6500732285 yjcs:b4083 hypothetical 73.7 kd protein in fdhf-phnp intergenic region:f665 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4083 b4083 Escherichia coli 562 -11536143 7000690971 yjcs hypothetical 73.7 kd protein in fdhf-phnp intergenic region (cl:hypothetical protein yol164w) (db:pir2.dat) B65217 B65217 Escherichia coli 562 -11536143 7500959833 yjcs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f665; 99 pct identical to yjcs_ecoli sw:) (le:260) (re:2257) (di:complement) AE000482 AE000482 g2367350 Escherichia coli 562 -11536143

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866655	12794	34950	795	264

Description

6500732286 yjct:b4084 hypothetical 33.8 kd protein in fdhf-phnp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4084 b4084 Escherichia coli 562 -11536144 113653 yjct (de:hypothetical 33.8 kd protein in fdhf-phnp intergenic region) (db:swissprot) YJCT_ECOLI P32718 ESCHERICHIA COLI 562 -11536144 7000688091 yjct hypothetical 33.8 kd protein in fdhf-phnp intergenic region (db:pir2.dat) C65217 C65217 Escherichia coli 562 -11536144 237290 yjct putative nagc-like transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f309; 100 pct identical to yjct_ecoli sw:) (le:2518) (re:3447) (di:complement) AE000482 AE000482 g1790522 Escherichia coli 562 -11536144 7500937914 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to bacillus subtilis xylose repressor) (le:172109) (re:173038) (di:complement) ECOUW89 U00006 g396419 Escherichia coli 562 -11536144 5000693876 (de:(ecoli_3970) (pn:hypothetical 33) (gn:yjct) (gtcfc:13.7:14.1) (ec:) (yjct_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3970 ECOLI_3970 Escherichia coli 562 10055381

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866659	12795	34951	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866662	12796	34952	732	243

Description

6500732287 yjcu:b4085 hypothetical 26.1 kd protein in fdhf-phnp intergenic region:f231 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4085 b4085 Escherichia coli 562 -11536145 113654 yjcu (de:hypothetical 26.1 kd protein in fdhf-phnp intergenic region (f231)) (db:swissprot) YJCU_ECOLI P32719 ESCHERICHIA COLI 562 -11536145 7000688092 yjcu hypothetical 26.1 kd protein in fdhf-phnp intergenic region (cl:yeast ribulose-5-phosphate-epimerase) (db:pir2.dat) D65217 D65217 Escherichia coli 562 -11536145 237291 yjcu putative epimerase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f231; 100 pct identical to yjcu_ecoli sw:) (le:3431) (re:4126) (di:complement) AE000482 AE000482 g1790523 Escherichia coli 562 -11536145 7500937915 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to alcaligenes eutrophus phg1) (le:173022) (re:173717) (di:complement) ECOUW89 U00006 g396420 Escherichia coli 562 -11536145 5000693877 (de:(ecoli_3971) (pn:hypothetical 26) (gn:yjcu) (gtcfc:13.7:14.1) (ec:) (yjcu_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3971 ECOLI_3971 Escherichia coli 562 10055382

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866681	12797	34953	375	124

Description

6500732288 yjcv:b4086 hypothetical 34.3 kd protein in fdhf-phnp intergenic region:hypothetical abc transporter permease protein yjcv (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4086 b4086 Escherichia coli 562 -11536146 113655 yjcv (de:hypothetical abc transporter permease protein yjcv) (db:swissprot) YJCV_ECOLI P32720 ESCHERICHIA COLI 562 -11536146 7000688093 yjcv probable sugar transport permease protein b4086 (cl:l-arabinose transport system permease arah) (db:pir2.dat) E65217 E65217 Escherichia coli 562 -11536146 237292 yjcv putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f326; 100 pct identical to yjcv_ecoli sw:) (le:4137) (re:5117) (di:complement) AE000482 AE000482 g1790524 Escherichia coli 562 -11536146 7500937916 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to e. coli high affinity ribose transport) (le:173728) (re:174708) (di:complement) ECOUW89 U00006 g396421 Escherichia coli 562 -11536146 5000693878 (de:(ecoli_3972) (pn:hypothetical 34) (gn:yjcv) (gtcfc:13.7:14.1) (ec:) (yjcv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3972 ECOLI_3972 Escherichia coli 562 10055383

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866684	12798	34954	438	145

Description

6500732289 yjcw:b4087 hypothetical abc transporter in fdhf-phnp intergenic region:hypothetical abc transporter atp-binding protein in fdhf-phnp intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4087 b4087 Escherichia coli 562 -11536147 113656 yjcw (de:hypothetical abc transporter atp-binding protein yjcw) (db:swissprot) YJCW_ECOLI P32721 ESCHERICHIA COLI 562 -11536147 163504 yjcw hypothetical abc transporter fdhf-phnp intergenic region:hypothetical protein 510 (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) S56315 S56315 Escherichia coli 562 -11536147 7500937917 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f510) (le:377) (re:1909) (di:complement) ECOUW93 U14003 g536931 Escherichia coli 562 -11536147 237295 yjcw putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f510; 100 pct identical to yjcw_ecoli sw:) (le:5096) (re:6628) (di:complement) AE000482 AE000482 g1790525 Escherichia coli 562 -11536147 5000693879 (de:(ecoli_3973) (pn:hypothetical abc transporter atp-binding protein in fdhf-phnp intergenic region:f510) (gn:yjcw) (gtcfc:13.7:14.1) (ec:) (yjcw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3973 ECOLI_3973 Escherichia coli 562 10055384

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866687	12799	34955	846	281

Description

6500732290 yjcx:b4088 hypothetical 32.9 kd protein in fdhf-phnp intergenic region:hypothetical 32.9 kd protein in fdhf-rpib intergenic region precursor:orf3 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4088 b4088 Escherichia coli 562 -11536148 113657 yjcx (de:precursor) (db:swissprot) YJCX_ECOLI P39265 ESCHERICHIA COLI 562 -11536148 163632 yjcx hypothetical 32.9k protein fdhf-phnp intergenic region:hypothetical protein f311 (db:pir2.dat) S56316 S56316 Escherichia coli 562 -11536148 7500937918 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f311) (le:2036) (re:2971) (di:complement) ECOUW93 U14003 g536932 Escherichia coli 562 -11536148 237296 yjcx putative lacI-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f311; 100 pct identical amino acid sequence and) (le:6755) (re:7690) (di:complement) AE000482 AE000482 g1790526 Escherichia coli 562 -11536148 5000693880 (de:(ecoli_3974) (pn:hypothetical 32) (gn:yjcx) (gtcfc:13.7:14.1) (ec:) (yjcx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3974 ECOLI_3974 Escherichia coli 562 10055385

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866692	12800	34956	516	171

Description

6500732291 rpir:b4089 hypothetical 33.5 kd protein in fdhf-phnp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4089 b4089 Escherichia coli 562 -11536149 163628 rpir rpir protein:hypothetical protein f307 (db:pir2.dat) S56317 S56317 Escherichia coli 562 -11536149 7500960454 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f307) (le:3030) (re:3953) (di:complement) ECOUW93 U14003 g536933 Escherichia coli 562 -11536149 237297 rpir transcriptional repressor of rpib expression (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f307; 100 pct identical amino acid sequence and) (le:7749) (re:8672) (di:complement) AE000482 AE000482 g1790527 Escherichia coli 562 -11536149 5000693881 (de:(ecoli_3975) (pn:rpir protein) (gn:rpir) (gtcfc:13.7:14.1) (ec:) (rpir_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3975 ECOLI_3975 Escherichia coli 562 10087015

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866693	12801	34957	669	222

Description

5000693883 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4103 b4103 Escherichia coli 562 -11536150 237311 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f73) (le:13371) (re:13592) (di:complement) ECOUW93 U14003 g536947 Escherichia coli 562 -11536150 7500974871 b4103 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f73; 98 pct identical to 73 c-terminal residues) (le:18090) (re:18311) (di:complement) AE000482 AE000482 g1790541 Escherichia coli 562 -11536150 6500732292 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4103 b4103 Escherichia coli 562 -11536150 154760 (de:hypothetical protein f73 - escherichia coli) S56331 S56331 Escherichia coli 562 -11536150

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866705	12802	34958	213	70

Description

6500732293 yjda:b4109 hypothetical 84.2 kd protein in phna-prop intergenic region:orf742 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4109 b4109 Escherichia coli 562 -11536151 113665 yjda (de:hypothetical 84.2 kd protein in phna-prop intergenic region (orf742)) (db:swissprot) YJDA_ECOLI P16694 ESCHERICHIA COLI 562 -11536151 164855 yjda hypothetical 84.2k protein phna-prop intergenic region:hypothetical protein 742:yjda protein (db:pir2.dat) S56337 S56337 Escherichia coli 562 -11536151 7500937931 yjda (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf of genbank accession number j05260) (le:17964) (re:20192) (di:direct) ECOUW93 U14003 g536953 Escherichia coli 562 -11536151 237317 yjda putative vimentin (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 373 of 400 of the completegenome.) (nt:o742; 100 pct identical amino acid sequence and) (le:1934) (re:4162) (di:direct) AE000483 AE000483 gl790548 Escherichia coli 562 -11536151 5000693886 (de:(ecoli_3995) (pn:hypothetical 84) (gn:yjda) (gtcfc:13.7:14.1) (ec:) (yjda_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3995 ECOLI_3995 Escherichia coli 562 10055393

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866711	12803	34959	279	92

Description

6500732294 yjcz:b4110 hypothetical 31.8 kd protein in phna-prop intergenic region:o281 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4110 b4110 Escherichia coli 562 -11536152 113658 yjcz (de:hypothetical 31.8 kd protein in phna-prop intergenic region (o281)) (db:swissprot) YJCZ_ECOLI P39267 ESCHERICHIA COLI 562 -11536152 163792 yjcz hypothetical 31.8k protein phna-prop intergenic region:hypothetical protein o281 (db:pir2.dat) S56338 S56338 Escherichia coli 562 -11536152 7500937919 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o281) (le:20222) (re:21067) (di:direct) ECOUW93 U14003 g536954 Escherichia coli 562 -11536152 237318 yjcz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 373 of 400 of the completegenome.) (nt:o281; 100 pct identical amino acid sequence and) (le:4192) (re:5037) (di:direct) AE000483 AE000483 gl790549 Escherichia coli 562 -11536152 5000693887 (de:(ecoli_3996) (pn:hypothetical 31) (gn:yjcz) (gtcfc:13.7:14.1) (ec:) (yjcz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3996 ECOLI_3996 Escherichia coli 562 10055386

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866712	12804	34960	1173	390

Description

6500732295 yjdb:b4114 hypothetical 61.7 kd protein in bass-adiy intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4114 b4114 Escherichia coli 562 -11536153 164856 yjdb hypothetical 61.7k protein bass-adiy intergenic region:yidb protein (db:pir2.dat) S56342 S56342 Escherichia coli 562 -11536153 7500959823 yjdb (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:24776) (re:26449) (di:complement) ECOUW93 U14003 g536958 Escherichia coli 562 -11536153 237322 yjdb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 373 of 400 of the completegenome.) (nt:f557; 100 pct identical to 547 amino acids of) (le:8746) (re:10419) (di:complement) AE000483 AE000483 g1790553 Escherichia coli 562 -11536153 5000693888 (de:(ecoli_4000) (pn:hypothetical 61) (gn:yjdb) (gtcfc:13.7:14.1) (ec:) (yjdb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4000 ECOLI_4000 Escherichia coli 562 10087490

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866764	12805	34961	660	219

Description

6500732296 hypothetical 46.8 kd protein in bass-adiy intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b4115 b4115 Escherichia coli 562 -11536154 7500937933 yjde (de:hypothetical 46.8 kd protein in bass-adiy intergenic region) (db:swissprot) YJDE_ECOLI P39269 ESCHERICHIA COLI 562 -11536154 7000690948 hypothetical 46.8 kd protein in bass-adiy intergenic region:hypothetical protein f326a (cl:l-lysine transport protein) (db:pir2.dat) B65221 B65221 Escherichia coli 562 -11536154 7500937935 yjde putative amino acid/amine transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 374 of 400 of the completegenome.) (nt:f445; sequence change joins orfs yjde and yjdd from) (le:67) (re:1404) (di:complement) AE000484 AE000484 g2367353 Escherichia coli 562 -11536154

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866769	12806	34962	318	105

Description

6500732297 yjdf:b4121 hypothetical 23.4 kd protein in melb-fumb intergenic region:f209 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4121 b4121 Escherichia coli 562 -11536155 113671 yjdf (de:hypothetical 23.4 kd protein in melb-fumb intergenic region (f209)) (db:swissprot) YJDF_ECOLI P39270 ESCHERICHIA COLI 562 -11536155 163587 yjdf hypothetical 23.4k protein melb-fumb intergenic region:hypothetical protein f209 (db:pir2.dat) S56350 S56350 Escherichia coli 562 -11536155 7500937936 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f209) (le:35757) (re:36386) (di:complement) ECOUW93 U14003 g536966 Escherichia coli 562 -11536155 237330 yjdf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 374 of 400 of the completegenome.) (nt:f209; 100 pct identical amino acid sequence and) (le:9302) (re:9931) (di:complement) AE000484 AE000484 g1790562 Escherichia coli 562 -11536155 5000693891 (de:(ecoli_4008) (pn:hypothetical 23) (gn:yjdf) (gtcfc:13.7:14.1) (ec:) (yjdf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4008 ECOLI_4008 Escherichia coli 562 10055399

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866775	12807	34963	2499	833

Description

GTC ORF with score 1503 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid c50f2.) (nt:coded for by c. elegans cdna yk13g5.3; coded for by) (le:771:884:1049:1753:2314) (re:836:1003:1705:1925:3089) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866790	12808	34964	258	85

Description

6500732298 yjdg:b4124 hypothetical 27.4 kd protein in dcub-lysu intergenic region:f239 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4124 b4124 Escherichia coli 562 -11536156 113672 dcur (de:transcriptional regulatory protein dcur) (db:swissprot) DCUR_ECOLI P39271 ESCHERICHIA COLI 562 -11536156 7000688094 yjdg hypothetical 27.4 kd protein in dcub-lysu intergenic region:hypothetical protein f239 (cl:transcription regulator crir:response regulator homology) (db:pir2.dat) C65222 C65222 Escherichia coli 562 -11536156 7500937937 yjdg putative 2-component transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 375 of 400 of the completegenome.) (nt:f239; 100 pct identical amino acid sequence and) (le:3726) (re:4445) (di:complement) AE000485 AE000485 g1790566 Escherichia coli 562 -11536156 5000693892 (de:(ecoli_4011) (pn:hypothetical 27) (gn:yjdg) (gtcfc:13.7:14.1) (ec:) (yjdg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4011 ECOLI_4011 Escherichia coli 562 10124151

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866799	12809	34965	306	101

Description

6500732299 yjdh:b4125 hypothetical 60.6 kd protein in dcub-lysu intergenic region:f543 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4125 b4125 Escherichia coli 562 -11536157 113673 dcus (ec:2.7.3.-) (de:sensor protein dcus,) (db:swissprot) DCUS_ECOLI P39272 ESCHERICHIA COLI 562 -11536157 7000688095 yjdh hypothetical 60.6 kd protein in dcub-lysu intergenic region:hypothetical protein f543 (cl:two-component sensor histidine kinase:sensor histidine kinase homology) (db:pir2.dat) D65222 D65222 Escherichia coli 562 -11536157 7500937938 yjdh putative 2-component sensor protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 375 of 400 of the completegenome.) (nt:f543; 100 pct identical amino acid sequence and) (le:4442) (re:6073) (di:complement) AE000485 AE000485 g1790567 Escherichia coli 562 -11536157 5000693893 (de:(ecoli_4012) (pn:hypothetical 60) (gn:yjdh) (gtcfc:13.7:14.1) (ec:) (yjdh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4012 ECOLI_4012 Escherichia coli 562 10124152

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866833	12810	34966	393	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866844	12811	34967	774	257

Description

6500732300 yjdi:b4126 hypothetical 8.6 kd protein in dcub-lysu intergenic region:o76 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4126 b4126 Escherichia coli 562 -11536158 113674 yjdi (de:hypothetical 8.6 kd protein in dcub-lysu intergenic region (o76)) (db:swissprot) YJDI_ECOLI P39273 ESCHERICHIA COLI 562 -11536158 163869 yjdi hypothetical 8.6k protein dcub-lysu intergenic region:hypothetical protein o76 (db:pir2.dat) S56355 S56355 Escherichia coli 562 -11536158 7500937939 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o76) (le:42671) (re:42901) (di:direct) ECOUW93 U14003 g536971 Escherichia coli 562 -11536158 237335 yjdi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 375 of 400 of the completegenome.) (nt:o76; 100 pct identical amino acid sequence and) (le:6254) (re:6484) (di:direct) AE000485 AE000485 gl790568 Escherichia coli 562 -11536158 5000693894 (de:(ecoli_4013) (pn:hypothetical 8) (gn:yjdi) (gtcfc:13.7:14.1) (ec:) (yjdi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4013 ECOLI_4013 Escherichia coli 562 10055402

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866856	12812	34968	540	179

Description

GTC ORF with score 347 to: (fn:required for o-glycosylation) (db:genpept-pln2) (de:candida albicans protein mannosyltransferase 1 (pmt1) gene,complete cds.) (nt:similar to saccharomyces cerevisiae pmt1p,) (le:151) (re:2784) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866861	12813	34969	543	180

Description

6500732301 yjdj:b4127 hypothetical 10.5 kd protein in dcub-lysu intergenic region:o90a (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4127 b4127 Escherichia coli 562 -11536159 113675 yjdj (de:hypothetical 10.5 kd protein in dcub-lysu intergenic region (o90a)) (db:swissprot) YJDJ_ECOLI P39274 ESCHERICHIA COLI 562 -11536159 163876 yjdj hypothetical 10.5k protein dcub-lysu intergenic region:hypothetical protein o90a (db:pir2.dat) S56356 S56356 Escherichia coli 562 -11536159 7500937940 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o90a) (le:42913) (re:43185) (di:direct) ECOUW93 U14003 g536972 Escherichia coli 562 -11536159 237336 yjdj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 375 of 400 of the completegenome.) (nt:o90a; 100 pct identical amino acid sequence and) (le:6496) (re:6768) (di:direct) AE000485 AE000485 g1790569 Escherichia coli 562 -11536159 5000693895 (de:(ecoli_4014) (pn:hypothetical 10) (gn:yjdj) (gtcfc:13.7:14.1) (ec:) (yjdj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4014 ECOLI_4014 Escherichia coli 562 10055403

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866866	12814	34970	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866867	12815	34971	420	139

Description

6500732302 yjdk:b4128 hypothetical 11.5 kd protein in dcub-lysu intergenic region:o98 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4128 b4128 Escherichia coli 562 -11536160 113676 yjdk (de:hypothetical 11.5 kd protein in dcub-lysu intergenic region (o98)) (db:swissprot) YJDK_ECOLI P39275 ESCHERICHIA COLI 562 -11536160 163879 yjdk hypothetical 11.5k protein dcub-lysu intergenic region:hypothetical protein o98 (db:pir2.dat) S56357 S56357 Escherichia coli 562 -11536160 7500937941 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o98) (le:43412) (re:43708) (di:direct) ECOUW93 U14003 g536973 Escherichia coli 562 -11536160 237337 yjdk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 375 of 400 of the completegenome.) (nt:o98; 100 pct identical amino acid sequence and) (le:6995) (re:7291) (di:direct) AE000485 AE000485 g1790570 Escherichia coli 562 -11536160 5000693896 (de:(ecoli_4015) (pn:hypothetical 11) (gn:yjdk) (gtcfc:13.7:14.1) (ec:) (yjdk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4015 ECOLI_4015 Escherichia coli 562 10055404

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866885	12816	34972	738	245

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866888	12817	34973	483	160

Description

GTC ORF with score 93 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid w02b8, complete sequence.) (nt:predicted using genefinder; similar to domain found) (le:8430:9219:10860:12131) (re:8510:10118:11888:12967) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866907	12818	34974	1662	553

Description

6500732303 yjdl:b4130 hypothetical protein:hypothetical 53.1 kd protein in lysu-cada intergenic region:f485 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4130 b4130 Escherichia coli 562 -11536161 113677 yjdl (de:hypothetical 53.1 kd protein in lysu-cada intergenic region) (db:swissprot) YJDL_ECOLI P39276 ESCHERICHIA COLI 562 -11536161 163671 yjdl probable proton/oligopeptide symporter yjdl:protein f485 (cl:peptide transporter protein) (db:pir2.dat) S56359 S56359 Escherichia coli 562 -11536161 7500937942 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f485) (le:45782) (re:47239) (di:complement) ECOUW93 U14003 g536975 Escherichia coli 562 -11536161 237339 yjdl putative peptide transporter (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 375 of 400 of the completegenome.) (nt:f485) (le:9365) (re:10822) (di:complement) AE000485 AE000485 g1790572 Escherichia coli 562 -11536161 5000693897 (de:(ecoli_4017) (pn:hypothetical 53) (gtcfc:13.7:14.1) (ec:) (yjdl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4017 ECOLI_4017 Escherichia coli 562 10055405

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866908	12819	34975	654	217

Description

GTC ORF with score 123 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome ii bac t28m21 genomic sequence,complete sequence.) (nt:unknown protein) (le:97328:98826:99416) (re:98518:98940:99530) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866912	12820	34976	747	248

Description

5000693901 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4140 b4140 Escherichia coli 562 -11536162 163721 hypothetical protein b4140:hypothetical protein aspa 5 region:hypothetical protein o125 (db:pir2.dat) (mp:94 min) S56368 S56368 Escherichia coli 562 -11536162 7500960324 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o125) (le:59591) (re:59968) (di:direct) ECOUW93 U14003 g536984 Escherichia coli 562 -11536162 237348 b4140 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.) (nt:o125) (le:253) (re:630) (di:direct) AE000487 AE000487 g1790583 Escherichia coli 562 -11536162 6500732304 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4140 b4140 Escherichia coli 562 -11536162

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866914	12821	34977	504	167

Description

GTC ORF with score 130 to: (fn:possibly involved in regulating granaticin) (db:genpept) (de:streptomyces violaceoruber tu22 granaticin biosynthetic genecluster.) (nt:contains possible cxxc motif) (le:15846) (re:16508) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866917	12822	34978	501	167

Description

6500732305 yjeh:b4141 hypothetical 44.8 kd protein in aspa-mopb intergenic region:f418 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4141 b4141 Escherichia coli 562 -11536163 113690 yjeh (de:hypothetical 44.8 kd protein in aspa-mopb intergenic region (f418)) (db:swissprot) YJEH_ECOLI P39277 ESCHERICHIA COLI 562 -11536163 163660 yjeh hypothetical 44.8k protein aspa-mopb intergenic region:hypothetical protein f418 (db:pir2.dat) S56369 S56369 Escherichia coli 562 -11536163 7500937957 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f418) (le:59984) (re:61240) (di:complement) ECOUW93 U14003 g536985 Escherichia coli 562 -11536163 237349 yjeh putative transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.) (nt:f418; 100 pct identical amino acid sequence and) (le:646) (re:1902) (di:complement) AE000487 AE000487 g1790584 Escherichia coli 562 -11536163 5000693902 (de:(ecoli_4027) (pn:hypothetical 44) (gn:yjeh) (gtcfc:13.7:14.1) (ec:) (yjeh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4027 ECOLI_4027 Escherichia coli 562 10055418

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866926	12823	34979	510	170

Description

GTC ORF with score 247 to: (sr:mice macrophage) (db:genpept-rod) (de:putative transcription regulator {clone t2, repetitive sequence}(mice, macrophage, mrna, 1263 nt).) (nt:method: conceptual translation supplied by author.) (le:55) (re:732) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866934	12824	34980	513	171

Description

GTC ORF with score 273 to: (sr:mice macrophage) (db:genpept-rod)
(de:putative transcription regulator {clone t2, repetitive sequence}(mice, macrophage, mrna, 1263 nt).) (nt:method: conceptual translation supplied by author.) (le:55) (re:732) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866935	12825	34981	489	162

Description

6500732306 yjei:b4144 hypothetical protein:hypothetical 13.1 kd protein in mopa-efp intergenic region precursor:o128 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4144 b4144 Escherichia coli 562 -11536164 113691 yjei (de:(o128)) (db:swissprot) YJEI_ECOLI P39278
ESCHERICHIA COLI 562 -11536164 163724 hypothetical protein o128:hypothetical protein b4144 (db:pir2.dat) S56372 S56372 Escherichia coli 562 -11536164 7500937958 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o128) (le:63604) (re:63990) (di:direct) ECOUW93 U14003 g536988 Escherichia coli 562 -11536164 237352 yjei orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.) (nt:o128) (le:4266) (re:4652) (di:direct) AE000487 AE000487 g1790587 Escherichia coli 562 -11536164 5000693903 (de:(ecoli_4030) (pn:hypothetical 13) (gtcfc:13.7:14.1) (ec:) (yjei_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4030 ECOLI_4030 Escherichia coli 562 10055419

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866939	12826	34982	492	163

Description

6500732307 yjej:b4145 hypothetical 32.9 kd protein in mopa-efp intergenic region:f289 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4145 b4145 Escherichia coli 562 -11536165 113692 yjej (de:hypothetical 32.9 kd protein in mopa-efp intergenic region (f289)) (db:swissprot) YJEJ_ECOLI P39279 ESCHERICHIA COLI 562 -11536165 163623 yjej hypothetical 32.9k protein mopa-efp intergenic region:hypothetical protein f289 (db:pir2.dat) S56373 S56373 Escherichia coli 562 -11536165 7500937959 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f289) (le:64193) (re:65062) (di:complement) ECOUW93 U14003 g536989 Escherichia coli 562 -11536165 237353 yjej orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.) (nt:f289; 100 pct identical amino acid sequence and) (le:4855) (re:5724) (di:complement) AE000487 AE000487 g1790588 Escherichia coli 562 -11536165 5000693904 (de:(ecoli_4031) (pn:hypothetical 32) (gn:yjej) (gtcfc:13.7:14.1) (ec:) (yjej_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4031 ECOLI_4031 Escherichia coli 562 10055420

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866943	12827	34983	534	177

Description

GTC ORF with score 178 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone f4d11 (essaiiproject).) (nt:similarity to protein kinase tmk1, arabidopsis) (le:33819:34133:34431) (re:34034:34294:34578) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501866944	12828	34984	1956	651

Description

6500732308 yjek:b4146 hypothetical 38.7 kd protein in mopa-efp intergenic region:f342 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4146 b4146 Escherichia coli 562 -11536166 113693 yjek (de:hypothetical 38.7 kd protein in mopa-efp intergenic region) (db:swissprot) YJEK_ECOLI P39280 ESCHERICHIA COLI 562 -11536166 163640 yjek hypothetical 38.7k protein mopa-efp intergenic region:hypothetical protein f342 (cl:conserved hypothetical protein yodo) (db:pir2.dat) S56374 S56374 Escherichia coli 562 -11536166 7500937960 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f342) (le:65457) (re:66485) (di:complement) ECOUW93 U14003 g536990 Escherichia coli 562 -11536166 237354 yjek orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.) (nt:f342; 100 pct identical amino acid sequence and) (le:6119) (re:7147) (di:complement) AE000487 AE000487 g1790589 Escherichia coli 562 -11536166 5000693905 (de:(ecoli_4032) (pn:hypothetical 38) (gn:yjek) (gtcfc:13.7:14.1) (ec:) (yje_k_e_coli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4032 ECOLI_4032 Escherichia coli 562 10055421

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866955	12829	34985	750	250

Description

6500732309 blc:b4149 hypothetical 19.9 kd protein in suge-ampc intergenic region:outer membrane lipoprotein precursor (gtcfc:14.3:11.2) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4149 b4149 Escherichia coli 562 -11536167 61819 blc (de:outer membrane lipoprotein blc precursor) (db:swissprot) BLC_ECOLI P39281 ESCHERICHIA COLI 562 -11536167 164213 blc outer membrane 19.9k lipoprotein suge-ampc intergenic region (cl:lipocalin:lipocalin homology) (db:pir2.dat) I84534 I84534 Escherichia coli 562 -11536167 238770 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f177) (le:68017) (re:68550) (di:complement) ECOUW93 U14003 g536993 Escherichia coli 562 -11536167 237357 blc outer membrane lipoprotein lipocalin (fn:membrane; macromolecule synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.) (nt:f177; 100 pct identical amino acid sequence and) (le:8679) (re:9212) (di:complement) AE000487 AE000487 g1790592 Escherichia coli 562 -11536167 7500877850 blc lipocalin precursor (db:genpept-bct2) (de:escherichia coli lipocalin precursor (blc), suge (suge), entericidin b precursor (ecnb), and entericidin a precursor (ecna)genes, complete cds.) (nt:blc) (le:59) (re:592) (di:direct) ECU21726 U21726 g717134 Escherichia coli 562 -11536167 5000693908 (de:(ecoli_4035) (pn:outer membrane lipoprotein precursor) (gn:blc) (gtcfc:13.7:14.1) (ec:) (blc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4035 ECOLI_4035 Escherichia coli 562 10004525

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866958	12830	34986	393	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866969	12831	34987	705	234

Description

GTC ORF with score 231 to: (fn:putative catabolite gene activator protein) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f237; alternate name yggc; orf3 of x14436) (le:28367) (re:29080) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501866994	12832	34988	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867002	12833	34989	210	70

Description

6500732310 yjem:b4156 hypothetical 56.3 kd protein in genx-psd intergenic region:o514 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4156 b4156 Escherichia coli 562 -11536168 113695 yjem (de:hypothetical 56.3 kd protein in genx-psd intergenic region (o514)) (db:swissprot) YJEM_ECOLI P39282 ESCHERICHIA COLI 562 -11536168 163855 yjem hypothetical 56.3k protein genx-psd intergenic region:hypothetical protein o514 (db:pir2.dat) S56384 S56384 Escherichia coli 562 -11536168 7500937962 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o514) (le:74625) (re:76169) (di:direct) ECOUW93 U14003 g537000 Escherichia coli 562 -11536168 237364 yjem putative transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 378 of 400 of the completegenome.) (nt:o514; 100 pct identical amino acid sequence and) (le:1456) (re:3000) (di:direct) AE000488 AE000488 g1790600 Escherichia coli 562 -11536168 5000693909 (de:(ecoli_4042) (pn:hypothetical 56) (gn:yjem) (gtcfc:13.7:14.1) (ec:) (yjem_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4042 ECOLI_4042 Escherichia coli 562 10055423

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867023	12834	34990	195	64

Description

6500732311 yjen:b4157 hypothetical 11.8 kd protein in genx-psd intergenic region:o104a (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4157 b4157 Escherichia coli 562 -11536169 113696 yjen (de:hypothetical 11.8 kd protein in genx-psd intergenic region (o104a)) (db:swissprot) YJEN_ECOLI P39283 ESCHERICHIA COLI 562 -11536169 163709 yjen hypothetical 11.8k protein genx-psd intergenic region:hypothetical protein o104a (db:pir2.dat) S56385 S56385 Escherichia coli 562 -11536169 7500937963 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o104a) (le:76221) (re:76535) (di:direct) ECOUW93 U14003 g537001 Escherichia coli 562 -11536169 237365 yjen orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 378 of 400 of the completegenome.) (nt:o104a; 100 pct identical amino acid sequence and) (le:3052) (re:3366) (di:direct) AE000488 AE000488 g1790601 Escherichia coli 562 -11536169 5000693910 (de:(ecoli_4043) (pn:hypothetical 11) (gn:yjen) (gtcfc:13.7:14.1) (ec:) (yjen_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4043 ECOLI_4043 Escherichia coli 562 10055424

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867030	12835	34991	354	117

Description

6500732312 yjeo:b4158 hypothetical 12.6 kd protein in genx-psd intergenic region:ol04b (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4158 b4158 Escherichia coli 562 -11536170 113697 yjeo (de:hypothetical 12.6 kd protein in genx-psd intergenic region (ol04b)) (db:swissprot) YJEO_ECOLI P39284 ESCHERICHIA COLI 562 -11536170 163710 yjeo hypothetical 12.6k protein genx-psd intergenic region:hypothetical protein ol04b (db:pir2.dat) S56386 S56386 Escherichia coli 562 -11536170 7500937964 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_ol04b) (le:76532) (re:76846) (di:direct) ECOUW93 U14003 g537002 Escherichia coli 562 -11536170 237366 yjeo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 378 of 400 of the completegenome.) (nt:ol04b; 100 pct identical amino acid sequence and) (le:3363) (re:3677) (di:direct) AE000488 AE000488 g1790602 Escherichia coli 562 -11536170 5000693911 (de:(ecoli_4044) (pn:hypothetical 12) (gn:yjeo) (gtcfc:13.7:14.1) (ec:) (yjeo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4044 ECOLI_4044 Escherichia coli 562 10055425

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867031	12836	34992	324	107

Description

6500732313 yjep:b4159 hypothetical 123.8 kd protein in genx-psd intergenic region:hypothetical 123.8 kd protein in genx-psd intergenic region precursor:f1107 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4159 b4159 Escherichia coli 562 -11536171 7500937965 yjep (de:hypothetical 123.8 kd protein in genx-psd intergenic region precursor) (db:swissprot) YJEP_ECOLI P39285 ESCHERICHIA COLI 562 -11536171 7000690910 yjep hypothetical 123.8 kd protein in genx-psd intergenic region:hypothetical protein f1107 (db:pir2.dat) E65226 E65226 Escherichia coli 562 -11536171 7500937967 yjep putative periplasmic binding protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 378 of 400 of the completegenome.) (nt:f1107; 99 pct identical to yjep_ecoli sw: p39285) (le:3706) (re:7029) (di:complement) AE000488 AE000488 g2367355 Escherichia coli 562 -11536171

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867039	12837	34993	258	85

Description

6500732314 yjeq:b4161 hypothetical 37.7 kd protein in psd-amib intergenic region:f337 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4161 b4161 Escherichia coli 562 -11536172 163639 yjeq hypothetical 37.7k protein psd-amib intergenic region:hypothetical protein f337 (cl:conserved hypothetical protein hi1714) (db:pir2.dat) S56389 S56389 Escherichia coli 562 -11536172 7500937969 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f337) (le:81285) (re:82298) (di:complement) ECOUW93 U14003 g537005 Escherichia coli 562 -11536172 237369 yjeq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 378 of 400 of the completengenome.) (nt:f337; 100 pct identical amino acid sequence and) (le:8116) (re:9129) (di:complement) AE000488 AE000488 g1790605 Escherichia coli 562 -11536172 113699 yjeq (de:hypothetical 37.7 kd protein in psd-amib intergenic region (f337)) (db:swissprot) YJEQ_ECOLI P39286 ESCHERICHIA COLI 562 -11536172 5000693913 (de:(ecoli_4047) (pn:hypothetical 37) (gn:yjeq) (gtcfc:13.7:14.1) (ec:) (yjeq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4047 ECOLI_4047 Escherichia coli 562 10055427

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867040	12838	34994	675	225

Description

6500732315 yjer:b4162 hypothetical 23.5 kd protein in psd-amib intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4162 b4162 Escherichia coli 562 -11536173 163760 yjer hypothetical 23.5k protein psd-amib intergenic region:hypothetical protein o204a (db:pir2.dat) S56390 S56390 Escherichia coli 562 -11536173 7500959799 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o204a) (le:82363) (re:82977) (di:direct) ECOUW93 U14003 g537006 Escherichia coli 562 -11536173 237370 yjer orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 378 of 400 of the completengenome.) (nt:o204a; 100 pct identical amino acid sequence and) (le:9194) (re:9808) (di:direct) AE000488 AE000488 g1790606 Escherichia coli 562 -11536173 5000693914 (de:(ecoli_4048) (pn:20) (gn:yjer) (gtcfc:13.7:14.1) (ec:) (yjer_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4048 ECOLI_4048 Escherichia coli 562 10087041

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867048	12839	34995	657	218

Description

6500732316 yjes:b4166 hypothetical 43.1 kd protein in psd-amib intergenic region:f379 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4166 b4166 Escherichia coli 562 -11536174 113703 yjes (de:hypothetical 43.1 kd protein in psd-amib intergenic region (f379)) (db:swissprot) YJES_ECOLI P39288 ESCHERICHIA COLI 562 -11536174 163649 yjes hypothetical 43.1k protein psd-amib intergenic region:hypothetical protein f379 (db:pir2.dat) S56391 S56391 Escherichia coli 562 -11536174 7500937971 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f379) (le:83756) (re:84895) (di:complement) ECOUW93 U14003 g537007 Escherichia coli 562 -11536174 237371 yjes orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 379 of 400 of the completegenome.) (nt:f379; 100 pct identical amino acid sequence and) (le:642) (re:1781) (di:complement) AE000489 AE000489 g1790608 Escherichia coli 562 -11536174 5000693915 (de:(ecoli_4049) (pn:hypothetical 43) (gn:yjes) (gtcfc:13.7:14.1) (ec:) (yjes_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4049 ECOLI_4049 Escherichia coli 562 10055431

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867054	12840	34996	969	323

Description

GTC ORF with score 134 to: (sr:information) (db:genpept) (de:homo sapiens pac clone dj0733b09 from 7p14-p13, complete sequence.) (nt:supported by genscan prediction and spliced est;) (le:<47312:51695) (re:47979:>51929) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867065	12841	34997	450	149

Description

6500732317 yjef:b4167 hypothetical 54.7 kd protein in psd-amib intergenic region:urf1 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4167 b4167 Escherichia coli 562 -11536175 113687 yjef (de:hypothetical 54.7 kd protein in psd-amib intergenic region (urf1)) (db:swissprot) YJEF_ECOLI P31806 ESCHERICHIA COLI 562 -11536175 163856 yjef hypothetical 54.7k protein psd-amib intergenic region:hypothetical protein o515 (db:pir2.dat) S56392 S56392 Escherichia coli 562 -11536175 7500937956 yjef (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:84894) (re:86441) (di:direct) ECOUW93 U14003 g537008 Escherichia coli 562 -11536175 237372 yjef orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 379 of 400 of the completgenome.) (nt:o515; 100 pct identical amino acid sequence and) (le:1780) (re:3327) (di:direct) AE000489 AE000489 g1790609 Escherichia coli 562 -11536175 5000693916 (de:(ecoli_4050) (pn:hypothetical 54) (gn:yjef) (gtcfc:13.7:14.1) (ec:) (yjef_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4050 ECOLI_4050 Escherichia coli 562 10055415

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867069	12842	34998	1434	478

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867085	12843	34999	1215	404

Description

6500732318 yjee:b4168 hypothetical 16.9 kd protein in psd-amib intergenic region:hypothetical 16.9 kd protein in psd-amib intergenic region precursor:urf2 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4168 b4168 Escherichia coli 562 -11536176 113685 yjee (de:(urf2)) (db:swissprot) YJEE_ECOLI P31805 ESCHERICHIA COLI 562 -11536176 163739 yjee hypothetical 16.9k protein psd-amib intergenic region:hypothetical protein o153a (cl:hypothetical protein hi0065) (db:pir2.dat) S56393 S56393 Escherichia coli 562 -11536176 237373 (fn:unknown) (sr:escherichia coli (strain k-12) (library: clarke-carbon) dna) (db:genpept-bct1) (de:escherichia coli n-acetylmuramoyl-l-alanine amidase (amib) gene,complete cds, dna repair protein (mutl) gene, partial cds, and twounidentified cds's.) (... ECOMUTL L19346 g304913 Escherichia coli 562 -11536176 7500937954 yjee (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:urf2 of genbank accession number l19346) (le:86413) (re:86874) (di:direct) ECOUW93 U14003 g537009 Escherichia coli 562 -11536176 235204 yjee orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 379 of 400 of the completegenome.) (nt:o153a; 100 pct identical amino acid sequence and) (le:3299) (re:3760) (di:direct) AE000489 AE000489 g1790610 Escherichia coli 562 -11536176 5000693917 (de:(ecoli_4051) (pn:hypothetical 16) (gn:yjee) (gtcfc:13.7:14.1) (ec:) (yjee_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4051 ECOLI_4051 Escherichia coli 562 10055413

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867089	12844	35000	429	142

Description

6500732319 yjet:b4176 hypothetical protein:hypothetical 7.2 kd protein in hflc-pura intergenic region:o65 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4176 b4176 Escherichia coli 562 -11536177 113704 yjet (de:hypothetical 7.2 kd protein in hflc-pura intergenic region (o65)) (db:swissprot) YJET_ECOLI P39289 ESCHERICHIA COLI 562 -11536177 163865 hypothetical protein b4176:hypothetical protein o65 (db:pir2.dat) S56401 S56401 Escherichia coli 562 -11536177 7500937972 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o65) (le:95214) (re:95411) (di:direct) ECOUW93 U14003 g537017 Escherichia coli 562 -11536177 237381 yjet orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:o65) (le:70) (re:267) (di:direct) AE000490 AE000490 g1790619 Escherichia coli 562 -11536177 5000693918 (de:(ecoli_4059) (pn:hypothetical 7) (gtcfc:13.7:14.1) (ec:) (yjet_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4059 ECOLI_4059 Escherichia coli 562 10055432

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867091	12845	35001	687	228

Description

6500732320 yjeb:b4178 hypothetical 15.6 kd protein in pura-vacb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4178 b4178 Escherichia coli 562 -11536178 113683 yjeb (de:hypothetical 15.6 kd protein in pura-vacb intergenic region) (db:swissprot) YJEB_ECOLI P21498 ESCHERICHIA COLI 562 -11536178 163733 yjeb hypothetical 15.6k protein pura-vacb intergenic region:hypothetical protein o141 (cl:hypothetical protein b2531) (db:pir2.dat) (mp:95 min) S56403 S56403 Escherichia coli 562 -11536178 260700 yjeb (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:97018) (re:97443) (di:direct) ECOUW93 U14003 g537019 Escherichia coli 562 -11536178 7500937953 orf-1 (sr:shigella flexneri (sub_species:2a) dna) (db:genpept-bct1) (de:shigella flexneri vacb gene.) (le:210) (re:635) (di:direct) SHFVACB D11024 g912442 Shigella flexneri 623 -11536178 237383 yjeb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:o141; 100 pct identical amino acid sequence and) (le:1874) (re:2299) (di:direct) AE000490 AE000490 g1790621 Escherichia coli 562 -11536178 5000693919 (de:(ecoli_4061) (pn:hypothetical 15) (gn:yjeb) (gtcfc:13.7:14.1) (ec:) (yjeb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4061 ECOLI_4061 Escherichia coli 562 10055411

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867092	12846	35002	723	240

Description

6500732321 yjfh:b4180 hypothetical 26.6 kd protein in vacb-aidb intergenic region:o243 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4180 b4180 Escherichia coli 562 -11536179 113718 yjfh (ec:2.1.1.-) (de:hypothetical trna/rRNA methyltransferase yjfh,) (db:swissprot) YJFH_ECOLI P39290 ESCHERICHIA COLI 562 -11536179 163782 yjfh hypothetical 26.6k protein vacb-aidb intergenic region:hypothetical protein o243 (cl:conserved hypothetical protein hi0860) (db:pir2.dat) S56405 S56405 Escherichia coli 562 -11536179 7500937984 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o243) (le:100103) (re:100834) (di:direct) ECOUW93 U14003 g537021 Escherichia coli 562 -11536179 237385 yjfh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:o243; 100 pct identical amino acid sequence and) (le:4959) (re:5690) (di:direct) AE000490 AE000490 g1790623 Escherichia coli 562 -11536179 5000693921 (de:(ecoli_4063) (pn:hypothetical 26) (gn:yjfh) (gtcfc:13.7:14.1) (ec:) (yjfh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4063 ECOLI_4063 Escherichia coli 562 10055446

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867111	12847	35003	540	179

Description

6500732322 yjfi:b4181 hypothetical 14.9 kd protein in vacb-aidb intergenic region:o133a (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4181 b4181 Escherichia coli 562 -11536180 113720 yjfi (de:hypothetical 14.9 kd protein in vacb-aidb intergenic region (o133a)) (db:swissprot) YJFI_ECOLI P39291 ESCHERICHIA COLI 562 -11536180 163728 yjfi hypothetical 14.9k protein vacb-aidb intergenic region:hypothetical protein o133a (db:pir2.dat) S56406 S56406 Escherichia coli 562 -11536180 7500937986 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o133a) (le:100961) (re:101362) (di:direct) ECOUW93 U14003 g537022 Escherichia coli 562 -11536180 237386 yjfi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:o133a; 100 pct identical amino acid sequence and) (le:5817) (re:6218) (di:direct) AE000490 AE000490 g1790624 Escherichia coli 562 -11536180 5000693922 (de:(ecoli_4064) (pn:hypothetical 14) (gn:yjfi) (gtcfc:13.7:14.1) (ec:) (yjfi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4064 ECOLI_4064 Escherichia coli 562 10055448

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867124	12848	35004	1284	427

Description

6500732323 yjfj:b4182 hypothetical 25.3 kd protein in vacb-aidb intergenic region:hypothetical 25.3 kd protein in vacb-aidb intergenic region precursor:o232 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4182 b4182 Escherichia coli 562 -11536181 113721 yjfj (de:(o232)) (db:swissprot) YJFJ_ECOLI P39292 ESCHERICHIA COLI 562 -11536181 163776 yjfj hypothetical 25.3k protein vacb-aidb intergenic region:hypothetical protein o232 (db:pir2.dat) S56407 S56407 Escherichia coli 562 -11536181 7500937987 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o232) (le:101381) (re:102079) (di:direct) ECOUW93 U14003 g537023 Escherichia coli 562 -11536181 237387 yjfj putative alpha helical protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:o232; 100 pct identical amino acid sequence and) (le:6237) (re:6935) (di:direct) AE000490 AE000490 g1790625 Escherichia coli 562 -11536181 5000693923 (de:(ecoli_4065) (pn:hypothetical 25) (gn:yjfj) (gtcfc:13.7:14.1) (ec:) (yjfj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4065 ECOLI_4065 Escherichia coli 562 10055449

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867144	12849	35005	1164	387

Description

6500732324 yjfk:b4183 hypothetical 25.0 kd protein in vacb-aidb intergenic region:o219 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4183 b4183 Escherichia coli 562 -11536182 113722 yjfk (de:hypothetical 25.0 kd protein in vacb-aidb intergenic region (o219)) (db:swissprot) YJFK_ECOLI P39293 ESCHERICHIA COLI 562 -11536182 163771 yjfk hypothetical 25.0k protein vacb-aidb intergenic region:hypothetical protein o219 (db:pir2.dat) S56408 S56408 Escherichia coli 562 -11536182 7500937988 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o219) (le:102130) (re:102789) (di:direct) ECOUW93 U14003 g537024 Escherichia coli 562 -11536182 237388 yjfk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completengenome.) (nt:o219; 100 pct identical amino acid sequence and) (le:6986) (re:7645) (di:direct) AE000490 AE000490 g1790626 Escherichia coli 562 -11536182 5000693924 (de:(ecoli_4066) (pn:hypothetical 25) (gn:yjfk) (gtcfc:13.7:14.1) (ec:) (yjfk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4066 ECOLI_4066 Escherichia coli 562 10055450

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867147	12850	35006	807	268

Description

6500732325 yjfl:b4184 hypothetical 14.2 kd protein in vacb-aidb intergenic region:o132 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4184 b4184 Escherichia coli 562 -11536183 113723 yjfl (de:hypothetical 14.2 kd protein in vacb-aidb intergenic region (o132)) (db:swissprot) YJFL_ECOLI P39294 ESCHERICHIA COLI 562 -11536183 163727 yjfl hypothetical 14.2k protein vacb-aidb intergenic region:hypothetical protein o132 (db:pir2.dat) S56409 S56409 Escherichia coli 562 -11536183 7500937989 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o132) (le:102807) (re:103205) (di:direct) ECOUW93 U14003 g537025 Escherichia coli 562 -11536183 237389 yjfl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completengenome.) (nt:o132; 100 pct identical amino acid sequence and) (le:7663) (re:8061) (di:direct) AE000490 AE000490 g1790627 Escherichia coli 562 -11536183 5000693925 (de:(ecoli_4067) (pn:hypothetical 14) (gn:yjfl) (gtcfc:13.7:14.1) (ec:) (yjfl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4067 ECOLI_4067 Escherichia coli 562 10055451

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867155	12851	35007	321	106

Description

6500732326 yjfm:b4185 hypothetical 23.4 kd protein in vacb-aidb intergenic region:o212 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4185 b4185 Escherichia coli 562 -11536184 113724 yjfm (de:hypothetical 23.4 kd protein in rnr-aidb intergenic region) (db:swissprot) YJFM_ECOLI P39295 ESCHERICHIA COLI 562 -11536184 163766 yjfm hypothetical 23.4k protein vacb-aidb intergenic region:hypothetical protein o212 (db:pir2.dat) S56410 S56410 Escherichia coli 562 -11536184 7500937990 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o212) (le:103215) (re:103853) (di:direct) ECOUW93 U14003 g537026 Escherichia coli 562 -11536184 237390 yjfm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:o212; 100 pct identical amino acid sequence and) (le:8071) (re:8709) (di:direct) AE000490 AE000490 g1790628 Escherichia coli 562 -11536184 5000693926 (de:(ecoli_4068) (pn:hypothetical 23) (gn:yjfm) (gtcfc:13.7:14.1) (ec:) (yjfm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4068 ECOLI_4068 Escherichia coli 562 10055452

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867156	12852	35008	549	182

Description

6500732327 yjfc:b4186 hypothetical 45.0 kd protein in vacb-aidb intergenic region:o387 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4186 b4186 Escherichia coli 562 -11536185 113714 yjfc (de:hypothetical 45.0 kd protein in vacb-aidb intergenic region (o387)) (db:swissprot) YJFC_ECOLI P33222 ESCHERICHIA COLI 562 -11536185 164857 yjfc hypothetical 45k protein vacb-aidb intergenic region:luxh protein:yifc protein (cl:conserved hypothetical protein hi0929) (db:pir2.dat) S56411 S56411 Escherichia coli 562 -11536185 7500937982 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:1st aidb orf of genbank accession number l20915;) (le:103856) (re:105019) (di:direct) ECOUW93 U14003 g537027 Escherichia coli 562 -11536185 237391 yjfc putative synthetase/amidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:o387; 100 pct identical amino acid sequence and) (le:8712) (re:9875) (di:direct) AE000490 AE000490 g1790629 Escherichia coli 562 -11536185 5000693927 (de:(ecoli_4069) (pn:hypothetical 45) (gn:yjfc) (gtcfc:13.7:14.1) (ec:) (yjfc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4069 ECOLI_4069 Escherichia coli 562 10055442

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867159	12853	35009	459	152

Description

6500732328 yjfn:b4188 hypothetical 11.0 kd protein in aidb-rpsf intergenic region:f100 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4188 b4188 Escherichia coli 562 -11536186 113725 yjfn (de:hypothetical 11.0 kd protein in aidb-sgat intergenic region) (db:swissprot) YJFN_ECOLI P39296 ESCHERICHIA COLI 562 -11536186 163547 yjfn hypothetical 11k protein aidb-rpsf intergenic region:hypothetical protein f100 (db:pir2.dat) S56413 S56413 Escherichia coli 562 -11536186 7500937991 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f100) (le:106849) (re:107151) (di:complement) ECOUW93 U14003 g537029 Escherichia coli 562 -11536186 237393 yjfn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:f100; 100 pct identical amino acid sequence and) (le:11701) (re:12003) (di:complement) AE000490 AE000490 g1790631 Escherichia coli 562 -11536186 5000693928 (de:(ecoli_4071) (pn:hypothetical 11) (gn:yjfn) (gtcfc:13.7:14.1) (ec:) (yjfn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4071 ECOLI_4071 Escherichia coli 562 10055453

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867167	12854	35010	393	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867171	12855	35011	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867187	12856	35012	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867216	12857	35013	1740	579

Description

6500732329 yjfo:b4189 hypothetical 16.0 kd protein in aidb-rpsf intergenic region:f142 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4189 b4189 Escherichia coli 562 -11536187 113726 yjfo (de:hypothetical 16.0 kd protein in aidb-sgat intergenic region) (db:swissprot) YJFO_ECOLI P39297 ESCHERICHIA COLI 562 -11536187 163564 yjfo hypothetical 16k protein aidb-rpsf intergenic region:hypothetical protein f142 (db:pir2.dat) S56414 S56414 Escherichia coli 562 -11536187 7500937992 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f142) (le:107273) (re:107701) (di:complement) ECOUW93 U14003 g537030 Escherichia coli 562 -11536187 237394 yjfo orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:f142; 100 pct identical amino acid sequence and) (le:107) (re:535) (di:complement) AE000491 AE000491 g1790633 Escherichia coli 562 -11536187 5000693929 (de:(ecoli_4072) (pn:hypothetical 16) (gn:yjfo) (gtcfc:13.7:14.1) (ec:) (yjfo_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4072 ECOLI_4072 Escherichia coli 562 10055454

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867222	12858	35014	1398	466

Description

6500732330 yjfp:b4190 hypothetical 27.6 kd protein in aidb-rpsf intergenic region:o249 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4190 b4190 Escherichia coli 562 -11536188 113727 yjfp (de:hypothetical 27.6 kd protein in aidb-sgat intergenic region) (db:swissprot) YJFP_ECOLI P39298 ESCHERICHIA COLI 562 -11536188 163784 yjfp hypothetical 27.6k protein aidb-rpsf intergenic region:hypothetical protein o249 (db:pir2.dat) S56415 S56415 Escherichia coli 562 -11536188 7500937993 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o249) (le:107784) (re:108533) (di:direct) ECOUW93 U14003 g537031 Escherichia coli 562 -11536188 237395 yjfp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:o249; 100 pct identical amino acid sequence and) (le:618) (re:1367) (di:direct) AE000491 AE000491 g1790634 Escherichia coli 562 -11536188 5000693930 (de:(ecoli_4073) (pn:hypothetical 27) (gn:yjfp) (gtcfc:13.7:14.1) (ec:) (yjfp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4073 ECOLI_4073 Escherichia coli 562 10055455

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867230	12859	35015	1560	519

Description

6500732331 yjfq:b4191 hypothetical transcriptional regulator in aidb-rpsf intergenic region:hypothetical transcriptional regulator in aidb-rpsf intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4191 b4191 Escherichia coli 562 -11536189 113728 yjfq (de:hypothetical transcriptional regulator in aidb-rpsf intergenic region) (db:swissprot) YJFQ_ECOLI P39299 ESCHERICHIA COLI 562 -11536189 163602 yjfq hypothetical transcription regulator:aidb-rpsf intergenic region:hypothetical protein f251 (db:pir2.dat) S56416 S56416 Escherichia coli 562 -11536189 7500937994 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f251) (le:108530) (re:109285) (di:complement) ECOUW93 U14003 g537032 Escherichia coli 562 -11536189 237396 yjfq putative deor-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:f251; 100 pct identical amino acid sequence and) (le:1364) (re:2119) (di:complement) AE000491 AE000491 g1790635 Escherichia coli 562 -11536189 5000693931 (de:(ecoli_4074) (pn:hypothetical transcriptional regulator in aidb-rpsf intergenic region:f251) (gn:yjfq) (gtcfc:13.7:14.1) (ec:) (yjfq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4074 ECOLI_4074 Escherichia coli 562 10055456

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867233	12860	35016	558	186

Description

6500732332 yjfr:b4192 hypothetical 40.3 kd protein in aidb-rpsf intergenic region:f356 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4192 b4192 Escherichia coli 562 -11536190 163645 yjfr hypothetical 40.3k protein aidb-rpsf intergenic region:hypothetical protein f356 (db:pir2.dat) S56417 S56417 Escherichia coli 562 -11536190 237397 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f356) (le:109393) (re:110463) (di:complement) ECOUW93 U14003 g537033 Escherichia coli 562 -11536190 7500959813 yjfr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:f356; 100 pct identical amino acid sequence and) (le:2227) (re:3297) (di:complement) AE000491 AE000491 g1790636 Escherichia coli 562 -11536190 113729 yjfr_ecoli (de:hypothetical 40.3 kd protein in aidb-rpsf intergenic region (f356).) P39300 P39300 Escherichia coli 562 -11536190 5000693932 (de:(ecoli_4075) (pn:hypothetical 40) (gn:yjfr) (gtcfc:13.7:14.1) (ec:) (yjfr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4075 ECOLI_4075 Escherichia coli 562 10055457

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867257	12861	35017	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867259	12862	35018	276	91

Description

6500732333 yjfs:sgat:b4193 hypothetical 52.9 kd protein in aidb-rpsf intergenic region:sgat protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4193 b4193 Escherichia coli 562 -11536191 7500891585 sgat (de:putative transport protein sgat) (db:swissprot) SGAT_ECOLI P39301 ESCHERICHIA COLI 562 -11536191 7000690956 yjfs hypothetical 52.9 kd protein in aidb-rpsf intergenic region:hypothetical protein o488 (db:pir2.dat) D65230 D65230 Escherichia coli 562 -11536191 7500891587 sgat orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completengenome.) (nt:o484; formerly designated yjfs) (le:3589) (re:5043) (di:direct) AE000491 AE000491 g2367358 Escherichia coli 562 -11536191

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867261	12863	35019	639	212

Description

6500732334 yjfw:sgau:b4197 hypothetical 32.0 kd protein in aidb-rpsf intergenic region:putative hexulose-6-phosphate isomerase:humpi (gtcfc:14.1) (ec:5.-.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4197 b4197 Escherichia coli 562 -11536192 113735 sgau (ec:5.-.-.-) (de:putative hexulose-6-phosphate isomerase, (humpi)) (db:swissprot) SGAU_ECOLI P39305 ESCHERICHIA COLI 562 -11536192 163794 yjfw hypothetical 32k protein aidb-rpsf intergenic region:hypothetical protein o284 (cl:hypothetical protein hil026) (db:pir2.dat) S56422 S56422 Escherichia coli 562 -11536192 7500891589 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o284) (le:113678) (re:114532) (di:direct) ECOUW93 U14003 g537038 Escherichia coli 562 -11536192 237402 sgau putative hexulose-6-phosphate isomerase (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completengenome.) (nt:o284; formerly designated yjfw) (le:6512) (re:7366) (di:direct) AE000491 AE000491 g1790641 Escherichia coli 562 -11536192 5000693936 (de:(ecoli_4080) (pn:hypothetical 32) (gn:yjfw) (gtcfc:13.7:14.1) (ec:) (yjfw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4080 ECOLI_4080 Escherichia coli 562 10055463

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867267	12864	35020	330	109

Description

6500732335 sgae:b4198 hypothetical protein:probable sugar isomerase sgae (gtcfc:14.1) (ec:5.1.-.-) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4198 b4198 Escherichia coli 562 -11536193 113736 sgae (ec:5.1.-.-) (de:probable sugar isomerase sgae,) (db:swissprot) SGAE_ECOLI P39306 ESCHERICHIA COLI 562 -11536193 142082 l-ribulose-phosphate 4-epimerase homolog:o228a:protein b4198:protein o228a (cl:l-ribulose-phosphate 4-epimerase) (ec:5.1.3.-) (db:pir2.dat) S56423 S56423 Escherichia coli 562 -11536193 7500891581 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o228a) (le:114532) (re:115218) (di:direct) ECOUW93 U14003 g537039 Escherichia coli 562 -11536193 237403 sgae putative epimerase/aldolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:o228a) (le:7366) (re:8052) (di:direct) AE000491 AE000491 g1790642 Escherichia coli 562 -11536193 5000693937 (de:(ecoli_4081) (pn:hypothetical 25) (gtcfc:13.7:14.1) (ec:) (yjfx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4081 ECOLI_4081 Escherichia coli 562 10055464

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867272	12865	35021	462	153

Description

6500732336 yjfy:b4199 hypothetical 10.1 kd protein in aidb-rpsf intergenic region:hypothetical 10.1 kd protein in aidb-rpsf intergenic region precursor:f91 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4199 b4199 Escherichia coli 562 -11536194 113737 yjfy (de:hypothetical 10.1 kd protein in sgae-rpsf intergenic region precursor) (db:swissprot) YJFY_ECOLI P39307 ESCHERICHIA COLI 562 -11536194 163693 yjfy hypothetical 10.1 kd protein in aidb-rpsf intergenic region:hypothetical protein f91 (db:pir2.dat) S56424 S56424 Escherichia coli 562 -11536194 7500937996 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f91) (le:115348) (re:115623) (di:complement) ECOUW93 U14003 g537040 Escherichia coli 562 -11536194 237404 yjfy orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:f91; 100 pct identical amino acid sequence and) (le:8182) (re:8457) (di:complement) AE000491 AE000491 g1790643 Escherichia coli 562 -11536194 5000693938 (de:(ecoli_4082) (pn:hypothetical 10) (gn:yjfy) (gtcfc:13.7:14.1) (ec:) (yjfy_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4082 ECOLI_4082 Escherichia coli 562 10055465

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867281	12866	35022	726	241

Description

6500732337 yjfc:b4204 hypothetical 29.7 kd protein in rpli-cpdb intergenic region:f264 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4204 b4204 Escherichia coli 562 -11536195 113738 yjfc (de:hypothetical 29.7 kd protein in rpli-fklb intergenic region) (db:swissprot) YJFZ_ECOLI P39308 ESCHERICHIA COLI 562 -11536195 163610 yjfc hypothetical 29.7k protein rpli-cpdb intergenic region:hypothetical protein f264 (db:pir2.dat) S56429 S56429 Escherichia coli 562 -11536195 7500937997 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f264) (le:117460) (re:118254) (di:complement) ECOUW93 U14003 g537045 Escherichia coli 562 -11536195 237409 yjfc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 381 of 400 of the completegenome.) (nt:f264; 100 pct identical amino acid sequence and) (le:10294) (re:11088) (di:complement) AE000491 AE000491 g1790648 Escherichia coli 562 -11536195 5000693939 (de:(ecoli_4087) (pn:hypothetical 29) (gn:yjfc) (gtcfc:13.7:14.1) (ec:) (yjfc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4087 ECOLI_4087 Escherichia coli 562 10055466

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867304	12867	35023	243	81

Description

6500732338 ytfa:b4205 hypothetical 12.2 kd protein in rpli-cpdb intergenic region:o108 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4205 b4205 Escherichia coli 562 -11536196 116397 ytfa (de:hypothetical 12.2 kd protein in rpli-cpdb intergenic region (o108)) (db:swissprot) YTFA_ECOLI P39309 ESCHERICHIA COLI 562 -11536196 163712 ytfa hypothetical 12.2k protein rpli-cpdb intergenic region:hypothetical protein o108 (db:pir2.dat) S56430 S56430 Escherichia coli 562 -11536196 7500952753 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o108) (le:118601) (re:118927) (di:direct) ECOUW93 U14003 g537046 Escherichia coli 562 -11536196 237410 ytfa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:o108; 100 pct identical amino acid sequence and) (le:341) (re:667) (di:direct) AE000492 AE000492 g1790650 Escherichia coli 562 -11536196 5000693940 (de:(ecoli_4088) (pn:hypothetical 12) (gn:ytfa) (gtcfc:13.7:14.1) (ec:) (ytfa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4088 ECOLI_4088 Escherichia coli 562 10058122

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867306	12868	35024	210	69

Description

6500732339 ytfb:b4206 hypothetical protein:hypothetical 24.9 kd protein in rpli-cpdb intergenic region:f224 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4206 b4206 Escherichia coli 562 -11536197 163591 hypothetical protein f224:hypothetical protein b4206 (db:pir2.dat) S56431 S56431 Escherichia coli 562 -11536197 237411 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f224) (le:118911) (re:119585) (di:complement) ECOUW93 U14003 g537047 Escherichia coli 562 -11536197 7500960336 ytfb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:f224) (le:651) (re:1325) (di:complement) AE000492 AE000492 g1790651 Escherichia coli 562 -11536197 116398 ytfb_ecoli (de:hypothetical 24.9 kd protein in rpli-cpdb intergenic region (f224).) P39310 P39310 Escherichia coli 562 -11536197 5000693941 (de:(ecoli_4089) (pn:hypothetical 24) (gtcfc:13.7:14.1) (ec:) (ytfb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4089 ECOLI_4089 Escherichia coli 562 10058123

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867307	12869	35025	1698	565

Description

6500732340 ytfb:b4209 hypothetical protein:hypothetical 24.9 kd protein in rpli-cpdb intergenic region:f220 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4209 b4209 Escherichia coli 562 -11536198 116399 ytfb (de:hypothetical 24.9 kd protein in rpli-cpdb intergenic region (f220)) (db:swissprot) YTFE_ECOLI P39313 ESCHERICHIA COLI 562 -11536198 163590 hypothetical protein f220:hypothetical protein b4209 (db:pir2.dat) S56434 S56434 Escherichia coli 562 -11536198 7500952755 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f220) (le:122153) (re:122815) (di:complement) ECOUW93 U14003 g537050 Escherichia coli 562 -11536198 237414 ytfb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:f220) (le:3893) (re:4555) (di:complement) AE000492 AE000492 g1790654 Escherichia coli 562 -11536198 5000693943 (de:(ecoli_4092) (pn:hypothetical 24) (gtcfc:13.7:14.1) (ec:) (ytfb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4092 ECOLI_4092 Escherichia coli 562 10058124

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867313	12870	35026	741	246

Description

6500732341 ytfb:b4210 hypothetical 35.5 kd protein in rpli-cpdb intergenic region:f324 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4210 b4210 Escherichia coli 562 -11536199 116401 ytfb (de:hypothetical 35.5 kd protein in rpli-cpdb intergenic region (f324)) (db:swissprot) YTFB_ECOLI P39314 ESCHERICHIA COLI 562 -11536199 163635 ytfb hypothetical 35.5k protein rpli-cpdb intergenic region:hypothetical protein f324 (db:pir2.dat) S56435 S56435 Escherichia coli 562 -11536199 7500952757 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f324) (le:122923) (re:123897) (di:complement) ECOUW93 U14003 g537051 Escherichia coli 562 -11536199 237415 ytfb putative transmembrane subunit (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:f324; 100 pct identical amino acid sequence and) (le:4663) (re:5637) (di:complement) AE000492 AE000492 g1790655 Escherichia coli 562 -11536199 5000693944 (de:(ecoli_4093) (pn:hypothetical 35) (gn:ytfb) (gtcfc:13.7:14.1) (ec:) (ytfb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4093 ECOLI_4093 Escherichia coli 562 10058126

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867319	12871	35027	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867332	12872	35028	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867335	12873	35029	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867345	12874	35030	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867347	12875	35031	333	110

Description

6500732342 ytfg:b4211 hypothetical 29.7 kd protein in rpli-cpdb intergenic region:f286 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4211 b4211 Escherichia coli 562 -11536200 116402 ytfg (de:hypothetical 29.7 kd protein in rpli-cpdb intergenic region (f286)) (db:swissprot) YTFG_ECOLI P39315 ESCHERICHIA COLI 562 -11536200 163621 ytfg hypothetical 29.7k protein rpli-cpdb intergenic region:hypothetical protein f286 (db:pir2.dat) S56436 S56436 Escherichia coli 562 -11536200 7500952758 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f286) (le:123996) (re:124856) (di:complement) ECOUW93 U14003 g537052 Escherichia coli 562 -11536200 237416 ytfg putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:f286; 100 pct identical amino acid sequence and) (le:5736) (re:6596) (di:complement) AE000492 AE000492 g1790656 Escherichia coli 562 -11536200 5000693945 (de:(ecoli_4094) (pn:hypothetical 29) (gn:ytfg) (gtcfc:13.7:14.1) (ec:) (ytfg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4094 ECOLI_4094 Escherichia coli 562 10058127

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867348	12876	35032	891	297

Description

6500732343 ytfh:b4212 hypothetical protein:hypothetical 17.6 kd protein in rpli-cpdb intergenic region:o156 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4212 b4212 Escherichia coli 562 -11536201 116403 ytfh (de:hypothetical 17.6 kd protein in rpli-cpdb intergenic region (o156)) (db:swissprot) YTFH_ECOLI P39316 ESCHERICHIA COLI 562 -11536201 163745 hypothetical protein o163:hypothetical protein b4212 (cl:conserved hypothetical protein mth1285) (db:pir2.dat) S56437 S56437 Escherichia coli 562 -11536201 7500952759 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o163) (le:124855) (re:125325) (di:direct) ECOUW93 U14003 g537053 Escherichia coli 562 -11536201 237417 ytfh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:o156) (le:6595) (re:7065) (di:direct) AE000492 AE000492 g1790657 Escherichia coli 562 -11536201 5000693946 (de:(ecoli_4095) (pn:hypothetical 17) (gtcfc:13.7:14.1) (ec:) (ytfh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4095 ECOLI_4095 Escherichia coli 562 10058128

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867352	12877	35033	432	143

Description

6500732344 ytfi:b4215 hypothetical protein:hypothetical 19.6 kd protein in cysq-msra intergenic region:o166 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4215 b4215 Escherichia coli 562 -11536202 116404 ytfi (de:hypothetical 19.6 kd protein in cysq-msra intergenic region (o166)) (db:swissprot) YTFI_ECOLI P39317 ESCHERICHIA COLI 562 -11536202 163747 hypothetical protein b4215:hypothetical protein o165 (db:pir2.dat) S56440 S56440 Escherichia coli 562 -11536202 7500952760 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o165) (le:128539) (re:129039) (di:direct) ECOUW93 U14003 g537056 Escherichia coli 562 -11536202 237420 ytfi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 383 of 400 of the completegenome.) (nt:o166) (le:156) (re:656) (di:direct) AE000493 AE000493 g1790661 Escherichia coli 562 -11536202 5000693947 (de:(ecoli_4098) (pn:hypothetical 19) (gtcfc:13.7:14.1) (ec:) (ytfi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4098 ECOLI_4098 Escherichia coli 562 10058129

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867355	12878	35034	234	77

Description

6500732345 ytfk:b4217 hypothetical 9.6 kd protein in cysq-msra intergenic region:o81 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4217 b4217 Escherichia coli 562 -11536203 7000688613 ytfk hypothetical 9.6 kd protein in cysq-msra intergenic region:hypothetical protein o81 (db:pir2.dat) D65233 D65233 Escherichia coli 562 -11536203 237422 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o81) (le:130379) (re:130624) (di:direct) ECOUW93 U14003 g537058 Escherichia coli 562 -11536203 7500959838 ytfk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 383 of 400 of the completegenome.) (nt:o81; 100 pct identical amino acid sequence and) (le:1996) (re:2241) (di:direct) AE000493 AE000493 g1790663 Escherichia coli 562 -11536203 116407 ytfk_ecoli (de:hypothetical 9.6 kd protein in cysq-msra intergenic region (o81).) P39318 P39318 Escherichia coli 562 -11536203 5000693949 (de:(ecoli_4100) (pn:hypothetical 9) (gn:ytfk) (gtcfc:13.7:14.1) (ec:) (ytfk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4100 ECOLI_4100 Escherichia coli 562 10058132

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867360	12879	35035	621	206

Description

6500732346 ytf1:b4218 hypothetical 49.8 kd protein in cysq-msra intergenic region:f447 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4218 b4218 Escherichia coli 562 -11536204 116408 ytf1 (de:hypothetical 49.8 kd protein in cysq-msra intergenic region) (db:swissprot) YTFL_ECOLI P39319 ESCHERICHIA COLI 562 -11536204 163665 ytf1 hypothetical 49.8k protein cysq-msra intergenic region:hypothetical protein f447 (cl:hypothetical protein hi0107) (db:pir2.dat) S56443 S56443 Escherichia coli 562 -11536204 7500952764 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f447) (le:130703) (re:132046) (di:complement) ECOUW93 U14003 g537059 Escherichia coli 562 -11536204 237423 ytf1 putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 383 of 400 of the completegenome.) (nt:f447; 100 pct identical amino acid sequence and) (le:2320) (re:3663) (di:complement) AE000493 AE000493 g1790664 Escherichia coli 562 -11536204 5000693950 (de:(ecoli_4101) (pn:hypothetical 49) (gn:ytf1) (gtcfc:13.7:14.1) (ec:) (ytf1_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4101 ECOLI_4101 Escherichia coli 562 10058133

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867363	12880	35036	537	178

Description

6500732347 ytfm:b4220 hypothetical 64.8 kd protein in msra-chpbi intergenic region:hypothetical 64.8 kd protein in msra-chpbi intergenic region precursor:o577 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4220 b4220 Escherichia coli 562 -11536205 116410 ytfm (de:(o577)) (db:swissprot) YTFM_ECOLI P39320 ESCHERICHIA COLI 562 -11536205 163861 ytfm hypothetical 64.8k protein msra-chpbi intergenic region:hypothetical protein o577 (db:pir2.dat) S56445 S56445 Escherichia coli 562 -11536205 7500952766 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o577) (le:133213) (re:134946) (di:direct) ECOUW93 U14003 g537061 Escherichia coli 562 -11536205 237425 ytfm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 383 of 400 of the completegenome.) (nt:o577; 100 pct identical amino acid sequence and) (le:4830) (re:6563) (di:direct) AE000493 AE000493 g1790666 Escherichia coli 562 -11536205 5000693951 (de:(ecoli_4103) (pn:hypothetical 64) (gn:ytfm) (gtcfc:13.7:14.1) (ec:) (ytfm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4103 ECOLI_4103 Escherichia coli 562 10058135

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867376	12881	35037	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867380	12882	35038	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867382	12883	35039	330	109

Description

6500732348 ytfp:b4222 hypothetical 12.9 kd protein in msra-chpbi intergenic region:o113 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4222 b4222 Escherichia coli 562 -11536206 116414 ytfp (de:hypothetical 12.9 kd protein in msra-chpbi intergenic region (o113)) (db:swissprot) YTFP_ECOLI P39323 ESCHERICHIA COLI 562 -11536206 163718 ytfp hypothetical 12.9k protein msra-chpbi intergenic region:hypothetical protein o113 (db:pir2.dat) S56448 S56448 Escherichia coli 562 -11536206 7500952770 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o113) (le:138726) (re:139067) (di:direct) ECOUW93 U14003 g537064 Escherichia coli 562 -11536206 237428 ytfp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 383 of 400 of the completegenome.) (nt:o113; 100 pct identical amino acid sequence and) (le:10342) (re:10683) (di:direct) AE000493 AE000493 g1790668 Escherichia coli 562 -11536206 5000693953 (de:(ecoli_4105) (pn:hypothetical 12) (gn:ytfp) (gtcfc:13.7:14.1) (ec:) (ytfp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4105 ECOLI_4105 Escherichia coli 562 10058139

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867386	12884	35040	930	309

Description

6500732349 ytftr:b4228 hypothetical abc transporter in ppa-fbp intergenic region:o4:hypothetical abc transporter atp-binding protein in ppa-fbp intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4228 b4228 Escherichia coli 562 -11536207 116416 ytftr (de:region) (db:swissprot) YTFR_ECOLI P39326 ESCHERICHIA COLI 562 -11536207 163836 ytftr hypothetical abc transporter ppa-fbp intergenic region:hypothetical protein o417a (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) S56454 S56454 Escherichia coli 562 -11536207 7500952772 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o417a) (le:141888) (re:143141) (di:direct) ECOUW93 U14003 g537070 Escherichia coli 562 -11536207 237434 ytftr putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 384 of 400 of the completegenome.) (nt:o417a; 100 pct identical amino acid sequence and) (le:2743) (re:3996) (di:direct) AE000494 AE000494 g1790675 Escherichia coli 562 -11536207 5000693958 (de:(ecoli_4111) (pn:hypothetical abc transporter atp-binding protein in ppa-fbp intergenic region:o417a) (gn:ytftr) (gtcfc:13.7:14.1) (ec:) (ytftr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4111 ECOLI_4111 Escherichia coli 562 10058141

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867393	12885	35041	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867395	12886	35042	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867397	12887	35043	282	93

Description

6500732350 ytfb:b4229 o90:hypothetical 9.9 kd protein in ppa-fbp intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4229 b4229 Escherichia coli 562 -11536208 116417 ytfb (de:hypothetical 9.9 kd protein in ppa-fbp intergenic region) (db:swissprot) YTFB_ECOLI P39327 ESCHERICHIA COLI 562 -11536208 163877 ytfb hypothetical 9.9k protein ppa-fbp intergenic region:hypothetical protein o90b (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) S56455 S56455 Escherichia coli 562 -11536208 7500952773 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o90b) (le:143117) (re:143389) (di:direct) ECOUW93 U14003 g537071 Escherichia coli 562 -11536208 237435 ytfb putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 384 of 400 of the complete genome.) (nt:o90b; 100 pct identical amino acid sequence and) (le:3972) (re:4244) (di:direct) AE000494 AE000494 g1790676 Escherichia coli 562 -11536208 5000693959 (de:(ecoli_4112) (pn:hypothetical 9) (gn:ytfb) (gtcfc:13.7:14.1) (ec:) (ytfb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4112 ECOLI_4112 Escherichia coli 562 10058142

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867401	12888	35044	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867435	12889	35045	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867442	12890	35046	879	292

Description

6500732351 ytft:b4230 hypothetical 35.7 kd protein in ppa-fbp intergenic region:o3:hypothetical abc transporter permease protein ytft (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4230 b4230 Escherichia coli 562 -11536209 116418 ytft (de:hypothetical abc transporter permease protein ytft) (db:swissprot) YTFT_ECOLI P39328 ESCHERICHIA COLI 562 -11536209 163817 ytft hypothetical 35.7k protein ppa-fbp intergenic region:hypothetical protein o341 (db:pir2.dat) S56456 S56456 Escherichia coli 562 -11536209 7500952774 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o341) (le:143400) (re:144425) (di:direct) ECOUW93 U14003 g537072 Escherichia coli 562 -11536209 237436 ytft putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 384 of 400 of the completegenome.) (nt:o341; 100 pct identical amino acid sequence and) (le:4255) (re:5280) (di:direct) AE000494 AE000494 g1790677 Escherichia coli 562 -11536209 5000693960 (de:(ecoli_4113) (pn:hypothetical 35) (gn:ytft) (gtcfc:13.7:14.1) (ec:)) (ytft_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4113 ECOLI_4113 Escherichia coli 562 10058143

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867448	12891	35047	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867451	12892	35048	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867499	12893	35049	804	267

Description

6500732352 yjff:b4231 hypothetical 34.0 kd protein in ppa-fbp intergenic region:o3:hypothetical abc transporter permease protein yjff (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4231 b4231 Escherichia coli 562 -11536210 113715 yjff (de:hypothetical abc transporter permease protein yjff) (db:swissprot) YJFF_ECOLI P37772 ESCHERICHIA COLI 562 -11536210 163807 yjff hypothetical 34.0k protein ppa-fbp intergenic region:hypothetical protein o323 (db:pir2.dat) S56457 S56457 Escherichia coli 562 -11536210 7500937983 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o323) (le:144436) (re:145407) (di:direct) ECOUW93 U14003 g537073 Escherichia coli 562 -11536210 237437 yjff putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 384 of 400 of the completegenome.) (nt:o323; 100 pct identical amino acid sequence and) (le:5291) (re:6262) (di:direct) AE000494 AE000494 g1790678 Escherichia coli 562 -11536210 5000693961 (de:(ecoli_4114) (pn:hypothetical 34) (gn:yjff) (gtcfc:13.7:14.1) (ec:) (yjff_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4114 ECOLI_4114 Escherichia coli 562 10055443

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867500	12894	35050	588	195

Description

6500732353 yjfg:b4233 hypothetical 48.5 kd protein in fbp-pmba intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4233 b4233 Escherichia coli 562 -11536211 7500885840 mpl (ec:6.3.2.-) (de:ligase,) (db:swissprot) MPL_ECOLI P37773 ESCHERICHIA COLI 562 -11536211 163843 yjfg hypothetical 48.5k protein fbp-pmba intergenic region:hypothetical protein o457 (db:pir2.dat) S56459 S56459 Escherichia coli 562 -11536211 237439 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o457) (le:146614) (re:147987) (di:direct) ECOUW93 U14003 g537075 Escherichia coli 562 -11536211 7500885842 yjfg putative ligase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 384 of 400 of the completegenome.) (nt:o457; 100 pct identical to 445 amino acids of) (le:7469) (re:8842) (di:direct) AE000494 AE000494 g1790680 Escherichia coli 562 -11536211 5000693962 (de:(ecoli_4116) (pn:hypothetical 48) (gn:yjfg) (gtcfc:13.7:14.1) (ec:) (yjfg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4116 ECOLI_4116 Escherichia coli 562 10087063

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867504	12895	35051	1968	655

Description

6500732354 yjga:x96:b4234 x:hypothetical 21.4 kd protein in fbp-pmba intergenic region:x96 protein:f183 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4234 b4234 Escherichia coli 562 -11536212 113747 yjga:x96 (de:protein) (f183)) (db:swissprot) YJGA_ECOLI P26650 ESCHERICHIA COLI 562 -11536212 164834 yjga hypothetical 21.4k protein fbp-pmba intergenic region:x96 protein (db:pir2.dat) S56460 S56460 Escherichia coli 562 -11536212 237440 21k protein (sr:escherichia coli (strain:k12, isolate:kp5254) dna, clone:pkp1838) (db:genpept-bct1) (de:escherichia coli dna for tlde protein and 21k protein, completecds.) (le:212) (re:763) (di:complement) ECOTLDE2 D44452 g1732439 Escherichia coli 562 -11536212 237631 x96 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:alternate gene name yjga) (le:148143) (re:148694) (di:complement) ECOUW93 U14003 g537076 Escherichia coli 562 -11536212 7500938011 x96 x96 (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e.coli x96 gene, complete cds.) (le:274) (re:825) (di:direct) ECOX96A M95096 g148266 Escherichia coli 562 -11536212 236105 yjga putative alpha helix protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 384 of 400 of the completegenome.) (nt:f183; 100 pct identical amino acid sequence and) (le:8998) (re:9549) (di:complement) AE000494 AE000494 g1790681 Escherichia coli 562 -11536212 5000693963 (de:(ecoli_4117) (pn:hypothetical 21) (gn:yjga) (gtcfc:13.7:14.1) (ec:) (yjga_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4117 ECOLI_4117 Escherichia coli 562 10055475

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867509	12896	35052	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867538	12897	35053	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867543	12898	35054	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867546	12899	35055	657	218

Description

6500732355 yjgg:b4247 hypothetical 12.8 kd protein in pyrl-argi intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4247 b4247 Escherichia coli 562 -11536213 163715 yjgg hypothetical 12.8k protein pyrl-argi intergenic region:hypothetical protein o110 (db:pir2.dat) S56473 S56473 Escherichia coli 562 -11536213 7500959772 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o110) (le:163342) (re:163674) (di:direct) ECOUW93 U14003 g537089 Escherichia coli 562 -11536213 237453 yjgg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 385 of 400 of the completengenome.) (nt:o110; 100 pct identical amino acid sequence and) (le:13155) (re:13487) (di:direct) AE000495 AE000495 g1790695 Escherichia coli 562 -11536213 5000693966 (de:(ecoli_4130) (pn:hypothetical 12) (gn:yjgg) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4130 ECOLI_4130 Escherichia coli 562 10087027

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867549	12900	35056	255	84

Description

6500732356 yjgh:b4248 hypothetical 14.6 kd protein in pyrl-argi intergenic region:f131 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4248 b4248 Escherichia coli 562 -11536214 113755 yjgh (de:hypothetical 14.6 kd protein in pyrl-argi intergenic region (f131)) (db:swissprot) YJGH_ECOLI P39332 ESCHERICHIA COLI 562 -11536214 163558 yjgh hypothetical 14.6k protein pyrl-argi intergenic region:hypothetical protein f131 (db:pir2.dat) S56474 S56474 Escherichia coli 562 -11536214 7500938016 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f131) (le:163643) (re:164038) (di:complement) ECOUW93 U14003 g537090 Escherichia coli 562 -11536214 237454 yjgh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 385 of 400 of the completengenome.) (nt:f131; 100 pct identical amino acid sequence and) (le:13456) (re:13851) (di:complement) AE000495 AE000495 g1790696 Escherichia coli 562 -11536214 5000693967 (de:(ecoli_4131) (pn:hypothetical 14) (gn:yjgh) (gtcfc:13.7:14.1) (ec:) (yjgh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4131 ECOLI_4131 Escherichia coli 562 10055483

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867560	12901	35057	363	120

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867561	12902	35058	699	232

Description

GTC ORF with score 498 to: (fn:mediates resistance to oxidative stress, i.e.) (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae hydroperoxide resistance (hyr1) gene,complete cds.) (nt:putative glutathione-peroxidase) (le:389) (re:880) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867563	12903	35059	609	202

Description

6500732357 yjgi:b4249 hypothetical 24.6 kd protein in pyr1-argi intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4249 b4249 Escherichia coli 562 -11536215 7500938017 yjgi (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YJGI_ECOLI P39333 ESCHERICHIA COLI 562 -11536215 7000690929 yjgi hypothetical 24.6 kd protein in pyr1-argi intergenic region:hypothetical protein f261a (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) D65237 D65237 Escherichia coli 562 -11536215 7500938019 yjgi putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 385 of 400 of the completegenome.) (nt:f237; sequence change shortens c-terminus relative) (le:13982) (re:14695) (di:complement) AE000495 AE000495 g2367365 Escherichia coli 562 -11536215

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867564	12904	35060	972	323

Description

5000693969 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4250 b4250 Escherichia coli 562 -11536216 7000691819 hypothetical protein b4250 (db:pir2.dat) E65237 E65237 Escherichia coli 562 -11536216 7500960325 b4250 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 386 of 400 of the completegenome.) (nt:o54; ??? pct identical amino acid sequence and) (le:82) (re:246) (di:direct) AE000496 AE000496 g1790699 Escherichia coli 562 -11536216 6500732358 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4250 b4250 Escherichia coli 562 -11536216

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867565	12905	35061	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867580	12906	35062	627	208

Description

5000693970 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b4251 b4251 Escherichia coli 562 -11536217
7000691820 hypothetical protein b4251 (db:pir2.dat) F65237 F65237
Escherichia coli 562 -11536217 7500960326 yjgj orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
386 of 400 of the completegenome.) (nt:o84; ??? pct identical amino acid
sequence and) (le:318) (re:572) (di:direct) AE000496 AE000496 g1790700
Escherichia coli 562 -11536217 6500732359 hypothetical protein (gtcfc:14.1)
(keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4251 b4251
Escherichia coli 562 -11536217

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867601	12907	35063	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867619	12908	35064	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867627	12909	35065	2112	703

Description

6500732360 yjgk:b4252 hypothetical 17.3 kd protein in pyrl-argi intergenic region:o153b (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4252 b4252 Escherichia coli 562 -11536218 113758 yjgk (de:hypothetical 17.3 kd protein in pyrl-argi intergenic region (o153b)) (db:swissprot) YJGK_ECOLI P39335 ESCHERICHIA COLI 562 -11536218 163740 yjgk hypothetical 17.3k protein pyrl-argi intergenic region:hypothetical protein o153b (cl:hypothetical protein hi0227) (db:pir2.dat) S56477 S56477 Escherichia coli 562 -11536218 7500938021 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o153b) (le:165688) (re:166149) (di:direct) ECOUW93 U14003 g537093 Escherichia coli 562 -11536218 237457 yjgk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 386 of 400 of the completegenome.) (nt:o153b; 100 pct identical amino acid sequence and) (le:708) (re:1169) (di:direct) AE000496 AE000496 g1790701 Escherichia coli 562 -11536218 5000693971 (de:(ecoli_4135) (pn:hypothetical 17) (gn:yjgk) (gtcfc:13.7:14.1) (ec:) (yjgk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4135 ECOLI_4135 Escherichia coli 562 10055486

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867651	12910	35066	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867656	12911	35067	1233	410

Description

6500732361 yjgl:b4253 hypothetical 71.1 kd protein in pyrl-argi intergenic region:o616 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4253 b4253 Escherichia coli 562 -11536219 113759 yjgl (de:hypothetical 71.1 kd protein in pyrl-argi intergenic region (o616)) (db:swissprot) YJGL_ECOLI P39336 ESCHERICHIA COLI 562 -11536219 163863 yjgl hypothetical 71.1k protein pyrl-argi intergenic region:hypothetical protein o616 (db:pir2.dat) S56478 S56478 Escherichia coli 562 -11536219 7500938022 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o616) (le:166236) (re:168086) (di:direct) ECOUW93 U14003 g537094 Escherichia coli 562 -11536219 237458 yjgl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 386 of 400 of the completegenome.) (nt:o616; 100 pct identical amino acid sequence and) (le:1256) (re:3106) (di:direct) AE000496 AE000496 g1790702 Escherichia coli 562 -11536219 5000693972 (de:(ecoli_4136) (pn:hypothetical 71) (gn:yjgl) (gtcfc:13.7:14.1) (ec:) (yjgl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4136 ECOLI_4136 Escherichia coli 562 10055487

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867660	12912	35068	300	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867682	12913	35069	627	208

Description

6500732362 yjgd:b4255 hypothetical 15.6 kd protein in argi-vals intergenic region:o138 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4255 b4255 Escherichia coli 562 -11536220 113750 yjgd (de:hypothetical 15.6 kd protein in argi-vals intergenic region (o138)) (db:swissprot) YJGD_ECOLI P37163 ESCHERICHIA COLI 562 -11536220 163732 yjgd hypothetical 15.6k protein argi-vals intergenic region:hypothetical protein o138 (db:pir2.dat) S56480 S56480 Escherichia coli 562 -11536220 7500938013 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o138) (le:169296) (re:169712) (di:direct) ECOUW93 U14003 g537096 Escherichia coli 562 -11536220 237460 yjgd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 386 of 400 of the completengenome.) (nt:o138; 100 pct identical amino acid sequence and) (le:4317) (re:4733) (di:direct) AE000496 AE000496 g1790704 Escherichia coli 562 -11536220 5000693973 (de:(ecoli_4138) (pn:hypothetical 15) (gn:yjgd) (gtcfc:13.7:14.1) (ec:) (yjgd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4138 ECOLI_4138 Escherichia coli 562 10055478

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867690	12914	35070	429	142

Description

5000693974 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4256 b4256 Escherichia coli 562 -11536221 163694 hypothetical protein b4256:hypothetical protein f97 (db:pir2.dat) S56481 S56481 Escherichia coli 562 -11536221 7500960327 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f97) (le:169856) (re:170149) (di:complement) ECOUW93 U14003 g537097 Escherichia coli 562 -11536221 237461 b4256 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 386 of 400 of the completengenome.) (nt:f97) (le:4878) (re:5171) (di:complement) AE000496 AE000496 g1790705 Escherichia coli 562 -11536221 6500732363 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4256 b4256 Escherichia coli 562 -11536221

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867691	12915	35071	447	148

Description

6500732364 hypothetical 44.4 kd protein in argi-vals intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b4257 b4257 Escherichia coli 562 -11536222 7500938023 yjgn (de:hypothetical 44.4 kd protein in argi-vals intergenic region) (db:swissprot) YJGN_ECOLI P39338 ESCHERICHIA COLI 562 -11536222 7000690943 hypothetical 44.4 kd protein in argi-vals intergenic region:hypothetical protein o204b (db:pir2.dat) D65238 D65238 Escherichia coli 562 -11536222 7500938025 yjgn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 386 of 400 of the completegenome.) (nt:o393; sequence change joins orfs yjgn and yjgo from) (le:5591) (re:6772) (di:direct) AE000496 AE000496 g2367367 Escherichia coli 562 -11536222

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867696	12916	35072	1617	539

Description

6500732365 yjgp:b4261 hypothetical 40.4 kd protein in pepa-gntv intergenic region:o366 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4261 b4261 Escherichia coli 562 -11536223 113765 yjgp (de:hypothetical 40.4 kd protein in pepa-gntv intergenic region (o366)) (db:swissprot) YJGP_ECOLI P39340 ESCHERICHIA COLI 562 -11536223 163825 yjgp hypothetical 40.4k protein pepa-gntv intergenic region:hypothetical protein o366 (db:pir2.dat) S56487 S56487 Escherichia coli 562 -11536223 7500938026 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o366) (le:177053) (re:178153) (di:direct) ECOUW93 U14003 g537103 Escherichia coli 562 -11536223 237467 yjgp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 387 of 400 of the completegenome.) (nt:o366; 100 pct identical amino acid sequence and) (le:196) (re:1296) (di:direct) AE000497 AE000497 g1790712 Escherichia coli 562 -11536223 5000693977 (de:(ecoli_4145) (pn:hypothetical 40) (gn:yjgp) (gtcfc:13.7:14.1) (ec:)) (yjgp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4145 ECOLI_4145 Escherichia coli 562 10055493

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867711	12917	35073	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867719	12918	35074	579	192

Description

6500732366 yjgq:b4262 hypothetical 39.8 kd protein in pepa-gntv intergenic region:o361 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4262 b4262 Escherichia coli 562 -11536224 113767 yjgq (de:hypothetical 39.8 kd protein in pepa-gntv intergenic region (o361)) (db:swissprot) YJGQ_ECOLI P39341 ESCHERICHIA COLI 562 -11536224 163823 yjgq hypothetical 39.8k protein pepa-gntv intergenic region:hypothetical protein o361 (db:pir2.dat) S56488 S56488 Escherichia coli 562 -11536224 7500938028 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o361) (le:178150) (re:179235) (di:direct) ECOUW93 U14003 g537104 Escherichia coli 562 -11536224 237468 yjgq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 387 of 400 of the completegenome.) (nt:o361; 100 pct identical amino acid sequence and) (le:1293) (re:2378) (di:direct) AE000497 AE000497 g1790713 Escherichia coli 562 -11536224 5000693978 (de:(ecoli_4146) (pn:hypothetical 39) (gn:yjgq) (gtcfc:13.7:14.1) (ec:) (yjgq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4146 ECOLI_4146 Escherichia coli 562 10055495

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867733	12919	35075	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867739	12920	35076	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867742	12921	35077	1221	406

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867763	12922	35078	672	223

Description

6500732367 yjgr:b4263 hypothetical 54.3 kd protein in pepa-gntv intergenic region:f500 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4263 b4263 Escherichia coli 562 -11536225 113769 yjgr (de:hypothetical 54.3 kd protein in pepa-gntv intergenic region (f500)) (db:swissprot) YJGR_ECOLI P39342 ESCHERICHIA COLI 562 -11536225 163673 yjgr hypothetical 54.3k protein pepa-gntv intergenic region:hypothetical protein f500 (db:pir2.dat) S56489 S56489 Escherichia coli 562 -11536225 7500938030 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f500) (le:179396) (re:180898) (di:complement) ECOUW93 U14003 g537105 Escherichia coli 562 -11536225 237469 yjgr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 387 of 400 of the completegenome.) (nt:f500; 100 pct identical amino acid sequence and) (le:2539) (re:4041) (di:complement) AE000497 AE000497 g1790714 Escherichia coli 562 -11536225 5000693979 (de:(ecoli_4147) (pn:hypothetical 54) (gn:yjgr) (gtcfc:13.7:14.1) (ec:) (yjgr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4147 ECOLI_4147 Escherichia coli 562 10055497

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867771	12923	35079	675	224

Description

6500732368 yjgs:b4264 hypothetical transcriptional regulator in pepa-gntv intergeni:hypothetical transcriptional regulator in pepa-gntv intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4264 b4264 Escherichia coli 562 -11536226 113770 yjgs (de:hypothetical transcriptional regulator in pepa-gntv intergenic region) (db:swissprot) YJGS_ECOLI P39343 ESCHERICHIA COLI 562 -11536226 163638 yjgs hypothetical transcription regulator pepa-gntv intergenic region:hypothetical protein f332 (cl:gntv protein) (db:pir2.dat) S56490 S56490 Escherichia coli 562 -11536226 7500938031 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f332) (le:180976) (re:181974) (di:complement) ECOUW93 U14003 g537106 Escherichia coli 562 -11536226 237470 idnr l-idonate transcriptional regulator (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 387 of 400 of the completegenome.) (nt:f332; formerly designated yjgs) (le:4119) (re:5117) (di:complement) AE000497 AE000497 g1790715 Escherichia coli 562 -11536226 5000693980 (de:(ecoli_4148) (pn:hypothetical transcriptional regulator in pepa-gntv intergenic region:f332) (gn:yjgs) (gtcfc:13.7:14.1) (ec:) (yjgs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4148 ECOLI_4148 Escherichia coli 562 10055498

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867780	12924	35080	474	157

Description

6500732369 yjgt:b4265 hypothetical 46.0 kd protein in pepa-gntv intergenic region:f439 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4265 b4265 Escherichia coli 562 -11536227 113771 yjgt (de:hypothetical 46.0 kd protein in pepa-gntv intergenic region) (db:swissprot) YJGT_ECOLI P39344 ESCHERICHIA COLI 562 -11536227 163664 yjgt hypothetical 46.0k protein pepa-gntv intergenic region:hypothetical protein f439 (cl:d-serine permease) (db:pir2.dat) S56491 S56491 Escherichia coli 562 -11536227 7500938032 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f439) (le:182041) (re:183360) (di:complement) ECOUW93 U14003 g537107 Escherichia coli 562 -11536227 237471 idnt l-idonate transporter (fn:transport; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 387 of 400 of the completegenome.) (nt:f439; formerly designated yjgt) (le:5184) (re:6503) (di:complement) AE000497 AE000497 g1790716 Escherichia coli 562 -11536227 5000693981 (de:(ecoli_4149) (pn:hypothetical 46) (gn:yjgt) (gtcfc:13.7:14.1) (ec:.) (yjgt_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4149 ECOLI_4149 Escherichia coli 562 10055499

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867794	12925	35081	702	233

Description

6500732370 yjgu:b4266 hypothetical 27.6 kd protein in pepa-gntv intergenic region:hypothetical oxidoreductase in pepa-gntv intergenic region (gtcfc:14.1) (ec:1.-.-.) (keggfc:14.1) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4266 b4266 Escherichia coli 562 -11536228 113772 yjgu (ec:1.-.-.) (de:(ec 1.-.-.) (db:swissprot) YJGU_ECOLI P39345 ESCHERICHIA COLI 562 -11536228 163603 yjgu hypothetical 27.6k protein pepa-gntv intergenic region:hypothetical protein f254 (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) S56492 S56492 Escherichia coli 562 -11536228 7500938033 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f254) (le:183422) (re:184186) (di:complement) ECOUW93 U14003 g537108 Escherichia coli 562 -11536228 237472 idno 5-keto-d-gluconate 5-reductase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 387 of 400 of the completegenome.) (nt:f254; formerly designated yjgu) (le:6565) (re:7329) (di:complement) AE000497 AE000497 g1790717 Escherichia coli 562 -11536228 5000693982 (de:(ecoli_4150) (pn:hypothetical oxidoreductase in pepa-gntv intergenic region:f254) (gn:yjgu) (gtcfc:13.7:14.1) (ec:1.-.-.) (yjgu_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4150 ECOLI_4150 Escherichia coli 562 10055500

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867796	12926	35082	402	133

Description

6500732371 yjgv:b4267 hypothetical zinc-type alcohol dehydrogenase-like protein in: hypothetical zinc-type alcohol dehydrogenase-like protein in pepa-gntv intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4267 b4267 Escherichia coli 562 -11536229 113773 yjgv (de:intergenic region) (db:swissprot) YJGV_ECOLI P39346 ESCHERICHIA COLI 562 -11536229 163641 yjgv probable alcohol dehydrogenase:yjgv:hypothetical protein f343a (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.-) (db:pir1.dat) S56493 S56493 Escherichia coli 562 -11536229 7500938034 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f343a) (le:184210) (re:185241) (di:complement) ECOUW93 U14003 g537109 Escherichia coli 562 -11536229 237473 idnd l-idonate dehydrogenase (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 387 of 400 of the complete genome.) (nt:f343a; formerly designated yjgv) (le:7353) (re:8384) (di:complement) AE000497 AE000497 g1790718 Escherichia coli 562 -11536229 5000693983 (de:(ecoli_4151) (pn:hypothetical zinc-type alcohol dehydrogenase-like protein in pepa-gntv intergenic region:f343a) (gn:yjgv) (gtcfc:13.7:14.1) (ec:) (yjgv_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4151 ECOLI_4151 Escherichia coli 562 10055501

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867798	12927	35083	912	303

Description

6500732372 yjgb:b4269 hypothetical zinc-type alcohol dehydrogenase-like protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4269 b4269 Escherichia coli 562 -11536230 164859 yjgb probable zinc-containing dehydrogenase:yjgb protein (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.-.-.-) (db:pir2.dat) S56495 S56495 Escherichia coli 562 -11536230 7500953780 yjgb (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:186025) (re:187086) (di:complement) ECOUW93 U14003 g537111 Escherichia coli 562 -11536230 237475 yjgb putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 387 of 400 of the complete genome.) (nt:f353; 100 pct identical to 339 amino acids of) (le:9168) (re:10229) (di:complement) AE000497 AE000497 g1790720 Escherichia coli 562 -11536230 5000693984 (de:(ecoli_4153) (pn:hypothetical zinc-type alcohol dehydrogenase-like protein in gntv-leux intergenic region:orf1) (gn:yjgb) (gtcfc:13.7:14.1) (ec:) (yjgb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4153 ECOLI_4153 Escherichia coli 562 10087491

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867804	12928	35084	183	60

Description

6500732373 yjgw:b4274 hypothetical 13.1 kd protein in leux-fece intergenic region:ol11 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4274 b4274 Escherichia coli 562 -11536231 163716 yjgw hypothetical 13.1k protein leux-fece intergenic region:hypothetical protein ol11 (db:pir2.dat) S56499 S56499 Escherichia coli 562 -11536231 237479 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_ol11) (le:190433) (re:190768) (di:direct) ECOUW93 U14003 g537115 Escherichia coli 562 -11536231 7500959778 yjgw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 388 of 400 of the completegenome.) (nt:ol11; 100 pct identical amino acid sequence and) (le:3301) (re:3636) (di:direct) AE000498 AE000498 g1790725 Escherichia coli 562 -11536231 113774 yjgw_ecoli (de:hypothetical 13.1 kd protein in leux-fece intergenic region (ol11).) P39348 P39348 Escherichia coli 562 -11536231 5000693986 (de:(ecoli_4157) (pn:hypothetical 13) (gn:yjgw) (gtcfc:13.7:14.1) (ec:) (yjgw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4157 ECOLI_4157 Escherichia coli 562 10055502

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867806	12929	35085	339	112

Description

6500732374 yjgx:b4275 hypothetical 16.4 kd protein in leux-fece intergenic region:f148 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4275 b4275 Escherichia coli 562 -11536232 113775 yjgx (de:hypothetical 16.4 kd protein in leux-fece intergenic region (f148)) (db:swissprot) YJGX_ECOLI P39349 ESCHERICHIA COLI 562 -11536232 163569 yjgx hypothetical 16.4k protein leux-fece intergenic region:hypothetical protein f148 (db:pir2.dat) S56500 S56500 Escherichia coli 562 -11536232 7500938035 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f148) (le:190877) (re:191323) (di:complement) ECOUW93 U14003 g537116 Escherichia coli 562 -11536232 237480 yjgx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 388 of 400 of the completegenome.) (nt:f148; 100 pct identical amino acid sequence and) (le:3745) (re:4191) (di:complement) AE000498 AE000498 g1790726 Escherichia coli 562 -11536232 5000693987 (de:(ecoli_4158) (pn:hypothetical 16) (gn:yjgx) (gtcfc:13.7:14.1) (ec:) (yjgx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4158 ECOLI_4158 Escherichia coli 562 10055503

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867807	12930	35086	405	135

Description

6500732375 yjgy:b4276 hypothetical 17.2 kd protein in leux-fece intergenic region:f149 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4276 b4276 Escherichia coli 562 -11536233 113777 yjgy (de:hypothetical 17.2 kd protein in leux-fece intergenic region (f149)) (db:swissprot) YJGY_ECOLI P39350 ESCHERICHIA COLI 562 -11536233 163570 yjgy hypothetical 17.2k protein leux-fece intergenic region:hypothetical protein f149 (db:pir2.dat) S56501 S56501 Escherichia coli 562 -11536233 7500938036 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f149) (le:191266) (re:191715) (di:complement) ECOUW93 U14003 g537117 Escherichia coli 562 -11536233 237481 yjgy orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 388 of 400 of the completegenome.) (nt:f149; 100 pct identical amino acid sequence and) (le:4134) (re:4583) (di:complement) AE000498 AE000498 g1790727 Escherichia coli 562 -11536233 5000693988 (de:(ecoli_4159) (pn:hypothetical 17) (gn:yjgy) (gtcfc:13.7:14.1) (ec:) (yjgy_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4159 ECOLI_4159 Escherichia coli 562 10055505

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867818	12931	35087	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867832	12932	35088	2202	733

Description

6500732376 yjgz:b4277 hypothetical 12.2 kd protein in leux-fece intergenic region:o109a (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4277 b4277 Escherichia coli 562 -11536234 113778 yjgz (de:hypothetical 12.2 kd protein in leux-fece intergenic region (o109a)) (db:swissprot) YJGZ_ECOLI P39351 ESCHERICHIA COLI 562 -11536234 163713 yjgz hypothetical 12.2k protein leux-fece intergenic region:hypothetical protein o109a (db:pir2.dat) S56502 S56502 Escherichia coli 562 -11536234 7500938037 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o109a) (le:192094) (re:192423) (di:direct) ECOUW93 U14003 g537118 Escherichia coli 562 -11536234 237482 yjgz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 388 of 400 of the completegenome.) (nt:o109a; 100 pct identical amino acid sequence and) (le:4962) (re:5291) (di:direct) AE000498 AE000498 g1790728 Escherichia coli 562 -11536234 5000693989 (de:(ecoli_4160) (pn:hypothetical 12) (gn:yjgz) (gtcfc:13.7:14.1) (ec:) (yjgz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4160 ECOLI_4160 Escherichia coli 562 10055506

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867839	12933	35089	804	268

Description

6500732377 yi41:b4278 insertion element is4 hypothetical 50.4 kd protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4278 b4278 Escherichia coli 562 -11536235 113083 b4278 (de:insertion element is4 hypothetical 50.4 kd protein) (db:swissprot) YI41_ECOLI P03835 ESCHERICHIA COLI 562 -11536235 135237 yi41 hypothetical protein 1:hypothetical protein f442 (db:pir1.dat) IIEC41 A04463 Escherichia coli 562 -11536235 243697 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f442) (le:192937) (re:194265) (di:complement) ECOUW93 U14003 g537119 Escherichia coli 562 -11536235 7500937250 unknown protein (sr:insertion sequence is4 (transposable element insertion sequenc) (db:genpept-bct1) (de:insertion sequence is4, complete sequence.) (nt:putative) (le:85) (re:1413) (di:direct) INS4CSORF M10575 g642118 Insertion sequence IS4 2684 -11536235 237483 yi41 is4 hypothetical protein (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 388 of 400 of the completegenome.) (nt:f442; 100 pct identical amino acid sequence and) (le:5805) (re:7133) (di:complement) AE000498 AE000498 g1790729 Escherichia coli 562 -11536235 5000693990 (de:(ecoli_4161) (pn:insertion element is4 hypothetical 50) (gn:yi41) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4161 ECOLI_4161 Escherichia coli 562 10054811

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867845	12934	35090	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867857	12935	35091	582	193

Description

6500732378 yjhb:b4279 hypothetical 46.6 kd protein in leux-fece intergenic region:o425 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4279 b4279 Escherichia coli 562 -11536236 163840 yjhb hypothetical 46.6k protein leux-fece intergenic region:hypothetical protein o425 (cl:escherichia coli hypothetical protein (leux-fece intergenic region)) (db:pir2.dat) S56504 S56504 Escherichia coli 562 -11536236 7500938054 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:ttg start codon) (le:194832) (re:196109) (di:direct) ECOUW93 U14003 g537120 Escherichia coli 562 -11536236 237484 yjhb putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 388 of 400 of the completegenome.) (nt:o425; 100 pct identical to yjhb_ecoli sw:) (le:7700) (re:8977) (di:direct) AE000498 AE000498 g1790730 Escherichia coli 562 -11536236 113790 yjhb (de:hypothetical 46.6 kd protein in leux-fece intergenic region (o425)) (db:swissprot) YJHB_ECOLI P39352 ESCHERICHIA COLI 562 -11536236 5000693991 (de:(ecoli_4162) (pn:hypothetical 46) (gn:yjhb) (gtcfc:13.7:14.1) (ec:) (yjhb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4162 ECOLI_4162 Escherichia coli 562 10055518

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867861	12936	35092	489	162

Description

6500732379 yjhc:b4280 hypothetical 41.9 kd protein in leux-fece intergenic region: o377 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4280 b4280 Escherichia coli 562 -11536237 163827 yjhc hypothetical 41.9k protein leux-fece intergenic region: hypothetical protein o377 (db:pir2.dat) S56505 S56505 Escherichia coli 562 -11536237 7500938055 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o377) (le:196106) (re:197239) (di:direct) ECOUW93 U14003 g537121 Escherichia coli 562 -11536237 237485 yjhc putative dehydrogenase (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 388 of 400 of the complete genome.) (nt:o377; 100 pct identical amino acid sequence and) (le:8974) (re:10107) (di:direct) AE000498 AE000498 g1790731 Escherichia coli 562 -11536237 113791 yjhc (de:hypothetical 41.9 kd protein in leux-fece intergenic region (o377)) (db:swissprot) YJHC_ECOLI P39353 ESCHERICHIA COLI 562 -11536237 5000693992 (de:(ecoli_4163) (pn:hypothetical 41) (gn:yjhc) (gtcfc:13.7:14.1) (ec:) (yjhc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4163 ECOLI_4163 Escherichia coli 562 10055519

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867867	12937	35093	690	230

Description

6500732380 yjhd:b4281 hypothetical 13.7 kd protein in leux-fece intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4281 b4281 Escherichia coli 562 -11536238 163557 yjhd hypothetical 13.7k protein leux-fece intergenic region: hypothetical protein f124 (db:pir2.dat) S56506 S56506 Escherichia coli 562 -11536238 7500959781 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f124) (le:197460) (re:197834) (di:complement) ECOUW93 U14003 g537122 Escherichia coli 562 -11536238 237486 yjhd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 389 of 400 of the complete genome.) (nt:f124; 100 pct identical amino acid sequence and) (le:122) (re:496) (di:complement) AE000499 AE000499 g1790733 Escherichia coli 562 -11536238 5000693993 (de:(ecoli_4164) (pn:hypothetical 8) (gn:yjhd) (gtcfc:13.7:14.1) (ec:) (yjhd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4164 ECOLI_4164 Escherichia coli 562 10086999

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867876	12938	35094	576	192

Description

6500732381 yjhe:b4282 hypothetical 7.1 kd protein in leux-fece intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4282 b4282 Escherichia coli 562 -11536239 163866 yjhe hypothetical 7.1k protein leux-fece intergenic region:hypothetical protein o67 (db:pir2.dat) S56507 S56507 Escherichia coli 562 -11536239 7500959827 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o67) (le:197740) (re:197943) (di:direct) ECOUW93 U14003 g537123 Escherichia coli 562 -11536239 237487 yjhe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 389 of 400 of the completegenome.) (nt:o67; 100 pct identical amino acid sequence and) (le:402) (re:605) (di:direct) AE000499 AE000499 g1790734 Escherichia coli 562 -11536239 5000693994 (de:(ecoli_4165) (pn:hypothetical 8) (gn:yjhe) (gtcfc:13.7:14.1) (ec:) (yjhe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4165 ECOLI_4165 Escherichia coli 562 10087066

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867878	12939	35095	1707	568

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867899	12940	35096	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867915	12941	35097	741	247

Description

6500732382 yi91:b4283 insertion element is911 hypothetical 11.6 kd protein:o100 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4283 b4283 Escherichia coli 562 -11536240 113106 b4283 (de:insertion element is911 hypothetical 11.6 kd protein) (db:swissprot) YI91_ECOLI P39212 ESCHERICHIA COLI 562 -11536240 163704 yi91 yi91 protein:hypothetical protein o100 (db:pir2.dat) S56508 S56508 Escherichia coli 562 -11536240 7500937266 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o100) (le:197995) (re:198297) (di:direct) ECOUW93 U14003 g537124 Escherichia coli 562 -11536240 237488 yi91b is911 hypothetical protein is911b (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 389 of 400 of the completegenome.) (nt:o100; 100 pct identical amino acid sequence and) (le:657) (re:959) (di:direct) AE000499 AE000499 g1790735 Escherichia coli 562 -11536240 5000693995 (de:(ecoli_4166) (pn:insertion element is911 hypothetical 11) (gn:yi91) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4166 ECOLI_4166 Escherichia coli 562 10054834

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867918	12942	35098	243	80

Description

5000693996 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4285 b4285 Escherichia coli 562 -11536241 163757 hypothetical protein o198:hypothetical protein b4285 (db:pir2.dat) S56510 S56510 Escherichia coli 562 -11536241 7500960361 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o198) (le:199792) (re:200388) (di:direct) ECOUW93 U14003 g537126 Escherichia coli 562 -11536241 237490 b4285 putative transposase (fn:is, phage, tn; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 389 of 400 of the completegenome.) (nt:o198; this 198 aa orf is 30 pct identical (3 gaps)) (le:2454) (re:3050) (di:direct) AE000499 AE000499 g1790737 Escherichia coli 562 -11536241 6500732383 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4285 b4285 Escherichia coli 562 -11536241

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867926	12943	35099	1689	563

Description

5000693997 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4286 b4286 Escherichia coli 562 -11536242
7000691821 hypothetical protein b4286:hypothetical protein o137 (db:pir2.dat) H65241 H65241 Escherichia coli 562 -11536242 7500960328 b4286 orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 389 of 400 of the completegenome.) (nt:o137; this 137 aa orf is 25 pct identical (9 gaps)) (le:3216) (re:3629) (di:direct) AE000499 AE000499 g1790738 Escherichia coli 562 -11536242 6500732384 hypothetical protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4286 b4286 Escherichia coli 562 -11536242

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867931	12944	35100	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867933	12945	35101	693	230

Description

6500732385 yjhu:b4295 hypothetical 29.1 kd protein in feci-fimb intergenic region:f266 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4295 b4295 Escherichia coli 562 -11536243 113810 yjhu (de:hypothetical transcriptional regulator in feci-fimb intergenic region) (db:swissprot) YJHU_ECOLI P39356 ESCHERICHIA COLI 562 -11536243 163611 yjhu hypothetical 29.1k protein feci-fimb intergenic region:hypothetical protein f266 (db:pir2.dat) S56520 S56520 Escherichia coli 562 -11536243 7500938070 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f266) (le:210172) (re:210972) (di:complement) ECOUW93 U14003 g537136 Escherichia coli 562 -11536243 237500 yjhu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f266; 100 pct identical amino acid sequence and) (le:2648) (re:3448) (di:complement) AE000500 AE000500 g1790748 Escherichia coli 562 -11536243 5000693999 (de:(ecoli_4178) (pn:hypothetical 29) (gn:yjhu) (gtcfc:13.7:14.1) (ec:) (yjhu_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4178 ECOLI_4178 Escherichia coli 562 10055538

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867944	12946	35102	453	150

Description

6500732386 yjhf:b4296 hypothetical 47.0 kd protein in feci-fimb intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4296 b4296 Escherichia coli 562 -11536244 7500938056 yjhf (de:hypothetical 47.0 kd protein in feci-fimb intergenic region) (db:swissprot) YJHF_ECOLI P39357 ESCHERICHIA COLI 562 -11536244 7000690949 yjhf hypothetical 47.0 kd protein in feci-fimb intergenic region:hypothetical protein f388 (cl:d-serine permease) (db:pir2.dat) B65243 B65243 Escherichia coli 562 -11536244 7500938058 yjhf putative transport system permease (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f449; sequence change lengthens c-terminus relative) (le:3981) (re:5330) (di:complement) AE000500 AE000500 g2367370 Escherichia coli 562 -11536244

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867946	12947	35103	408	135

Description

6500732387 yjhg:b4297 hypothetical 70.1 kd protein in feci-fimb intergenic region:f655 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4297 b4297 Escherichia coli 562 -11536245 7500938059 yjhg (de:hypothetical 70.0 kd protein in feci-fimb intergenic region) (db:swissprot) YJHG_ECOLI P39358 ESCHERICHIA COLI 562 -11536245 7000690970 yjhg hypothetical 70.1 kd protein in feci-fimb intergenic region:hypothetical protein f655 (cl:dihydroxy-acid dehydratase) (db:pir2.dat) C65243 C65243 Escherichia coli 562 -11536245 7500938061 yjhg putative dehydratase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f655; 99 pct identical to yjhg_ecoli sw: p39358) (le:5437) (re:7404) (di:complement) AE000500 AE000500 g2367371 Escherichia coli 562 -11536245

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867965	12948	35104	540	179

Description

6500732388 yjhh:b4298 hypothetical 34.9 kd protein in feci-fimb intergenic region:f319 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4298 b4298 Escherichia coli 562 -11536246 113796 yjhh (de:hypothetical 34.9 kd protein in feci-fimb intergenic region (f319)) (db:swissprot) YJHH_ECOLI P39359 ESCHERICHIA COLI 562 -11536246 163633 yjhh probable dihydrodipicolinate synthase yjhh:hypothetical protein f319 (cl:dihydrodipicolinate synthase) (db:pir2.dat) S56523 S56523 Escherichia coli 562 -11536246 7500938062 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f319) (le:214937) (re:215896) (di:complement) ECOUW93 U14003 g537139 Escherichia coli 562 -11536246 237503 yjhh putative lyase/synthase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f319; 100 pct identical amino acid sequence and) (le:7415) (re:8374) (di:complement) AE000500 AE000500 g1790751 Escherichia coli 562 -11536246 5000694002 (de:(ecoli_4181) (pn:hypothetical 34) (gn:yjhh) (gtcfc:13.7:14.1) (ec:) (yjhh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4181 ECOLI_4181 Escherichia coli 562 10055524

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501867968	12949	35105	750	249

Description

6500732389 yjhi:b4299 hypothetical transcriptional regulator in feci-fimb intergenic region:hypothetical transcriptional regulator in feci-fimb intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4299 b4299 Escherichia coli 562 -11536247 113797 yjhi (de:hypothetical transcriptional regulator in feci-fimb intergenic region) (db:swissprot) YJHI_ECOLI P39360 ESCHERICHIA COLI 562 -11536247 163608 yjhi hypothetical transcription regulator:feci-fimb intergenic region:hypothetical protein f262a (db:pir2.dat) S56524 S56524 Escherichia coli 562 -11536247 7500938063 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f262a) (le:215847) (re:216635) (di:complement) ECOUW93 U14003 g537140 Escherichia coli 562 -11536247 237504 yjhi putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f262a; 100 pct identical amino acid sequence and) (le:8325) (re:9113) (di:complement) AE000500 AE000500 g1790752 Escherichia coli 562 -11536247 5000694003 (de:(ecoli_4182) (pn:hypothetical transcriptional regulator in feci-fimb intergenic region:f262a) (gn:yjhi) (gtcfc:13.7:14.1) (ec:) (yjhi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4182 ECOLI_4182 Escherichia coli 562 10055525

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867970	12950	35106	570	189

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867977	12951	35107	426	142

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867989	12952	35108	558	186

Description

6500732390 yjhj:sgcr:b4300 hypothetical transcriptional regulator in feci-fimb intergenic region:putative sgc region transcriptional regulator (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4300 b4300 Escherichia coli 562 -11536248 113798 sgcr (de:putative sgc region transcriptional regulator) (db:swissprot) SGCR_ECOLI P39361 ESCHERICHIA COLI 562 -11536248 163605 yjhj hypothetical transcription regulator:feci-fimb intergenic region:hypothetical protein f260 (db:pir2.dat) S56525 S56525 Escherichia coli 562 -11536248 7500891601 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f260) (le:216938) (re:217720) (di:complement) ECOUW93 U14003 g537141 Escherichia coli 562 -11536248 237505 sgcr putative deor-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:f260; formerly designated yjhj) (le:9416) (re:10198) (di:complement) AE000500 AE000500 g1790753 Escherichia coli 562 -11536248 5000694004 (de:(ecoli_4183) (pn:hypothetical transcriptional regulator in feci-fimb intergenic region:f260) (gn:yjhj) (gtcfc:13.7:14.1) (ec:)(yjhj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4183 ECOLI_4183 Escherichia coli 562 10055526

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501867996	12953	35109	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868028	12954	35110	471	156

Description

6500732391 yjhm:sgcq:b4303 hypothetical 29.4 kd protein in feci-fimb intergenic region:putative sgc region protein sgcq (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4303 b4303 Escherichia coli 562 -11536249 113801 sgcq (de:putative sgc region protein sgcq) (db:swissprot) SGCQ_ECOLI P39364 ESCHERICHIA COLI 562 -11536249 163612 yjhm hypothetical 29.4k protein feci-fimb intergenic region:hypothetical protein f268a (db:pir2.dat) S56528 S56528 Escherichia coli 562 -11536249 7500891600 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f268a) (le:218943) (re:219749) (di:complement) ECOUW93 U14003 g537144 Escherichia coli 562 -11536249 237508 sgcq putative nucleoside triphosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 391 of 400 of the completegenome.) (nt:f268a; formerly designated yjhm) (le:96) (re:902) (di:complement) AE000501 AE000501 g1790757 Escherichia coli 562 -11536249 5000694006 (de:(ecoli_4186) (pn:hypothetical 29) (gn:yjhm) (gtcfc:13.7:14.1) (ec:) (yjhm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4186 ECOLI_4186 Escherichia coli 562 10055529

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868029	12955	35111	789	262

Description

6500732392 yjhn:sgcc:b4304 hypothetical phosphotransferase enzyme ii:putative phosphotransferase enzyme ii:c component sgcc (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4304 b4304 Escherichia coli 562 -11536250 113802 sgcc (de:putative phosphotransferase enzyme ii, c component sgcc) (db:swissprot) SGCC_ECOLI P39365 ESCHERICHIA COLI 562 -11536250 163663 yjhn probable phosphotransferase enzyme ii:hypothetical protein f437 (cl:phosphotransferase enzyme ii galactitol-specific) (db:pir2.dat) S56529 S56529 Escherichia coli 562 -11536250 7500891598 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f437) (le:219762) (re:221075) (di:complement) ECOUW93 U14003 g537145 Escherichia coli 562 -11536250 237509 sgcc putative pts system enzyme iic component (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 391 of 400 of the completegenome.) (nt:f437; formerly designated yjhn) (le:915) (re:2228) (di:complement) AE000501 AE000501 g1790758 Escherichia coli 562 -11536250 5000694007 (de:(ecoli_4187) (pn:hypothetical phosphotransferase enzyme ii, c component in feci-fimb intergenic region:f437) (gn:yjhn) (gtcfc:13.7:14.1) (ec:) (yjhn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4187 ECOLI_4187 Escherichia coli 562 10055530

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868056	12956	35112	564	188

Description

6500732393 yjho:sgcx:b4305 hypothetical 41.7 kd protein in feci-fimb intergenic region:putative sgc region protein sgcx (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4305 b4305 Escherichia coli 562 -11536251 7500891602 sgcx (de:putative sgc region protein sgcx) (db:swissprot) SGCX_ECOLI P39366 ESCHERICHIA COLI 562 -11536251 7000690940 yjho hypothetical 41.7 kd protein in feci-fimb intergenic region:hypothetical protein f383 (cl:thermophilic aminopeptidase i alpha chain) (db:pir2.dat) C65244 C65244 Escherichia coli 562 -11536251 7500891604 sgcx putative lyase/synthase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 391 of 400 of the completegenome.) (nt:f383; formerly designated yjho) (le:2515) (re:3666) (di:complement) AE000501 AE000501 g2367373 Escherichia coli 562 -11536251

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868059	12957	35113	954	318

Description

6500732394 yjhp:b4306 hypothetical 27.4 kd protein in feci-fimb intergenic region:f248 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4306 b4306 Escherichia coli 562 -11536252 113804 yjhp (de:hypothetical 27.4 kd protein in feci-fimb intergenic region (f248)) (db:swissprot) YJHP_ECOLI P39367 ESCHERICHIA COLI 562 -11536252 163601 yjhp hypothetical 27.4k protein feci-fimb intergenic region:hypothetical protein f248 (cl:bioc homology) (db:pir2.dat) S56531 S56531 Escherichia coli 562 -11536252 7500938064 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f248) (le:223269) (re:224015) (di:complement) ECOUW93 U14003 g537147 Escherichia coli 562 -11536252 237511 yjhp putative methyltransferase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 391 of 400 of the completegenome.) (nt:f248; 100 pct identical amino acid sequence and) (le:4422) (re:5168) (di:complement) AE000501 AE000501 g1790760 Escherichia coli 562 -11536252 5000694009 (de:(ecoli_4189) (pn:hypothetical 27) (gn:yjhp) (gtcfc:13.7:14.1) (ec:)) (yjhp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4189 ECOLI_4189 Escherichia coli 562 10055532

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868108	12958	35114	924	307

Description

6500732395 yjhg:b4307 hypothetical 20.0 kd protein in feci-fimb intergenic region:f181 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4307 b4307 Escherichia coli 562 -11536253 113805 yjhg (de:hypothetical 20.0 kd protein in feci-fimb intergenic region (f181)) (db:swissprot) YJHQ_ECOLI P39368 ESCHERICHIA COLI 562 -11536253 163576 yjhg hypothetical 20k protein feci-fimb intergenic region:hypothetical protein f181 (db:pir2.dat) S56532 S56532 Escherichia coli 562 -11536253 7500938065 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f181) (le:224071) (re:224616) (di:complement) ECOUW93 U14003 g537148 Escherichia coli 562 -11536253 237512 yjhg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 391 of 400 of the completengenome.) (nt:f181; 100 pct identical amino acid sequence and) (le:5224) (re:5769) (di:complement) AE000501 AE000501 g1790761 Escherichia coli 562 -11536253 5000694010 (de:(ecoli_4190) (pn:hypothetical 20) (gn:yjhg) (gtcfc:13.7:14.1) (ec:) (yjhg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4190 ECOLI_4190 Escherichia coli 562 10055533

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868110	12959	35115	537	178

Description

6500732396 yjhr:b4308 hypothetical 38.0 kd protein in feci-fimb intergenic region:o338 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4308 b4308 Escherichia coli 562 -11536254 113806 yjhr (de:hypothetical 38.0 kd protein in feci-fimb intergenic region (o338)) (db:swissprot) YJHR_ECOLI P39369 ESCHERICHIA COLI 562 -11536254 163816 yjhr hypothetical 38k protein feci-fimb intergenic region:hypothetical protein o338 (db:pir2.dat) S56533 S56533 Escherichia coli 562 -11536254 7500938066 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o338) (le:225847) (re:226863) (di:direct) ECOUW93 U14003 g537149 Escherichia coli 562 -11536254 237513 yjhr putative frameshift suppressor (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 391 of 400 of the completengenome.) (nt:o338; 100 pct identical amino acid sequence and) (le:7000) (re:8016) (di:direct) AE000501 AE000501 g1790762 Escherichia coli 562 -11536254 5000694011 (de:(ecoli_4191) (pn:hypothetical 38) (gn:yjhr) (gtcfc:13.7:14.1) (ec:) (yjhr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4191 ECOLI_4191 Escherichia coli 562 10055534

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868112	12960	35116	573	190

Description

6500732397 yjhs:b4309 hypothetical 36.9 kd protein in feci-fimb intergenic region:hypothetical 36.9 kd protein in feci-fimb intergenic region
precursor:f326b (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b4309 b4309 Escherichia coli 562 -11536255 113807
yjhs (de:(f326b)) (db:swissprot) YJHS_ECOLI P39370 ESCHERICHIA COLI 562
-11536255 163637 yjhs hypothetical 36.9k protein feci-fimb intergenic
region:hypothetical protein f326b (db:pir2.dat) S56534 S56534 Escherichia
coli 562 -11536255 7500938067 (db:genpept-bct1) (de:escherichia coli k-12
chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f326b) (le:227446)
(re:228426) (di:complement) ECOUW93 U14003 g537150 Escherichia coli 562
-11536255 237514 yjhs orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 391 of 400 of the
completegenome.) (nt:f326b; 100 pct identical amino acid sequence and)
(le:8599) (re:9579) (di:complement) AE000501 AE000501 g1790763 Escherichia
coli 562 -11536255 5000694012 (de:(ecoli_4192) (pn:hypothetical 36)
(gn:yjhs) (gtcfc:13.7:14.1) (ec:) (yjhs_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_4192 ECOLI_4192 Escherichia coli 562
10055535

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868120	12961	35117	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868121	12962	35118	258	85

Description

6500732398 yjht:b4310 hypothetical 43.7 kd protein in feci-fimb intergenic region:f404 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4310 b4310 Escherichia coli 562 -11536256 113808 yjht (de:hypothetical 43.7 kd protein in feci-fimb intergenic region (f404)) (db:swissprot) YJHT_ECOLI P39371 ESCHERICHIA COLI 562 -11536256 163656 yjht hypothetical 43.7k protein feci-fimb intergenic region:hypothetical protein f404 (db:pir2.dat) S56535 S56535 Escherichia coli 562 -11536256 7500938068 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f404) (le:228491) (re:229705) (di:complement) ECOUW93 U14003 g537151 Escherichia coli 562 -11536256 237515 yjht orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 391 of 400 of the completegenome.) (nt:f404; 100 pct identical amino acid sequence and) (le:9644) (re:10858) (di:complement) AE000501 AE000501 g1790764 Escherichia coli 562 -11536256 5000694013 (de:(ecoli_4193) (pn:hypothetical 43) (gn:yjht) (gtcfc:13.7:14.1) (ec:) (yjht_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4193 ECOLI_4193 Escherichia coli 562 10055536

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868123	12963	35119	315	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868131	12964	35120	774	257

Description

6500732399 yjha:b4311 hypothetical 28.3 kd protein in feci-fimb intergenic region:hypothetical 28.3 kd protein in feci-fimb intergenic region
precursor:f241 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli) b4311 b4311 Escherichia coli 562 -11536257 113789
yjha (de:hypothetical 28.3 kd protein in feci-fimb intergenic region
precursor) (db:swissprot) YJHA_ECOLI P39372 ESCHERICHIA COLI 562 -11536257
163597 yjha hypothetical 28.3k protein feci-fimb intergenic
region:hypothetical protein f241 (db:pir2.dat) S56536 S56536 Escherichia
coli 562 -11536257 7500938053 (db:genpept-bct1) (de:escherichia coli k-12
chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f241) (le:229617)
(re:230342) (di:complement) ECOUW93 U14003 g537152 Escherichia coli 562
-11536257 237516 yjha orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 391 of 400 of the
completegenome.) (nt:f241; 100 pct identical amino acid sequence and)
(le:10770) (re:11495) (di:complement) AE000501 AE000501 g1790765 Escherichia
coli 562 -11536257 5000694014 (de:(ecoli_4194) (pn:hypothetical 28)
(gn:yjha) (gtcfc:13.7:14.1) (ec:) (yjha_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_4194 ECOLI_4194 Escherichia coli 562
10055517

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868138	12965	35121	366	122

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868144	12966	35122	747	248

Description

6500732400 yjic:b4325 hypothetical 30.6 kd protein in uxur-iada intergenic region:f276 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4325 b4325 Escherichia coli 562 -11536258 113817 yjic (de:hypothetical 30.6 kd protein in uxur-iada intergenic region (f276)) (db:swissprot) YJIC_ECOLI P39374 ESCHERICHIA COLI 562 -11536258 163617 yjic hypothetical 30.6 kd protein uxur-iada intergenic region:hypothetical protein f276 (db:pir2.dat) S56550 S56550 Escherichia coli 562 -11536258 7500938079 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f276) (le:246322) (re:247152) (di:complement) ECOUW93 U14003 g537166 Escherichia coli 562 -11536258 237530 yjic orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.) (nt:f276; 100 pct identical amino acid sequence and) (le:4030) (re:4860) (di:complement) AE000503 AE000503 g1790781 Escherichia coli 562 -11536258 5000694017 (de:(ecoli_4208) (pn:hypothetical 30) (gn:yjic) (gtcfc:13.7:14.1) (ec:) (yjic_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4208 ECOLI_4208 Escherichia coli 562 10055545

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868145	12967	35123	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868161	12968	35124	429	143

Description

GTC ORF with score 187 to: (or:Caenorhabditis elegans) (db:genpept-inv) (de:caenorhabditis elegans cosmid f55a11, complete sequence.) (nt:possible zinc finger protein; cdna est embl:m89115) (le:3919:4192:4928:5136) (re:4146:4624:5090:5323) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868169	12969	35125	1791	596

Description

6500732401 yjid:b4326 hypothetical 15.2 kd protein in uxur-iada intergenic region:ol33b (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4326 b4326 Escherichia coli 562 -11536259 113818 yjid (de:hypothetical 15.2 kd protein in uxur-iada intergenic region (ol33b)) (db:swissprot) YJID_ECOLI P39375 ESCHERICHIA COLI 562 -11536259 163729 yjid hypothetical 15.2k protein uxur-iada intergenic region:hypothetical protein ol33b (db:pir2.dat) S56551 S56551 Escherichia coli 562 -11536259 7500938080 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_ol33b) (le:247816) (re:248217) (di:direct) ECOUW93 U14003 g537167 Escherichia coli 562 -11536259 237531 yjid orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.) (nt:ol33b; 100 pct identical amino acid sequence and) (le:5524) (re:5925) (di:direct) AE000503 AE000503 g1790782 Escherichia coli 562 -11536259 5000694018 (de:(ecoli_4209) (pn:hypothetical 15) (gn:yjid) (gtcfc:13.7:14.1) (ec:) (yjid_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4209 ECOLI_4209 Escherichia coli 562 10055546

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868181	12970	35126	906	301

Description

6500732402 yjie:b4327 hypothetical transcriptional regulator in uxur-iada intergeni:hypothetical transcriptional regulator in uxur-iada intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4327 b4327 Escherichia coli 562 -11536260 113819 yjie (de:hypothetical transcriptional regulator in uxur-iada intergenic region) (db:swissprot) YJIE_ECOLI P39376 ESCHERICHIA COLI 562 -11536260 163321 yjie hypothetical transcriptional regulator uxur-iada intergenic region:hypothetical protein iada 3 region (db:pir2.dat) S56552 S56552 Escherichia coli 562 -11536260 7500938081 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f303) (le:248210) (re:249121) (di:complement) ECOUW93 U14003 g537168 Escherichia coli 562 -11536260 237532 yjie putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.) (nt:f303; 100 pct identical amino acid sequence and) (le:5918) (re:6829) (di:complement) AE000503 AE000503 g1790783 Escherichia coli 562 -11536260 5000694019 (de:(ecoli_4210) (pn:hypothetical transcriptional regulator in uxur-iada intergenic region:f303) (gn:yjie) (gtcfc:13.7:14.1) (ec:) (yjie_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4210 ECOLI_4210 Escherichia coli 562 10055547

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868182	12971	35127	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868184	12972	35128	636	211

Description

6500732403 yjig:b4329 hypothetical 16.2 kd protein in iada-mcrd intergenic region:f153 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4329 b4329 Escherichia coli 562 -11536261 113820 yjig (de:hypothetical 16.2 kd protein in iada-mcrd intergenic region (f153)) (db:swissprot) YJIG_ECOLI P39378 ESCHERICHIA COLI 562 -11536261 163571 yjig hypothetical 16.2k protein iada-mcrd intergenic region:hypothetical protein f153 iada 5 region (db:pir2.dat) A55889 A55889 Escherichia coli 562 -11536261 238677 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f153) (le:250371) (re:250832) (di:complement) ECUW93 U14003 g537170 Escherichia coli 562 -11536261 237534 yjig orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.) (nt:f153; 100 pct identical amino acid sequence and) (le:8079) (re:8540) (di:complement) AE000503 AE000503 g1790785 Escherichia coli 562 -11536261 7500938082 orf1 (db:genpept-bct2) (de:escherichia coli (orf1) and isoaspartyl dipeptidase (iada) genes,complete cds, and (orf2) gene, partial cds.) (nt:identical to cds orf_f153 encoded by genbank) (le:544) (re:1005) (di:direct) ECU15029 U15029 g640030 Escherichia coli 562 -11536261 5000694021 (de:(ecoli_4212) (pn:hypothetical 16) (gn:yjig) (gtcfc:13.7:14.1) (ec:) (yjig_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4212 ECOLI_4212 Escherichia coli 562 10055548

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868204	12973	35129	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868224	12974	35130	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868228	12975	35131	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868229	12976	35132	408	135

Description

6500732404 yjih:b4330 hypothetical 24.2 kd protein in iada-mcrd intergenic region:f231 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4330 b4330 Escherichia coli 562 -11536262 113821 yjih (de:hypothetical 24.2 kd protein in iada-mcrd intergenic region (f231)) (db:swissprot) YJIH_ECOLI P39379 ESCHERICHIA COLI 562 -11536262 163593 yjih hypothetical 24.2k protein iada-mcrd intergenic region:hypothetical protein f231 (db:pir2.dat) S56555 S56555 Escherichia coli 562 -11536262 7500938083 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f231) (le:250829) (re:251524) (di:complement) ECOUW93 U14003 g537171 Escherichia coli 562 -11536262 237535 yjih orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.) (nt:f231; 100 pct identical amino acid sequence and) (le:8537) (re:9232) (di:complement) AE000503 AE000503 g1790786 Escherichia coli 562 -11536262 5000694022 (de:(ecoli_4213) (pn:hypothetical 24) (gn:yjih) (gtcfc:13.7:14.1) (ec:) (yjih_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4213 ECOLI_4213 Escherichia coli 562 10055549

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868239	12977	35133	474	157

Description

6500732405 yjii:b4331 hypothetical 24.6 kd protein in iada-mcrd intergenic region:o218 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4331 b4331 Escherichia coli 562 -11536263 113822 yjii (de:hypothetical 24.6 kd protein in iada-mcrd intergenic region (o218)) (db:swissprot) YJII_ECOLI P39380 ESCHERICHIA COLI 562 -11536263 163769 yjii hypothetical 24.6k protein iada-mcrd intergenic region:hypothetical protein o218 (db:pir2.dat) S56556 S56556 Escherichia coli 562 -11536263 7500938084 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o218) (le:251660) (re:252316) (di:direct) ECOUW93 U14003 g537172 Escherichia coli 562 -11536263 237536 yjii orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.) (nt:o218; 100 pct identical amino acid sequence and) (le:9368) (re:10024) (di:direct) AE000503 AE000503 g1790787 Escherichia coli 562 -11536263 5000694023 (de:(ecoli_4214) (pn:hypothetical 24) (gn:yjii) (gtcfc:13.7:14.1) (ec:) (yjii_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4214 ECOLI_4214 Escherichia coli 562 10055550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868246	12978	35134	312	103

Description

6500732406 yjij:b4332 hypothetical 41.4 kd protein in iada-mcrd intergenic region:f392 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4332 b4332 Escherichia coli 562 -11536264 113823 yjij (de:hypothetical 41.4 kd protein in iada-mcrd intergenic region (f392)) (db:swissprot) YJIJ_ECOLI P39381 ESCHERICHIA COLI 562 -11536264 163653 yjij hypothetical 41.4k protein iada-mcrd intergenic region:hypothetical protein f392 (db:pir2.dat) S56557 S56557 Escherichia coli 562 -11536264 7500938085 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f392) (le:252329) (re:253507) (di:complement) ECOUW93 U14003 g537173 Escherichia coli 562 -11536264 237537 yjij putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.) (nt:f392; 100 pct identical amino acid sequence and) (le:10037) (re:11215) (di:complement) AE000503 AE000503 g1790788 Escherichia coli 562 -11536264 5000694024 (de:(ecoli_4215) (pn:hypothetical 41) (gn:yjij) (gtcfc:13.7:14.1) (ec:) (yjij_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4215 ECOLI_4215 Escherichia coli 562 10055551

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868249	12979	35135	450	149

Description

6500732407 yjik:b4333 hypothetical 36.0 kd protein in iada-mcrd intergenic region:f323 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4333 b4333 Escherichia coli 562 -11536265 113824 yjik (de:hypothetical 36.0 kd protein in iada-mcrd intergenic region (f323)) (db:swissprot) YJIK_ECOLI P39382 ESCHERICHIA COLI 562 -11536265 163634 yjik hypothetical 36k protein iada-mcrd intergenic region:hypothetical protein f323 (db:pir2.dat) S56558 S56558 Escherichia coli 562 -11536265 7500938086 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f323) (le:253575) (re:254546) (di:complement) ECOUW93 U14003 g537174 Escherichia coli 562 -11536265 237538 yjik orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 394 of 400 of the completegenome.) (nt:f323; 100 pct identical amino acid sequence and) (le:64) (re:1035) (di:complement) AE000504 AE000504 g1790790 Escherichia coli 562 -11536265 5000694025 (de:(ecoli_4216) (pn:hypothetical 36) (gn:yjik) (gtcfc:13.7:14.1) (ec:) (yjik_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4216 ECOLI_4216 Escherichia coli 562 10055552

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868250	12980	35136	1635	544

Description

6500732408 yjil:b4334 hypothetical 27.4 kd protein in iada-mcrd intergenic region:f257 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4334 b4334 Escherichia coli 562 -11536266 113825 yjil (de:hypothetical 27.4 kd protein in iada-mcrd intergenic region (f257)) (db:swissprot) YJIL_ECOLI P39383 ESCHERICHIA COLI 562 -11536266 163604 yjil hypothetical 27.4k protein iada-mcrd intergenic region:hypothetical protein f257 (cl:hgdc protein) (db:pir2.dat) S56559 S56559 Escherichia coli 562 -11536266 7500938087 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f257) (le:254754) (re:255527) (di:complement) ECOUW93 U14003 g537175 Escherichia coli 562 -11536266 237539 yjil putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 394 of 400 of the completegenome.) (nt:f257; 100 pct identical amino acid sequence and) (le:1243) (re:2016) (di:complement) AE000504 AE000504 g1790791 Escherichia coli 562 -11536266 5000694026 (de:(ecoli_4217) (pn:hypothetical 27) (gn:yjil) (gtcfc:13.7:14.1) (ec:) (yjil_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4217 ECOLI_4217 Escherichia coli 562 10055553

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868259	12981	35137	444	147

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868270	12982	35138	273	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868273	12983	35139	531	176

Description

6500732409 yjim:b4335 hypothetical 43.6 kd protein in iada-mcrd intergenic region:f390b (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4335 b4335 Escherichia coli 562 -11536267 113826 yjim (de:hypothetical 43.6 kd protein in iada-mcrd intergenic region (f390b)) (db:swissprot) YJIM_ECOLI P39384 ESCHERICHIA COLI 562 -11536267 163652 yjim hypothetical 43.6k protein iada-mcrd intergenic region:hypothetical protein f390b (db:pir2.dat) S56560 S56560 Escherichia coli 562 -11536267 7500938088 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f390b) (le:255531) (re:256703) (di:complement) ECOUW93 U14003 g537176 Escherichia coli 562 -11536267 237540 yjim orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 394 of 400 of the completegenome.) (nt:f390b; 100 pct identical amino acid sequence and) (le:2020) (re:3192) (di:complement) AE000504 AE000504 g1790792 Escherichia coli 562 -11536267 5000694027 (de:(ecoli_4218) (pn:hypothetical 43) (gn:yjim) (gtcfc:13.7:14.1) (ec:) (yjim_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4218 ECOLI_4218 Escherichia coli 562 10055554

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868278	12984	35140	816	271

Description

6500732410 yjin:b4336 hypothetical 48.2 kd protein in iada-mcrd intergenic region:f426 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4336 b4336 Escherichia coli 562 -11536268 113827 yjin (de:hypothetical 48.2 kd protein in iada-mcrd intergenic region (f426)) (db:swissprot) YJIN_ECOLI P39385 ESCHERICHIA COLI 562 -11536268 163662 yjin hypothetical 48.2k protein iada-mcrd intergenic region:hypothetical protein f426 (db:pir2.dat) S56561 S56561 Escherichia coli 562 -11536268 7500938089 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f426) (le:256798) (re:258078) (di:complement) ECOUW93 U14003 g537177 Escherichia coli 562 -11536268 237541 yjin orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 394 of 400 of the completegenome.) (nt:f426; 100 pct identical amino acid sequence and) (le:3287) (re:4567) (di:complement) AE000504 AE000504 g1790793 Escherichia coli 562 -11536268 5000694028 (de:(ecoli_4219) (pn:hypothetical 48) (gn:yjin) (gtcfc:13.7:14.1) (ec:) (yjin_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4219 ECOLI_4219 Escherichia coli 562 10055555

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868304	12985	35141	312	103

Description

6500732411 yjio:b4337 hypothetical 44.7 kd protein in iada-mcrd intergenic region:f410 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4337 b4337 Escherichia coli 562 -11536269 113828 yjio (de:hypothetical 44.7 kd protein in iada-mcrd intergenic region (f410)) (db:swissprot) YJIO_ECOLI P39386 ESCHERICHIA COLI 562 -11536269 163658 yjio hypothetical 44.7k protein iada-mcrd intergenic region:hypothetical protein f410 (cl:escherichia coli hypothetical protein (iada-mcrd intergenic region)) (db:pir2.dat) S56562 S56562 Escherichia coli 562 -11536269 7500938090 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f410) (le:258119) (re:259351) (di:complement) ECOUW93 U14003 g537178 Escherichia coli 562 -11536269 237542 yjio putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 394 of 400 of the completegenome.) (nt:f410; 100 pct identical amino acid sequence and) (le:4608) (re:5840) (di:complement) AE000504 AE000504 g1790794 Escherichia coli 562 -11536269 5000694029 (de:(ecoli_4220) (pn:hypothetical 44) (gn:yjio) (gtcfc:13.7:14.1) (ec:) (yjio_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4220 ECOLI_4220 Escherichia coli 562 10055556

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868305	12986	35142	1083	360

Description

6500732412 yjip:b4338 hypothetical 12.1 kd protein in iada-mcrd intergenic region:o103 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4338 b4338 Escherichia coli 562 -11536270 113829 yjip (de:hypothetical 12.1 kd protein in iada-mcrd intergenic region (o103)) (db:swissprot) YJIP_ECOLI P39387 ESCHERICHIA COLI 562 -11536270 163707 yjip hypothetical 12.1k protein iada-mcrd intergenic region:hypothetical protein o103 (db:pir2.dat) S56563 S56563 Escherichia coli 562 -11536270 7500938091 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o103) (le:259830) (re:260141) (di:direct) ECOUW93 U14003 g537179 Escherichia coli 562 -11536270 237543 yjip orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 394 of 400 of the completegenome.) (nt:o103; 100 pct identical amino acid sequence and) (le:6319) (re:6630) (di:direct) AE000504 AE000504 g1790795 Escherichia coli 562 -11536270 5000694030 (de:(ecoli_4221) (pn:hypothetical 12) (gn:yjip) (gtcfc:13.7:14.1) (ec:) (yjip_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4221 ECOLI_4221 Escherichia coli 562 10055557

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868321	12987	35143	1056	351

Description

6500732413 yjiq:b4339 hypothetical 21.8 kd protein in iada-mcrd intergenic region:o186 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4339 b4339 Escherichia coli 562 -11536271 113830 yjiq (de:hypothetical 21.8 kd protein in iada-mcrd intergenic region (o186)) (db:swissprot) YJIQ_ECOLI P39388 ESCHERICHIA COLI 562 -11536271 163754 yjiq hypothetical 21.8k protein iada-mcrd intergenic region:hypothetical protein o186 (db:pir2.dat) S56564 S56564 Escherichia coli 562 -11536271 7500938092 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o186) (le:260190) (re:260750) (di:direct) ECOUW93 U14003 g537180 Escherichia coli 562 -11536271 237544 yjiq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 394 of 400 of the completegenome.) (nt:o186; 100 pct identical amino acid sequence and) (le:6679) (re:7239) (di:direct) AE000504 AE000504 g1790796 Escherichia coli 562 -11536271 5000694031 (de:(ecoli_4222) (pn:hypothetical 21) (gn:yjiq) (gtcfc:13.7:14.1) (ec:) (yjiq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4222 ECOLI_4222 Escherichia coli 562 10055558

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868329	12988	35144	1128	375

Description

6500732414 yjir:b4340 hypothetical 53.0 kd protein in iada-mcrd intergenic region:f470 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4340 b4340 Escherichia coli 562 -11536272 113831 yjir (de:hypothetical 53.0 kd protein in iada-mcrd intergenic region (f470)) (db:swissprot) YJIR_ECOLI P39389 ESCHERICHIA COLI 562 -11536272 163666 yjir hypothetical 53k protein iada-mcrd intergenic region:hypothetical protein f470 (cl:hypothetical protein b1439) (db:pir2.dat) S56565 S56565 Escherichia coli 562 -11536272 7500938093 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f470) (le:260994) (re:262406) (di:complement) ECOUW93 U14003 g537181 Escherichia coli 562 -11536272 237545 yjir putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 394 of 400 of the completengenome.) (nt:f470; 100 pct identical amino acid sequence and) (le:7483) (re:8895) (di:complement) AE000504 AE000504 g1790797 Escherichia coli 562 -11536272 5000694032 (de:(ecoli_4223) (pn:hypothetical 53) (gn:yjir) (gtcfc:13.7:14.1) (ec:) (yjir_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4223 ECOLI_4223 Escherichia coli 562 10055559

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868330	12989	35145	480	159

Description

6500732415 yjis:b4341 hypothetical protein:hypothetical 6.7 kd protein in iada-mcrd intergenic region:o54 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4341 b4341 Escherichia coli 562 -11536273 113832 yjis (de:hypothetical 6.7 kd protein in iada-mcrd intergenic region) (db:swissprot) YJIS_ECOLI P39390 ESCHERICHIA COLI 562 -11536273 163859 hypothetical protein o54:hypothetical protein b4341 (db:pir2.dat) S56566 S56566 Escherichia coli 562 -11536273 7500938094 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o54) (le:262583) (re:262747) (di:direct) ECOUW93 U14003 g537182 Escherichia coli 562 -11536273 237546 yjis orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 394 of 400 of the completengenome.) (nt:o54) (le:9072) (re:9236) (di:direct) AE000504 AE000504 g1790798 Escherichia coli 562 -11536273 5000694033 (de:(ecoli_4224) (pn:hypothetical 6) (gtcfc:13.7:14.1) (ec:) (yjis_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4224 ECOLI_4224 Escherichia coli 562 10055560

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868345	12990	35146	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868353	12991	35147	1335	445

Description

6500732416 yjit:b4342 hypothetical 58.6 kd protein in iada-mcrd intergenic region:o521 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4342 b4342 Escherichia coli 562 -11536274 113833 yjit (de:hypothetical 58.6 kd protein in iada-mcrd intergenic region) (db:swissprot) YJIT_ECOLI P39391 ESCHERICHIA COLI 562 -11536274 163857 yjit hypothetical 58.6k protein iada-mcrd intergenic region:hypothetical protein o521 (db:pir2.dat) S56567 S56567 Escherichia coli 562 -11536274 7500938095 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o521) (le:263198) (re:264763) (di:direct) ECOUW93 U14003 g537183 Escherichia coli 562 -11536274 237547 yjit orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 394 of 400 of the completegenome.) (nt:o521; 100 pct identical amino acid sequence and) (le:9687) (re:11252) (di:direct) AE000504 AE000504 g1790799 Escherichia coli 562 -11536274 5000694034 (de:(ecoli_4225) (pn:hypothetical 58) (gn:yjit) (gtcfc:13.7:14.1) (ec:) (yjit_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4225 ECOLI_4225 Escherichia coli 562 10055561

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868383	12992	35148	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868391	12993	35149	348	115

Description

GTC ORF with score 170 to: (fn:involved in heterokaryon incompatibility) (sr:podospora anserina dna) (db:genpept-vrl) (de:podospora anserina beta transducin-like protein (het-e1) gene,complete cds.) (nt:putative) (le:810:3142) (re:3092:4929) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868396	12994	35150	897	298

Description

6500732417 hypothetical 58.2 kd protein in iada-mcrd intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b4343 b4343 Escherichia coli 562 -11536275 7500938096 yjiv (de:hypothetical 58.2 kd protein in iada-mcrd intergenic region) (db:swissprot) YJIV_ECOLI P39393 ESCHERICHIA COLI 562 -11536275 7000690961 hypothetical 58.2 kd protein in iada-mcrd intergenic region:hypothetical protein o109b (db:pir2.dat) A65249 A65249 Escherichia coli 562 -11536275 7500938098 yjiu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 395 of 400 of the completegenome.) (nt:o513; sequence change joins orfs yjiu and yjiv from) (le:145) (re:1686) (di:direct) AE000505 AE000505 g2367376 Escherichia coli 562 -11536275

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868403	12995	35151	531	176

Description

6500732418 yjiw:b4347 hypothetical 14.6 kd protein in mcrb-hsds intergenic region:f132 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4347 b4347 Escherichia coli 562 -11536276 113836 yjiw (de:hypothetical 14.6 kd protein in mcrb-hsds intergenic region (f132)) (db:swissprot) YJIW_ECOLI P39394 ESCHERICHIA COLI 562 -11536276 163560 yjiw hypothetical 14.6k protein mcrb-hsds intergenic region:hypothetical protein f132 (db:pir2.dat) S56573 S56573 Escherichia coli 562 -11536276 7500938099 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f132) (le:270332) (re:270730) (di:complement) ECOUW93 U14003 g537189 Escherichia coli 562 -11536276 237553 yjiw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 395 of 400 of the completegenome.) (nt:f132; 100 pct identical amino acid sequence and) (le:5510) (re:5908) (di:complement) AE000505 AE000505 g1790806 Escherichia coli 562 -11536276 5000694038 (de:(ecoli_4231) (pn:hypothetical 14) (gn:yjiw) (gtcfc:13.7:14.1) (ec:) (yjiw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4231 ECOLI_4231 Escherichia coli 562 10055564

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868404	12996	35152	1491	496

Description

6500732419 yjia:b4352 f2:hypothetical 32.0 kd protein in mrr-tsr intergenic region:f284 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4352 b4352 Escherichia coli 562 -11536277 113816 yjia (de:hypothetical 32.0 kd protein in mrr-tsr intergenic region (f284)) (db:swissprot) YJIA_ECOLI P24203 ESCHERICHIA COLI 562 -11536277 164860 yjia yjia protein:hypothetical 32k protein mrr-tsr intergenic region (db:pir2.dat) S56578 S56578 Escherichia coli 562 -11536277 7500938078 yjia (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:278742) (re:279596) (di:complement) ECOUW93 U14003 g537194 Escherichia coli 562 -11536277 237558 yjia orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 396 of 400 of the completengenome.) (nt:f284; f284; 100 pct identical amino acid) (le:1057) (re:1911) (di:complement) AE000506 AE000506 g1790812 Escherichia coli 562 -11536277 5000694039 (de:(ecoli_4236) (pn:hypothetical 32) (gn:yjia) (gtcfc:13.7:14.1) (ec:) (yjia_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4236 ECOLI_4236 Escherichia coli 562 10055544

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868405	12997	35153	507	168

Description

6500732420 yjix:b4353 hypothetical 7.7 kd protein in mrr-tsr intergenic region:f67 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4353 b4353 Escherichia coli 562 -11536278 113837 yjix (de:hypothetical 7.7 kd protein in mrr-tsr intergenic region (f67)) (db:swissprot) YJIX_ECOLI P39395 ESCHERICHIA COLI 562 -11536278 163685 yjix hypothetical 7.7k protein mrr-tsr intergenic region:hypothetical protein f67 (db:pir2.dat) S56579 S56579 Escherichia coli 562 -11536278 7500938100 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f67) (le:279710) (re:279913) (di:complement) ECOUW93 U14003 g537195 Escherichia coli 562 -11536278 237559 yjix orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 396 of 400 of the completengenome.) (nt:f67; 100 pct identical amino acid sequence and) (le:2024) (re:2227) (di:complement) AE000506 AE000506 g1790813 Escherichia coli 562 -11536278 5000694040 (de:(ecoli_4237) (pn:hypothetical 7) (gn:yjix) (gtcfc:13.7:14.1) (ec:) (yjix_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4237 ECOLI_4237 Escherichia coli 562 10055565

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868430	12998	35154	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868433	12999	35155	1668	555

Description

6500732421 yjiy:b4354 hypothetical 77.9 kd protein in mrr-tsr intergenic region:f721 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4354 b4354 Escherichia coli 562 -11536279 113838 yjiy (de:hypothetical 77.9 kd protein in mrr-tsr intergenic region (f721)) (db:swissprot) YJIY_ECOLI P39396 ESCHERICHIA COLI 562 -11536279 163688 yjiy carbon starvation protein-like protein yjiy:protein f721 (cl:carbon starvation protein) (db:pir2.dat) S56580 S56580 Escherichia coli 562 -11536279 7500938101 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f721) (le:279963) (re:282128) (di:complement) ECOUW93 U14003 g537196 Escherichia coli 562 -11536279 237560 yjiy putative carbon starvation protein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 396 of 400 of the completegenome.) (nt:f721; 100 pct identical amino acid sequence and) (le:2277) (re:4442) (di:complement) AE000506 AE000506 g1790814 Escherichia coli 562 -11536279 5000694041 (de:(ecoli_4238) (pn:hypothetical 77) (gn:yjiy) (gtcfc:13.7:14.1) (ec:) (yjiy_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4238 ECOLI_4238 Escherichia coli 562 10055566

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868447	13000	35156	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868469	13001	35157	2199	732

Description

6500732422 hypothetical 49.4 kd protein in tsr-mdob intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0:5.7.0) (db:gtc-escherichia coli) b4356 b4356 Escherichia coli 562 -11536280 7500938120 yj1 (de:hypothetical 49.4 kd protein in tsr-mdob intergenic region) (db:swissprot) YJ1L_ECOLI P39398 ESCHERICHIA COLI 562 -11536280 7000690952 hypothetical 49.4 kd protein in tsr-mdob intergenic region (cl:hexuronate transporter) (db:pir2.dat) F65250 F65250 Escherichia coli 562 -11536280 7500938122 yj2 putative transport protein:cryptic:orf:joins (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 396 of 400 of the completegenome.) (nt:f453; sequence change joins orfs yj1 and yj2 from) (le:6509) (re:7870) (di:complement) AE000506 AE000506 g2367379 Escherichia coli 562 -11536280

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868476	13002	35158	1092	363

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868485	13003	35159	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868487	13004	35160	732	243

Description

6500732423 yjjm:b4357 hypothetical 31.4 kd protein in tsr-mdob intergenic region:f268b (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4357 b4357 Escherichia coli 562 -11536281 113854 yjjm (de:hypothetical 31.4 kd protein in tsr-mdob intergenic region (f268b)) (db:swissprot) YJJM_ECOLI P39399 ESCHERICHIA COLI 562 -11536281 163613 yjjm hypothetical 31.4k protein tsr-mdob intergenic region:hypothetical protein f268b (db:pir2.dat) S56584 S56584 Escherichia coli 562 -11536281 7500938123 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f268b) (le:285770) (re:286576) (di:complement) ECOUW93 U14003 g537200 Escherichia coli 562 -11536281 237564 yjjm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 396 of 400 of the completegenome.) (nt:f268b; 100 pct identical amino acid sequence and) (le:8085) (re:8891) (di:complement) AE000506 AE000506 g1790818 Escherichia coli 562 -11536281 5000694044 (de:(ecoli_4242) (pn:hypothetical 31) (gn:yjjm) (gtcfc:13.7:14.1) (ec:) (yjjm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4242 ECOLI_4242 Escherichia coli 562 10055582

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868507	13005	35161	324	107

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868517	13006	35162	492	163

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868519	13007	35163	432	143

Description

6500732424 yjjn:b4358 hypothetical zinc-type alcohol dehydrogenase-like protein in tsr-mdob intergenic region:hypothetical zinc-type alcohol dehydrogenase-like protein in tsr-mdob intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4358 b4358 Escherichia coli 562 -11536282 113855 yjjn (de:intergenic region) (db:swissprot) YJJN_ECOLI P39400 ESCHERICHIA COLI 562 -11536282 163818 yjjn l-iditol 2-dehydrogenase:homolog yjjn:hypothetical protein o345:sorbitol dehydrogenase (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.14) (db:pir1.dat) S56585 S56585 Escherichia coli 562 -11536282 7500938124 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o345) (le:286807) (re:287844) (di:direct) ECOUW93 U14003 g537201 Escherichia coli 562 -11536282 237565 yjjn putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 396 of 400 of the completegenome.) (nt:o345; 100 pct identical amino acid sequence and) (le:9122) (re:10159) (di:direct) AE000506 AE000506 g1790819 Escherichia coli 562 -11536282 5000694045 (de:(ecoli_4243) (pn:hypothetical zinc-type alcohol dehydrogenase-like protein in tsr-mdob intergenic region:o345) (gn:yjjn) (gtcfc:13.7:14.1) (ec:) (yjjn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4243 ECOLI_4243 Escherichia coli 562 10055583

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868530	13008	35164	663	220

Description

6500732425 yjja:b4360 hypothetical 17.5 kd protein in mdob-dnac intergenic region: hypothetical 17.5 kd protein in mdob-dnac intergenic region precursor: protein p-18:f165 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4360 b4360 Escherichia coli 562 -11536283 113845 yjja (de:(protein p-18) (f165)) (db:swissprot) YJJA_ECOLI P18390 ESCHERICHIA COLI 562 -11536283 154687 yjja primosomal operon 17.5k protein mdob-dnac intergenic region:p18 protein (cl:primosomal operon 18k protein) (db:pir1.dat) (mp:99 min) RMEC18 S56587 Escherichia coli 562 -11536283 7500938109 yjja p18 protein (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:290527) (re:291024) (di:complement) ECOUW93 U14003 g537203 Escherichia coli 562 -11536283 237568 yjja putative glycoprotein/receptor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 397 of 400 of the complete genome.) (nt:f165; 100 pct identical amino acid sequence and) (le:2644) (re:3141) (di:complement) AE000507 AE000507 g1790822 Escherichia coli 562 -11536283 5000694046 (de:(ecoli_4245) (pn:hypothetical 17) (gn:yjja) (gtcfc:13.7:14.1) (ec:) (yjja_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4245 ECOLI_4245 Escherichia coli 562 10055573

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868535	13009	35165	288	95

Description

6500732426 yjyp:b4364 hypothetical 30.5 kd protein in dnat-hold intergenic region: hypothetical 30.5 kd protein in dnat-bglj intergenic region:f277 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4364 b4364 Escherichia coli 562 -11536284 113856 yjyp (de:hypothetical 30.5 kd protein in dnat-bglj intergenic region (f277)) (db:swissprot) YJYP_ECOLI P39402 ESCHERICHIA COLI 562 -11536284 163618 yjyp hypothetical 30.5k protein dnat-hold intergenic region:hypothetical protein f277 (db:pir2.dat) S56591 S56591 Escherichia coli 562 -11536284 7500938125 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f277) (le:292920) (re:293753) (di:complement) ECOUW93 U14003 g537207 Escherichia coli 562 -11536284 237572 yjyp putative structural protein (fn:putative structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 397 of 400 of the complete genome.) (nt:f277; 100 pct identical amino acid sequence and) (le:5037) (re:5870) (di:complement) AE000507 AE000507 g1790826 Escherichia coli 562 -11536284 5000694048 (de:(ecoli_4249) (pn:hypothetical 30) (gn:yjyp) (gtcfc:13.7:14.1) (ec:) (yjyp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4249 ECOLI_4249 Escherichia coli 562 10055584

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868539	13010	35166	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868555	13011	35167	660	219

Description

6500732427 yjjq:b4365 hypothetical 27.0 kd protein in dnat-hold intergenic region:hypothetical 27.0 kd protein in dnat-bglj intergenic region:o241 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4365 b4365 Escherichia coli 562 -11536285 113858 yjjq (de:hypothetical 27.0 kd protein in dnat-bglj intergenic region (o241)) (db:swissprot) YJJQ_ECOLI P39403 ESCHERICHIA COLI 562 -11536285 163781 yjjq hypothetical 27k protein dnat-hold intergenic region:hypothetical protein o241 (db:pir2.dat) S56592 S56592 Escherichia coli 562 -11536285 7500938127 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o241) (le:294309) (re:295034) (di:direct) ECOUW93 U14003 g537208 Escherichia coli 562 -11536285 237573 yjjq putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 397 of 400 of the completegenome.) (nt:o241; 100 pct identical amino acid sequence and) (le:6426) (re:7151) (di:direct) AE000507 AE000507 g1790827 Escherichia coli 562 -11536285 5000694049 (de:(ecoli_4250) (pn:hypothetical 27) (gn:yjjq) (gtcfc:13.7:14.1) (ec:)) (yjjq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4250 ECOLI_4250 Escherichia coli 562 10055586

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868557	13012	35168	636	211

Description

6500732428 yjrr:bglj:b4366 hypothetical 25.6 kd protein in dnat-hold intergenic region:bglj protein (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4366 b4366 Escherichia coli 562 -11536286 163774 bglj:yjrr bglj protein:protein o225a (db:pir2.dat) (mp:99 min) S56593 S56593 Escherichia coli 562 -11536286 239459 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o225a) (le:294992) (re:295669) (di:direct) ECOUW93 U14003 g537209 Escherichia coli 562 -11536286 297664 bglj (db:genpept-bct1) (de:escherichia coli bglj gene, complete cds.) (le:38) (re:715) (di:direct) ECU35834 U35834 g1754973 Escherichia coli 562 -11536286 237574 bglj 2-component transcriptional regulator (fn:regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 397 of 400 of the completegenome.) (nt:o225a; 100 pct identical amino acid sequence and) (le:7109) (re:7786) (di:direct) AE000507 AE000507 g1790828 Escherichia coli 562 -11536286 113859 bglj (de:bglj protein) (db:swissprot) BGLJ_ECOLI P39404 ESCHERICHIA COLI 562 -11536286 5000694050 (de:(ecoli_4251) (pn:hypothetical 25) (gn:yjrr) (gtcfc:13.7:14.1) (ec:) (yjrr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4251 ECOLI_4251 Escherichia coli 562 10055587

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868564	13013	35169	363	120

Description

6500732429 yjjs:fhuf:b4367 hypothetical 30.1 kd protein in dnat-hold intergenic region:ferric hydroxamate transport protein fhuf (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4367 b4367 Escherichia coli 562 -11536287 113860 fhuf (de:ferric hydroxamate transport protein fhuf) (db:swissprot) FHUF_ECOLI P39405 ESCHERICHIA COLI 562 -11536287 163609 yjjs hypothetical 30.1k protein dnat-hold intergenic region:hypothetical protein f262b (db:pir2.dat) S56594 S56594 Escherichia coli 562 -11536287 7500881446 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f262b) (le:295707) (re:296495) (di:complement) ECOUW93 U14003 g537210 Escherichia coli 562 -11536287 237575 fhuf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 397 of 400 of the completegenome.) (nt:f262b; 100 pct identical amino acid sequence and) (le:7824) (re:8612) (di:complement) AE000507 AE000507 g1790829 Escherichia coli 562 -11536287 5000694051 (de:(ecoli_4252) (pn:hypothetical 30) (gn:yjjs) (gtcfc:13.7:14.1) (ec:) (yjjs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4252 ECOLI_4252 Escherichia coli 562 10055588

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868565	13014	35170	1221	406

Description

6500732430 yjtt:b4371 hypothetical 37.6 kd protein in dnat-hold intergenic region: hypothetical 37.6 kd protein in fhuf-hold intergenic region: f343b (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4371 b4371 Escherichia coli 562 -11536288 113861 yjtt (de: hypothetical 37.6 kd protein in fhuf-hold intergenic region (f343b)) (db:swissprot) YJTT_ECOLI P39406 ESCHERICHIA COLI 562 -11536288 163642 yjtt hypothetical 37.6k protein dnat-hold intergenic region: hypothetical protein f343b (db:pir2.dat) S56595 S56595 Escherichia coli 562 -11536288 7500938128 (db:genpept-bct1) (de: escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f343b) (le:297501) (re:298532) (di:complement) ECOUW93 U14003 g537211 Escherichia coli 562 -11536288 237576 yjtt putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de: escherichia coli k-12 mg1655 section 397 of 400 of the complete genome.) (nt:f343b; 100 pct identical amino acid sequence and) (le:9618) (re:10649) (di:complement) AE000507 AE000507 g1790830 Escherichia coli 562 -11536288 5000694052 (de: (ecoli_4253) (pn: hypothetical 37) (gn: yjtt) (gtcfc:13.7:14.1) (ec:) (yjtt_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4253 ECOLI_4253 Escherichia coli 562 10055589

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868570	13015	35171	300	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868573	13016	35172	363	120

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868579	13017	35173	1266	421

Description

GTC ORF with score 116 to: (sr:thale cress) (db:genpept-pln1) (de:the sequence of bac fln21 from arabidopsis thaliana chromosome 1, complete sequence.) (nt:similar to est gb|n38308) (le:66075:66260:66445:66612) (re:66161:66357:66531:66774) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868584	13018	35174	534	178

Description

6500732431 yjjg:b4374 hypothetical 22.2 kd protein in rimi-prfc intergenic region (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4374 b4374 Escherichia coli 562 -11536289 7500938111 yjjg (de:hypothetical 25.3 kd protein in rimi-prfc intergenic region) (db:swissprot) YJJG_ECOLI P33999 ESCHERICHIA COLI 562 -11536289 164861 yjjg hypothetical 22.2k protein rimi-prfc intergenic region:yjjg protein (db:pir2.dat) S56598 S56598 Escherichia coli 562 -11536289 237579 yjjg (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:299477) (re:300154) (di:direct) ECOUW93 U14003 g537214 Escherichia coli 562 -11536289 7500938113 yjjg putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 397 of 400 of the completegenome.) (nt:o225b; o225; 100 pct identical to 200 amino acids) (le:11595) (re:12272) (di:direct) AE000507 AE000507 g1790833 Escherichia coli 562 -11536289 5000694053 (de:(ecoli_4256) (pn:hypothetical 22) (gn:yjjg) (gtcfc:13.7:14.1) (ec:) (yjjg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4256 ECOLI_4256 Escherichia coli 562 10087492

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868587	13019	35175	1089	362

Description

6500732432 yjju:b4377 hypothetical 39.8 kd protein in osmy-deoc intergenic region:o357 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4377 b4377 Escherichia coli 562 -11536290 113863 yjju (de:hypothetical 39.8 kd protein in osmy-deoc intergenic region (o357)) (db:swissprot) YJJU_ECOLI P39407 ESCHERICHIA COLI 562 -11536290 163822 yjju hypothetical 39.8k protein osmy-deoc intergenic region:hypothetical protein o357 (db:pir2.dat) S56601 S56601 Escherichia coli 562 -11536290 7500938130 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o357) (le:303242) (re:304315) (di:direct) ECOUW93 U14003 g537217 Escherichia coli 562 -11536290 237582 yjju orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:o357; 100 pct identical amino acid sequence and) (le:3059) (re:4132) (di:direct) AE000508 AE000508 g1790837 Escherichia coli 562 -11536290 5000694054 (de:(ecoli_4259) (pn:hypothetical 39) (gn:yjju) (gtcfc:13.7:14.1) (ec:) (yjju_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4259 ECOLI_4259 Escherichia coli 562 10055591

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868588	13020	35176	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868590	13021	35177	339	113

Description

6500732433 yjjw:b4379 hypothetical 31.5 kd protein in osmy-deoc intergenic region:f287 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4379 b4379 Escherichia coli 562 -11536291 113866 yjjw (de:hypothetical 31.5 kd protein in osmy-deoc intergenic region (f287)) (db:swissprot) YJJW_ECOLI P39409 ESCHERICHIA COLI 562 -11536291 163622 yjjw hypothetical 31.5k protein osmy-deoc intergenic region:hypothetical protein f287 (db:pir2.dat) S56603 S56603 Escherichia coli 562 -11536291 7500938132 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f287) (le:305511) (re:306374) (di:complement) ECOUW93 U14003 g537219 Escherichia coli 562 -11536291 237584 yjjw putative activating enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:f287; 100 pct identical amino acid sequence and) (le:5328) (re:6191) (di:complement) AE000508 AE000508 g1790839 Escherichia coli 562 -11536291 5000694056 (de:(ecoli_4261) (pn:hypothetical 31) (gn:yjjw) (gtcfc:13.7:14.1) (ec:) (yjjw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4261 ECOLI_4261 Escherichia coli 562 10055594

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868598	13022	35178	300	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868617	13023	35179	483	160

Description

6500732434 yjji:b4380 hypothetical 58.0 kd protein in osmy-deoc intergenic region:f516 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4380 b4380 Escherichia coli 562 -11536292 113848 yjji (de:hypothetical 58.0 kd protein in osmy-deoc intergenic region (f516)) (db:swissprot) YJJI_ECOLI P37342 ESCHERICHIA COLI 562 -11536292 163675 yjji hypothetical 58.0k protein osmy-deoc intergenic region:hypothetical protein f516 (db:pir2.dat) S56604 S56604 Escherichia coli 562 -11536292 7500938115 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f516) (le:306346) (re:307896) (di:complement) ECOUW93 U14003 g537220 Escherichia coli 562 -11536292 237585 yjji orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:f516; 100 pct identical amino acid sequence and) (le:6163) (re:7713) (di:complement) AE000508 AE000508 g1790840 Escherichia coli 562 -11536292 5000694057 (de:(ecoli_4262) (pn:hypothetical 58) (gn:yjji) (gtcfc:13.7:14.1) (ec:) (yjji_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4262 ECOLI_4262 Escherichia coli 562 10055576

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868618	13024	35180	294	97

Description

6500732435 yjjj:b4385 hypothetical 49.8 kd protein in deod-lpla intergenic region:o443 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4385 b4385 Escherichia coli 562 -11536293 113850 yjjj (de:hypothetical 49.8 kd protein in deod-lpla intergenic region (o443)) (db:swissprot) YJJJ_ECOLI P39410 ESCHERICHIA COLI 562 -11536293 164862 yjjj hypothetical 49.8k protein deod-lpla intergenic region:yjjj protein (db:pir2.dat) S56609 S56609 Escherichia coli 562 -11536293 7500938117 yjjj (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:312601) (re:313932) (di:direct) ECOUW93 U14003 g537225 Escherichia coli 562 -11536293 237590 yjjj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:o443; 100 pct identical amino acid sequence and) (le:12417) (re:13748) (di:direct) AE000508 AE000508 g1790845 Escherichia coli 562 -11536293 5000694058 (de:(ecoli_4267) (pn:hypothetical 49) (gn:yjjj) (gtcfc:13.7:14.1) (ec:) (yjjj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4267 ECOLI_4267 Escherichia coli 562 10055578

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868620	13025	35181	453	150

Description

6500732436 yjxx:b4394 hypothetical 18.6 kd protein in trpr-gpmb intergenic region:f173 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4394 b4394 Escherichia coli 562 -11536294 113867 yjxx (de:hypothetical 18.6 kd protein in trpr-gpmb intergenic region (f173)) (db:swissprot) YJXX_ECOLI P39411 ESCHERICHIA COLI 562 -11536294 163575 yjxx yjxx protein:protein f173 (cl:escherichia coli conserved yjxx protein) (db:pir2.dat) S56618 S56618 Escherichia coli 562 -11536294 7500938133 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f173) (le:324066) (re:324587) (di:complement) ECOUW93 U14003 g537234 Escherichia coli 562 -11536294 237599 yjxx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 399 of 400 of the completengenome.) (nt:f173; 100 pct identical amino acid sequence and) (le:8421) (re:8942) (di:complement) AE000509 AE000509 g1790855 Escherichia coli 562 -11536294 5000694061 (de:(ecoli_4276) (pn:hypothetical 18) (gn:yjxx) (gtcfc:13.7:14.1) (ec:) (yjxx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4276 ECOLI_4276 Escherichia coli 562 10055595

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868623	13026	35182	1680	559

Description

6500732437 yjyy:b4402 hypothetical 4.9 kd protein in arca-last intergenic region:o46 (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4402 b4402 Escherichia coli 562 -11536295 113871 yjyy (de:hypothetical 4.9 kd protein in arca-last intergenic region (o46)) (db:swissprot) YJYY_ECOLI P39412 ESCHERICHIA COLI 562 -11536295 164179 yjyy hypothetical protein o46:hypothetical protein yjyy (db:pir2.dat) S56626 S56626 Escherichia coli 562 -11536295 7500938134 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o46) (le:331235) (re:331375) (di:direct) ECOUW93 U14003 g537242 Escherichia coli 562 -11536295 237607 yjyy orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 400 of 400 of the completengenome.) (nt:o46; 100 pct identical amino acid sequence and) (le:5059) (re:5199) (di:direct) AE000510 AE000510 g1790864 Escherichia coli 562 -11536295 5000694065 (de:(ecoli_4284) (pn:hypothetical 4) (gn:yjyy) (gtcfc:13.7:14.1) (ec:) (yjyy_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4284 ECOLI_4284 Escherichia coli 562 10055599

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868630	13027	35183	1311	436

Description

6500732438 last:b4403 hypothetical 25.3 kd protein in arca-thrl intergenic region:o228b (gtcfc:14.1) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b4403 b4403 Escherichia coli 562 -11536296 81523 last (ec:2.1.1.-) (de:hypothetical trna/rrna methyltransferase last,) (db:swissprot) LAST_ECOLI P37005 ESCHERICHIA COLI 562 -11536296 163775 last hypothetical protein o228b:hypothetical protein last (cl:conserved hypothetical protein mth1849) (db:pir2.dat) S56627 S56627 Escherichia coli 562 -11536296 7500884812 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o228b) (le:331775) (re:332461) (di:direct) ECOUW93 U14003 g537243 Escherichia coli 562 -11536296 237608 last orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 400 of 400 of the completegenome.) (nt:o228b; 100 pct identical amino acid sequence and) (le:5599) (re:6285) (di:direct) AE000510 AE000510 g1790865 Escherichia coli 562 -11536296 5000694066 (de:(ecoli_4285) (pn:hypothetical 25) (gn:last) (gtcfc:13.7:14.1) (ec:) (last_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4285 ECOLI_4285 Escherichia coli 562 10023759

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868631	13028	35184	1155	384

Description

6500732439 insb_1:insb_5:insb:b0021 insb_6:insertion element is1 protein insb (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0021 b0021 Escherichia coli 562 -11536297 79960 insb:b0021:b0988:b1893:b3445 (de:insertion element is1 protein insb) (db:swissprot) ISB_ECOLI P03830 ESCHERICHIA COLI 562 -11536297 157308 insb_6 insb protein (cl:insb protein) (db:pir2.dat) JN0135 JN0135 Escherichia coli 562 -11536297 224812 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #404(51.7-52.1 min.)) (nt:similar to (pir accession number jn0135)) (le:9346) (re:9849) (di:complement) D90860 D90860 g1799658 Escherichia coli 562 -11536297 407157 insb (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:19474) (re:19977) (di:complement) ECO110K D10483 g216447 Escherichia coli 562 -11536297 7000685648 insb (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o167; overlaps insa) (le:364414) (re:364917) (di:direct) ECOUW67 U18997 g606380 Escherichia coli 562 -11536297 7000685649 insb insb protein (db:genpept-bct1) (de:escherichia coli insa, insb, and yiaj genes (plasmid pjb4).) (le:603) (re:1106) (di:direct) ECPJB4 AJ223474 g2980623 Escherichia coli 562 -11536297 7500884279 insb insb protein (db:genpept-bct1) (de:escherichia coli yiaj, yiaj, insb, and insa genes (plasmid pjb6).) (le:542) (re:1045) (di:complement) ECPJB6 AJ223475 g2980628 Escherichia coli 562 -11536297 233557 insb_1 is1 protein insb (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the completegenome.) (nt:f167; 100 pct identical to isb_ecoli sw: p03830) (le:9273) (re:9776) (di:complement) AE000112 AE000112 g1786203 Escherichia coli 562 -11536297 236679 insb_5 is1 protein insb (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:f167; 100 pct identical to isb_ecoli sw: p03830) (le:1346) (re:1849) (di:complement) AE000283 AE000283 g1788203 Escherichia coli 562 -11536297 304040 insb_6 is1 protein insb (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completegenome.) (nt:o167) (le:10067) (re:10570) (di:direct) AE000420 AE000420 g1789853 Escherichia coli 562 -11536297 7500884280 insb insb peptide (db:genpept-syn) (de:binary vector binhygtop aph4, teta, tetr, traj, insb, insa, apha-3and trfa genes.) (le:7405) (re:7908) (di:complement) BINHYGDNA Z37515 g886848 unidentified 32644 -11536297 5000691337 (de:(ecoli_21) (pn:insertion element is1 protein insb:insertion element is1 protein insb:function not assigned) (gn:isb:insb_4:insb_5) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_21 ECOLI_21 Escherichia coli 562 10022212

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868636	13029	35185	696	232

Description

5000691344 caif (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b0034 b0034 Escherichia coli 562 -11536298
7000691922 caif transcription activator caif (db:pir2.dat) B64724 B64724
Escherichia coli 562 -11536298 7500960469 caif transcriptional regulator of
cai operon (fn:regulator; central intermediary metabolism:)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 4 of 400 of the
completeness.) (nt:ol66; 100 pct identical to gb: eccaif_1) (le:109)
(re:609) (di:direct) AE000114 AE000114 g1786218 Escherichia coli 562
-11536298 6500732440 caif (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b0034 b0034 Escherichia coli 562 -11536298

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868642	13030	35186	324	107

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868654	13031	35187	873	290

Description

GTC ORF with score 875 to: (fn:catalysis of the last step in arginine)
(sr:fission yeast) (db:genpept-pln1) (ec:4.3.2.1) (de:schizosaccharomyces
pombe 972h- l-argininosuccinate lyase (argx)gene, complete cds.) (nt:asl
(le:451) (re:1833) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868656	13032	35188	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868657	13033	35189	528	175

Description

6500732441 yaau:b0045 hypothetical metabolite transport protein in carb-kefc intergenic region:orf65/66 (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0045 b0045 Escherichia coli 562 -11536299 109514 yaau (de:region (orf65/66)) (db:swissprot) YAAU_ECOLI P31679 ESCHERICHIA COLI 562 -11536299 7000687122 yaau yaau protein (cl:yaau protein) (db:pir2.dat) E64725 E64725 Escherichia coli 562 -11536299 7500895981 yaau putative transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 4 of 400 of the completgenome.) (nt:o443; residues 1-141 are 94 pct identical to) (le:11721) (re:13052) (di:direct) AE000114 AE000114 g1786229 Escherichia coli 562 -11536299 5000691353 (de:(ecoli_45) (pn:hypothetical 18) (gn:yaau) (gtcfc:13.7:14.1) (ec:) (yaau_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_45 ECOLI_45 Escherichia coli 562 10122630

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868664	13034	35190	405	135

Description

GTC ORF with score 421 to: (fn:catalysis of the last step in arginine) (sr:fission yeast) (db:genpept-pln1) (ec:4.3.2.1) (de:schizosaccharomyces pombe 972h- l-argininosuccinate lyase (argx)gene, complete cds.) (nt:asl) (le:451) (re:1833) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868676	13035	35191	1026	341

Description

5000691373 yacg (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0101 b0101 Escherichia coli 562 -11536300 7000691932 yacg yacg protein (db:pir2.dat) E64732 E64732 Escherichia coli 562 -11536300 7500960483 yacg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completgenome.) (nt:f65; 100 pct identical to yacg_ecoli sw: p36681) (le:6405) (re:6602) (di:complement) AE000119 AE000119 g1786290 Escherichia coli 562 -11536300 6500732442 yacg (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0101 b0101 Escherichia coli 562 -11536300

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868692	13036	35192	1659	552

Description

6500732443 yace:b0103 hypothetical 22.5 kd protein in mutt-guac intergenic region precursor (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0103 b0103 Escherichia coli 562 -11536301 109594 yace (de:hypothetical 22.6 kd protein in mutt-guac intergenic region) (db:swissprot) YACE_ECOLI P36679 ESCHERICHIA COLI 562 -11536301 7000687152 yace yace protein (cl:conserved hypothetical protein ydr196c) (db:pir2.dat) G64732 G64732 Escherichia coli 562 -11536301 7500896031 yace putative dna repair protein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.) (nt:f206; 97 pct identical (1 gap) to yace_ecoli) (le:7355) (re:7975) (di:complement) AE000119 AE000119 g1786292 Escherichia coli 562 -11536301 5000691375 (de:(ecoli_103) (pn:hypothetical 22) (gn:yace) (gtcfc:13.7:14.1) (ec: (yace_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_103 ECOLI_103 Escherichia coli 562 10122658

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868694	13037	35193	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868698	13038	35194	1668	555

Description

GTC ORF with score 709 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868699	13039	35195	798	265

Description

GTC ORF with score 116 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868702	13040	35196	420	139

Description

GTC ORF with score 102 to: (db:genpept-bct2) (de:bordetella pertussis d-3-phosphoglycerate dehydrogenase homolog(sera) and brg1 (brg1) genes, complete cds.) (nt:orf4; similar to salicylate hydroxylase) (le:7172) (re:8392) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868720	13041	35197	573	190

Description

6500732444 yadh:b0128 hypothetical 28.5 kd protein in hpt-pand intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0128 b0128 Escherichia coli 562 -11536302 109649 yadh (de:hypothetical 28.5 kd protein in hpt-pand intergenic region) (db:swissprot) YADH_ECOLI P36880 ESCHERICHIA COLI 562 -11536302 7000687170 yadh probable abc-2-type transport protein yadh (db:pir2.dat) H64735 H64735 Escherichia coli 562 -11536302 7500896069 yadh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 12 of 400 of the completegenome.) (nt:o256; 100 pct identical to yadh_ecoli sw:) (le:4998) (re:5768) (di:direct) AE000122 AE000122 g1786320 Escherichia coli 562 -11536302 5000691387 (de:(ecoli_128) (pn:hypothetical 22) (gn:yadh) (gtcfc:13.7:14.1) (ec:) (yadh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_128 ECOLI_128 Escherichia coli 562 10122673

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868721	13042	35198	300	99

Description

6500732445 yade:b0130 hypothetical 46.3 kd protein in hpt-pand intergenic region precursor (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0130 b0130 Escherichia coli 562 -11536303 109643 yade (de:hypothetical 46.3 kd protein in hpt-pand intergenic region precursor) (db:swissprot) YADE_ECOLI P31666 ESCHERICHIA COLI 562 -11536303 7000687168 yade yade protein (db:pir2.dat) B64736 B64736 Escherichia coli 562 -11536303 7500896066 yade orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 12 of 400 of the completegenome.) (nt:o409; 100 pct identical to 237 residues) (le:6377) (re:7606) (di:direct) AE000122 AE000122 g1786322 Escherichia coli 562 -11536303 5000691389 (de:(ecoli_130) (pn:hypothetical 27) (gn:yade) (gtcfc:13.7:14.1) (ec:) (yade_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_130 ECOLI_130 Escherichia coli 562 10122675

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868723	13043	35199	582	193

Description

6500732446 yaee:b0198 hypothetical abc transporter permease protein yaee (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0198 b0198 Escherichia coli 562 -11536304 109685 yaee (de:hypothetical abc transporter permease protein yaee) (db:swissprot) YAEE_ECOLI P31547 ESCHERICHIA COLI 562 -11536304 7000687180 yaee probable transport protein yaee (cl:probable transport protein yaee) (db:pir2.dat) F64744 F64744 Escherichia coli 562 -11536304 239825 hypothetical 23.3 kd protein (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:alternate gene name yaee) (le:30515) (re:31168) (di:complement) ECOTSF D83536 g1208965 Escherichia coli 562 -11536304 303260 yaee (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:52043) (re:52696) (di:complement) ECU70214 U70214 g1552774 Escherichia coli 562 -11536304 236183 yaee putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 19 of 400 of the completegenome.) (nt:f218; 100 pct identical to yaee_ecoli sw: p31547) (le:944) (re:1597) (di:complement) AE000129 AE000129 g1786397 Escherichia coli 562 -11536304 5000691421 (de:(ecoli_198) (pn:hypothetical 23) (gn:yaee) (gtcfc:13.7:14.1) (ec:) (yaee_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_198 ECOLI_198 Escherichia coli 562 10051417

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868731	13044	35200	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868746	13045	35201	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868757	13046	35202	246	81

Description

6500732447 dinj:b0226 dna-damage-inducible protein j (gtcfc:13.4)
(keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0226 b0226
Escherichia coli 562 -11536305 120156 dinj (de:dna-damage-inducible protein
j) (db:swissprot) DINJ_ECOLI Q47150 ESCHERICHIA COLI 562 -11536305
7000685055 dinj dna-damage-inducible protein dinj (db:pir2.dat) C64747
C64747 Escherichia coli 562 -11536305 7500880327 dinj dinj (sr:escherichia
coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1)
(de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yafI,
yafm, fhia, mbha, dinp, yafn, yafo and yafp.) (nt:hypothetical) (le:3884)
(re:4144) (di:c... ECODINJ D38582 g984582 Escherichia coli 562 -11536305
234160 dinj damage-inducible protein j (fn:phenotype; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the
completegenome.) (nt:f86; 100 pct identical to gb: ecodinj_6) (le:2831)
(re:3091) (di:complement) AE000131 AE000131 g1786420 Escherichia coli 562
-11536305 5000691438 (de:(ecoli_219) (pn:function not assigned) (gn:dinj)
(gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia
coli)) ECOLI_219 ECOLI_219 Escherichia coli 562 10063030

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868760	13047	35203	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868786	13048	35204	1128	375

Description

5000691442 mbha (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b0230 b0230 Escherichia coli 562 -11536306
7000691859 mbha mbha protein (db:pir2.dat) G64747 G64747 Escherichia coli
562 -11536306 7500960377 mbha putative motility protein (fn:putative
structure; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 21 of 400 of the completegenome.) (nt:o211; residues 2-211
are 100 pct identical to) (le:6631) (re:7416) (di:direct) AE000131 AE000131
g1786424 Escherichia coli 562 -11536306 6500732448 mbha (gtcfc:14.2)
(keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0230 b0230
Escherichia coli 562 -11536306

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868787	13049	35205	408	135

Description

6500732449 yafw:b0246 hypothetical 11.9 kd protein in proa-perr intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0246 b0246 Escherichia coli 562 -11536307 1500686250 yafw (de:hypothetical 11.9 kd protein in proa-perr intergenic region) (db:swissprot) YAFW_ECOLI Q47684 ESCHERICHIA COLI 562 -11536307 7000687199 yafw yafw protein (db:pir2.dat) F64749 F64749 Escherichia coli 562 -11536307 239864 unknown (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:alternate gene name yagb) (le:72428) (re:72745) (di:complement) ECOTSF D83536 g1208990 Escherichia coli 562 -11536307 303285 yagb (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to e. coli orf_o105) (le:93989) (re:94306) (di:complement) ECU70214 U70214 g1552813 Escherichia coli 562 -11536307 236208 yafw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 22 of 400 of the completegenome.) (nt:f105; 68 pct identical to 54 residues of the 58 aa) (le:9630) (re:9947) (di:complement) AE000132 AE000132 g1786440 Escherichia coli 562 -11536307 5000691450 (de:(ecoli_238) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_238 ECOLI_238 Escherichia coli 562 10060993

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868791	13050	35206	429	142

Description

6500732450 yafx:b0248 hypothetical 17.4 kd protein in proa-perr intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0248 b0248 Escherichia coli 562 -11536308 4000709259 yafx (de:hypothetical 17.4 kd protein in proa-perr intergenic region) (db:swissprot) YAFX_ECOLI P75676 ESCHERICHIA COLI 562 -11536308 7000687200 yafx yafx protein (cl:klca protein) (db:pir2.dat) H64749 H64749 Escherichia coli 562 -11536308 7500896140 yafx orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 23 of 400 of the completegenome.) (nt:f152) (le:542) (re:1000) (di:complement) AE000133 AE000133 g1786442 Escherichia coli 562 -11536308 5000691451 (de:(ecoli_239) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_239 ECOLI_239 Escherichia coli 562 10122721

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868792	13051	35207	507	168

Description

6500732451 ykfb:b0250 hypothetical 17.0 kd protein in proa-perr intergenic region precursor (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0250 b0250 Escherichia coli 562 -11536309 4000709260 ykfb (de:hypothetical 17.0 kd protein in proa-perr intergenic region precursor) (db:swissprot) YKFB_ECOLI P77162 ESCHERICHIA COLI 562 -11536309 7000688096 ykfb ykfb protein (db:pir2.dat) B64750 B64750 Escherichia coli 562 -11536309 7500938461 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to e. coli orf_o155) (le:95919) (re:96386) (di:complement) ECU70214 U70214 g1552817 Escherichia coli 562 -11536309 239868 ykfb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 23 of 400 of the completegenome.) (nt:f155; 24 pct identical (11 gaps) to 128 residues) (le:1414) (re:1881) (di:complement) AE000133 AE000133 g1786444 Escherichia coli 562 -11536309 5000691453 (de:(ecoli_241) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_241 ECOLI_241 Escherichia coli 562 10122723

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868795	13052	35208	702	233

Description

6500732452 yafy:b0251 hypothetical transcriptional regulator in proa-perr intergenic region (gtcfc:10.2:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0251 b0251 Escherichia coli 562 -11536310 4000708156 yafy (de:hypothetical transcriptional regulator in proa-perr intergenic region) (db:swissprot) YAFY_ECOLI P77365 ESCHERICHIA COLI 562 -11536310 7000687201 yafy probable transcription regulator yafy:probable membrane protein yafy (db:pir2.dat) C64750 C64750 Escherichia coli 562 -11536310 7500896141 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to e. coli orf_o278) (le:96409) (re:97266) (di:complement) ECU70214 U70214 g1552818 Escherichia coli 562 -11536310 239869 yafy orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 23 of 400 of the completegenome.) (nt:f285; 39 pct identical (9 gaps) to 63 residues of) (le:1904) (re:2761) (di:complement) AE000133 AE000133 g1786445 Escherichia coli 562 -11536310 5000691454 (de:(ecoli_242) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_242 ECOLI_242 Escherichia coli 562 10122724

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868798	13053	35209	1083	360

Description

6500732453 yafz:b0252 hypothetical 31.7 kd protein in proa-perr intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0252 b0252 Escherichia coli 562 -11536311 4000709261 yafz (de:hypothetical 31.7 kd protein in proa-perr intergenic region) (db:swissprot) YAFZ_ECOLI P77206 ESCHERICHIA COLI 562 -11536311 7000687202 yafz yafz protein (db:pir2.dat) D64750 D64750 Escherichia coli 562 -11536311 7500896142 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to e. coli orf_o273) (le:97483) (re:98319) (di:complement) ECU70214 U70214 g1552819 Escherichia coli 562 -11536311 239870 yafz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 23 of 400 of the completegenome.) (nt:f278; 65 pct identical (1 gap) to 270 residues of) (le:2978) (re:3814) (di:complement) AE000133 AE000133 g1786446 Escherichia coli 562 -11536311 5000691455 (de:(ecoli_243) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_243 ECOLI_243 Escherichia coli 562 10122725

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868806	13054	35210	309	102

Description

6500732454 ykfa:b0253 hypothetical 32.0 kd protein in proa-perr intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0253 b0253 Escherichia coli 562 -11536312 7000691965 ykfa ykfa protein (cl:ykfa protein:translation elongation factor tu homology) (db:pir2.dat) E64750 E64750 Escherichia coli 562 -11536312 7500960524 ykfa putative gtp-binding protein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 23 of 400 of the completegenome.) (nt:f288; 24 pct identical (6 gaps) to 158 residues of) (le:3891) (re:4757) (di:complement) AE000133 AE000133 g1786447 Escherichia coli 562 -11536312 5000691456 (de:(ecoli_244) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_244 ECOLI_244 Escherichia coli 562 10122726

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868807	13055	35211	1209	402

Description

6500732455 perr:b0254 peroxide resistance protein perr (gtcfc:13.3:12.12) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0254 b0254 Escherichia coli 562 -11536313 500684954 perr (de:peroxide resistance protein perr) (db:swissprot) PERR_ECOLI Q57083 ESCHERICHIA COLI 562 -11536313 7000686116 perr regulatory protein perr:peroxidase resistance protein perr (cl:regulatory protein ampr) (db:pir2.dat) F64750 F64750 Escherichia coli 562 -11536313 239731 unknown (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:orf307; similar to dsdc, pir accession number) (le:78025) (re:78918) (di:complement) ECOTSF D83536 g1208994 Escherichia coli 562 -11536313 239872 perr perr (fn:apparent regulatory gene involved in peroxide) (sr:escherichia coli strain=k-12) (db:genpept-bct1) (de:escherichia coli perr (perr) gene, complete cds.) (nt:lysr homolog) (le:823) (re:1716) (di:direct) ECU57080 U57080 g1354820 Escherichia coli 562 -11536313 303289 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical, similar to dsdc) (le:99588) (re:100481) (di:complement) ECU70214 U70214 g1552821 Escherichia coli 562 -11536313 236212 perr putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 23 of 400 of the completegenome.) (nt:f297; 35 pct identical (5 gaps) to 283 residues of) (le:5083) (re:5976) (di:complement) AE000133 AE000133 g1786448 Escherichia coli 562 -11536313 5000691457 (de:(ecoli_245) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_245 ECOLI_245 Escherichia coli 562 10060920

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868810	13056	35212	600	199

Description

6500732456 ykfc:b0258 hypothetical 43.2 kd protein in perr-argf intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0258 b0258 Escherichia coli 562 -11536314 1500686251 ykfc (de:hypothetical 43.2 kd protein in perr-argf intergenic region) (db:swissprot) YKFC_ECOLI Q47688 ESCHERICHIA COLI 562 -11536314 7000688097 ykfc ykfc protein (db:pir2.dat) B64751 B64751 Escherichia coli 562 -11536314 7500938462 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical protein) (le:103161) (re:104291) (di:direct) ECU70214 U70214 g1552826 Escherichia coli 562 -11536314 239877 ykfc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 23 of 400 of the completegenome.) (nt:o376; poor stats; 38 pct identical (35 gaps) to) (le:8656) (re:9786) (di:direct) AE000133 AE000133 g1786452 Escherichia coli 562 -11536314 5000691461 (de:(ecoli_249) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_249 ECOLI_249 Escherichia coli 562 10060994

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868814	13057	35213	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868816	13058	35214	363	120

Description

6500732457 ykfd:b0260 hypothetical 51.5 kd transport protein in perr-argf intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0260 b0260 Escherichia coli 562 -11536315 4000707492 ykfd (de:hypothetical 51.5 kd transport protein in perr-argf intergenic region) (db:swissprot) YKFD_ECOLI Q47689 ESCHERICHIA COLI 562 -11536315 7000688098 ykfd amino acid permease ykfd (cl:arginine permease) (db:pir2.dat) D64751 D64751 Escherichia coli 562 -11536315 239880 unknown (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (nt:orf331; similar to lysp, pir accession number) (le:84124) (re:85551) (di:direct) ECOTSF D83536 g1208999 Escherichia coli 562 -11536315 303294 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to b. subtilis histidine permease) (le:105600) (re:107027) (di:direct) ECU70214 U70214 g1552829 Escherichia coli 562 -11536315 236217 ykfd putative amino acid/amine transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 24 of 400 of the completegenome.) (nt:o475; 99 pct identical to gb: ecotsf_57) (le:106) (re:1533) (di:direct) AE000134 AE000134 g1786455 Escherichia coli 562 -11536315 5000691463 (de:(ecoli_251) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_251 ECOLI_251 Escherichia coli 562 10122730

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868831	13059	35215	486	161

Description

6500732458 yagd:b0261 hypothetical 33.4 kd protein in perr-argf intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0261 b0261 Escherichia coli 562 -11536316 4000709263 yagd (de:hypothetical 33.4 kd protein in perr-argf intergenic region) (db:swissprot) YAGD_ECOLI Q47690 ESCHERICHIA COLI 562 -11536316 7000687204 yagd probable membrane protein yagd (db:pir2.dat) E64751 E64751 Escherichia coli 562 -11536316 7500896149 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to s. cerevisiae yll062c) (le:107014) (re:107946) (di:direct) ECU70214 U70214 g1552830 Escherichia coli 562 -11536316 239881 yagd putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 24 of 400 of the completegenome.) (nt:o310; 100 pct identical to gb:) (le:1520) (re:2452) (di:direct) AE000134 AE000134 g1786456 Escherichia coli 562 -11536316 5000691464 (de:(ecoli_252) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_252 ECOLI_252 Escherichia coli 562 10122731

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868835	13060	35216	978	325

Description

GTC ORF with score 259 to: (or:Arabidopsis thaliana) (sr:thale cress)
(db:genpept-pln2) (de:arabidopsis thaliana bac f8m12.) (nt:similar to
uridine diphosphate glucose epimerase;) (le:28907:29751:29928:30157)
(re:29089:29800:30063:30258) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868837	13061	35217	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868839	13062	35218	447	148

Description

5000691469 yagb (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b0266 b0266 Escherichia coli 562 -11536317
7000691933 yagb yagb protein (db:pir2.dat) B64752 B64752 Escherichia coli
562 -11536317 7500960491 (db:genpept-bct1) (de:escherichia coli chromosome
minutes 4-6.) (nt:similar to e. coli orf_o105) (le:110684) (re:111061)
(di:complement) ECU70214 U70214 g1552835 Escherichia coli 562 -11536317
239886 yagb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 24 of 400 of the completegenome.)
(nt:f125; 125 aa orf is 98 pct identical to 58 residues) (le:5190) (re:5567)
(di:complement) AE000134 AE000134 g1786461 Escherichia coli 562 -11536317
6500732459 yagb (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b0266 b0266 Escherichia coli 562 -11536317

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868845	13063	35219	702	233

Description

6500732460 yage:b0268 hypothetical 33.3 kd protein in perr-argf intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0268 b0268 Escherichia coli 562 -11536318 4000707863 yage (de:hypothetical 33.3 kd protein in perr-argf intergenic region) (db:swissprot) YAGE_ECOLI P75682 ESCHERICHIA COLI 562 -11536318 7000687205 yage probable dihydrodipicolinate synthase yage (cl:dihydrodipicolinate synthase) (db:pir2.dat) D64752 D64752 Escherichia coli 562 -11536318 7500896150 yage putative lyase/synthase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 24 of 400 of the completegenome.) (nt:o309; 58 pct identical to 290 residues of the 319) (le:7062) (re:7991) (di:direct) AE000134 AE000134 g1786463 Escherichia coli 562 -11536318 5000691471 (de:(ecoli_259) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_259 ECOLI_259 Escherichia coli 562 10122736

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868870	13064	35220	561	186

Description

6500732461 yagf:b0269 hypothetical 69.4 kd protein in perr-argf intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0269 b0269 Escherichia coli 562 -11536319 4000708710 yagf (de:hypothetical 69.4 kd protein in perr-argf intergenic region) (db:swissprot) YAGF_ECOLI P77596 ESCHERICHIA COLI 562 -11536319 7000687206 yagf probable dihydroxy-acid dehydratase yagf (cl:dihydroxy-acid dehydratase) (db:pir2.dat) E64752 E64752 Escherichia coli 562 -11536319 7500896151 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to e. coli yjhg) (le:113499) (re:115466) (di:direct) ECU70214 U70214 g1552838 Escherichia coli 562 -11536319 239889 yagf putative dehydratase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 24 of 400 of the completegenome.) (nt:o655; 67 pct identical (2 gaps) to 642 residues of) (le:8006) (re:9973) (di:direct) AE000134 AE000134 g1786464 Escherichia coli 562 -11536319 5000691472 (de:(ecoli_260) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_260 ECOLI_260 Escherichia coli 562 10122737

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501868871	13065	35221	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868876	13066	35222	612	203

Description

6500732462 yagg:b0270 hypothetical 50.6 kd protein in perr-argf intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0270 b0270 Escherichia coli 562 -11536320 4000709755 yagg (de:hypothetical symporter in perr-argf intergenic region) (db:swissprot) YAGG_ECOLI P75683 ESCHERICHIA COLI 562 -11536320 7000687207 yagg probable melibiose carrier protein yagg:probable membrane protein yagg (cl:melibiose carrier protein) (db:pir2.dat) F64752 F64752 Escherichia coli 562 -11536320 7500896152 yagg putative permease (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 25 of 400 of the completegenome.) (nt:o460; 43 pct identical (8 gaps) to 441 residues of) (le:144) (re:1526) (di:direct) AE000135 AE000135 g1786466 Escherichia coli 562 -11536320 5000691473 (de:(ecoli_261) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_261 ECOLI_261 Escherichia coli 562 10122738

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868889	13067	35223	1281	426

Description

6500732463 yagi:b0272 hypothetical transcriptional regulator in perr-argf intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0272 b0272 Escherichia coli 562 -11536321 4000708137 yagi (de:hypothetical transcriptional regulator in perr-argf intergenic region) (db:swissprot) YAGI_ECOLI P77300 ESCHERICHIA COLI 562 -11536321 7000687209 yagi probable transcription regulator yagi (cl:acetate operon repressor) (db:pir2.dat) H64752 H64752 Escherichia coli 562 -11536321 7500896154 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to e. coli yiaj) (le:118702) (re:119460) (di:complement) ECU70214 U70214 g1552841 Escherichia coli 562 -11536321 239892 yagi putative regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 25 of 400 of the completegenome.) (nt:f252; 39 pct identical (1 gap) to 247 residues of) (le:3153) (re:3911) (di:complement) AE000135 AE000135 g1786468 Escherichia coli 562 -11536321 5000691475 (de:(ecoli_263) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_263 ECOLI_263 Escherichia coli 562 10122740

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868895	13068	35224	1767	588

Description

GTC ORF with score 125 to: (sr:saccharomyces cerevisiae (strain:grf88) dna, clone_lib:ycp5) (db:genpept-pln1) (de:saccharomyces cerevisiae dna for thi2 positive regulatory protein of thiamin synthesis, complete cds.) (le:721) (re:2073) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868902	13069	35225	882	293

Description

6500732464 yagj:b0276 hypothetical 27.9 kd protein in argf-intf intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0276 b0276 Escherichia coli 562 -11536322 4000709264 yagj (de:hypothetical 27.9 kd protein in argf-intf intergenic region) (db:swissprot) YAGJ_ECOLI P77169 ESCHERICHIA COLI 562 -11536322 7000687210 yagj yagj protein (db:pir2.dat) D64753 D64753 Escherichia coli 562 -11536322 7500896155 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical protein) (le:121798) (re:122529) (di:direct) ECU70214 U70214 g1552844 Escherichia coli 562 -11536322 239895 yagj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 25 of 400 of the complete genome.) (nt:o243; 32 pct identical (2 gaps) to 61 residues of) (le:6249) (re:6980) (di:direct) AE000135 AE000135 g1786472 Escherichia coli 562 -11536322 5000691476 (de:(ecoli_267) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_267 ECOLI_267 Escherichia coli 562 10122742

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868928	13070	35226	477	158

Description

6500732465 yagk:b0277 hypothetical 24.5 kd protein in argf-intf intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0277 b0277 Escherichia coli 562 -11536323 4000709265 yagk (de:hypothetical 24.5 kd protein in argf-intf intergenic region) (db:swissprot) YAGK_ECOLI P77657 ESCHERICHIA COLI 562 -11536323 7000687211 yagk yagk protein (cl:yagk protein) (db:pir2.dat) E64753 E64753 Escherichia coli 562 -11536323 7500896156 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to e. coli orf_o208) (le:120) (re:746) (di:complement) ECU73857 U73857 g1657478 Escherichia coli 562 -11536323 239899 yagk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 25 of 400 of the completegenome.) (nt:f208; phage stats; 24 pct identical (16 gaps) to) (le:7071) (re:7697) (di:complement) AE000135 AE000135 g1786473 Escherichia coli 562 -11536323 5000691477 (de:(ecoli_268) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_268 ECOLI_268 Escherichia coli 562 10122743

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868932	13071	35227	771	256

Description

6500732466 yagl:b0278 hypothetical 27.3 kd protein in argf-intf intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0278 b0278 Escherichia coli 562 -11536324 4000709266 yagl (de:hypothetical 27.3 kd protein in argf-intf intergenic region) (db:swissprot) YAGL_ECOLI P77607 ESCHERICHIA COLI 562 -11536324 7000687212 yagl yagl protein (db:pir2.dat) F64753 F64753 Escherichia coli 562 -11536324 7500896157 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:1018) (re:1716) (di:complement) ECU73857 U73857 g1657479 Escherichia coli 562 -11536324 239900 yagl dna-binding protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 25 of 400 of the completegenome.) (nt:f232; phage stats; 25 pct identical (10 gaps) to) (le:7969) (re:8667) (di:complement) AE000135 AE000135 g1786474 Escherichia coli 562 -11536324 5000691478 (de:(ecoli_269) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_269 ECOLI_269 Escherichia coli 562 10122744

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868938	13072	35228	606	201

Description

6500732467 yagp:b0282 hypothetical 15.4 kd protein in intf-eaeh intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0282 b0282 Escherichia coli 562 -11536325 4000709267 yagp (de:hypothetical 15.4 kd protein in intf-eaeh intergenic region) (db:swissprot) YAGP_ECOLI P75684 ESCHERICHIA COLI 562 -11536325 7000687213 yagp yagp protein (db:pir2.dat) B64754 B64754 Escherichia coli 562 -11536325 7500896166 yagp putative transcriptional regulator lysr-type (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completegenome.) (nt:f136; 25 pct identical (4 gaps) to 107 residues of) (le:1762) (re:2172) (di:complement) AE000136 AE000136 g1786476 Escherichia coli 562 -11536325 5000691479 (de:(ecoli_270) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_270 ECOLI_270 Escherichia coli 562 10122745

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868945	13073	35229	897	298

Description

6500732468 yagq:b0283 hypothetical 35.0 kd protein in intf-eaeh intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0283 b0283 Escherichia coli 562 -11536326 4000709268 yagq (de:hypothetical 35.0 kd protein in intf-eaeh intergenic region) (db:swissprot) YAGQ_ECOLI P77183 ESCHERICHIA COLI 562 -11536326 7000687214 yagq yagq protein (db:pir2.dat) C64754 C64754 Escherichia coli 562 -11536326 7500896167 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:5568) (re:6524) (di:complement) ECU73857 U73857 g1657484 Escherichia coli 562 -11536326 239905 yagq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completegenome.) (nt:f318; 42 pct identical (2 gaps) to 54 residues of) (le:2151) (re:3107) (di:complement) AE000136 AE000136 g1786477 Escherichia coli 562 -11536326 5000691480 (de:(ecoli_271) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_271 ECOLI_271 Escherichia coli 562 10122746

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868965	13074	35230	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868971	13075	35231	402	133

Description

6500732469 yagr:b0284 hypothetical 78.1 kd protein in intf-eaeh intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0284 b0284 Escherichia coli 562 -11536327 4000709269 yagr (de:hypothetical 78.1 kd protein in intf-eaeh intergenic region) (db:swissprot) YAGR_ECOLI P77489 ESCHERICHIA COLI 562 -11536327 7000687215 yagr probable oxidoreductase yagr (db:pir2.dat) D64754 D64754 Escherichia coli 562 -11536327 7500896168 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to e. coli o765) (le:6534) (re:8732) (di:complement) ECU73857 U73857 g1657485 Escherichia coli 562 -11536327 239906 yagr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completegenome.) (nt:f732; 26 pct identical (39 gaps) to 714 residues of) (le:3117) (re:5315) (di:complement) AE000136 AE000136 g1786478 Escherichia coli 562 -11536327 5000691481 (de:(ecoli_272) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_272 ECOLI_272 Escherichia coli 562 10122747

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868974	13076	35232	441	146

Description

6500732470 yags:b0285 hypothetical 33.9 kd protein in intf-eaeh intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0285 b0285 Escherichia coli 562 -11536328 4000709270 yags (de:hypothetical 33.9 kd protein in intf-eaeh intergenic region) (db:swissprot) YAGS_ECOLI P77324 ESCHERICHIA COLI 562 -11536328 7000687216 yags yags protein (db:pir2.dat) E64754 E64754 Escherichia coli 562 -11536328 7500896169 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:8729) (re:9685) (di:complement) ECU73857 U73857 g1657486 Escherichia coli 562 -11536328 239907 yags orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completegenome.) (nt:f318; 29 pct identical (1 gap) to 68 residues of) (le:5312) (re:6268) (di:complement) AE000136 AE000136 g1786479 Escherichia coli 562 -11536328 5000691482 (de:(ecoli_273) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_273 ECOLI_273 Escherichia coli 562 10122748

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868978	13077	35233	420	139

Description

6500732471 yagt:b0286 hypothetical 24.3 kd protein in intf-eaeh intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0286 b0286 Escherichia coli 562 -11536329 4000709271 yagt (de:hypothetical 24.3 kd protein in intf-eaeh intergenic region) (db:swissprot) YAGT_ECOLI P77165 ESCHERICHIA COLI 562 -11536329 7000687217 yagt probable oxidoreductase:yagt:yagt protein (cl:isoquinoline 1-oxidoreductase alpha chain) (ec:1.-.-.-) (db:pir2.dat) F64754 F64754 Escherichia coli 562 -11536329 7500896170 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to a. nicotinovorans nicotine) (le:9682) (re:10371) (di:complement) ECU73857 U73857 g1657487 Escherichia coli 562 -11536329 239908 yagt putative xanthine dehydrogenase ec 1.1.1.20 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completegenome.) (nt:f229; 43 pct identical (28 gaps) to 155 residues of) (le:6265) (re:6954) (di:complement) AE000136 AE000136 g1786480 Escherichia coli 562 -11536329 5000691483 (de:(ecoli_274) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_274 ECOLI_274 Escherichia coli 562 10122749

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501868985	13078	35234	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869002	13079	35235	612	203

Description

6500732472 yagu:b0287 hypothetical 23.0 kd protein in intf-eaeh intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0287 b0287 Escherichia coli 562 -11536330 4000709272 yagu (de:hypothetical 23.0 kd protein in intf-eaeh intergenic region) (db:swissprot) YAGU_ECOLI P77262 ESCHERICHIA COLI 562 -11536330 7000687218 yagu probable membrane protein yagu (db:pir2.dat) G64754 G64754 Escherichia coli 562 -11536330 7500896171 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:10789) (re:11403) (di:direct) ECU73857 U73857 g1657488 Escherichia coli 562 -11536330 239909 yagu orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completegenome.) (nt:o204; 26 pct identical to 46 residues of approx.) (le:7372) (re:7986) (di:direct) AE000136 AE000136 g1786481 Escherichia coli 562 -11536330 5000691484 (de:(ecoli_275) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_275 ECOLI_275 Escherichia coli 562 10122750

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869008	13080	35236	675	224

Description

6500732473 yagv:b0289 hypothetical 28.2 kd protein in intf-eaeh intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0289 b0289 Escherichia coli 562 -11536331 7000687219 yagv probable membrane protein yagv (db:pir2.dat) A64755 A64755 Escherichia coli 562 -11536331 239911 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:12293) (re:13048) (di:complement) ECU73857 U73857 g1657490 Escherichia coli 562 -11536331 7500960493 yagv orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completegenome.) (nt:f251; 30 pct identical (6 gaps) to 75 residues of) (le:8876) (re:9631) (di:complement) AE000136 AE000136 g1786482 Escherichia coli 562 -11536331 4000709273 yagv_ecoli (de:(gn:yagv) (de:hypothetical 28.2 kd protein in intf-eaeh intergenic region) (sp:p77263)) P77263 P77263 Escherichia coli 562 -11536331 5000691485 (de:(ecoli_276) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_276 ECOLI_276 Escherichia coli 562 10122751

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869012	13081	35237	330	109

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869039	13082	35238	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869042	13083	35239	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869047	13084	35240	231	76

Description

6500732474 yagw:b0290 hypothetical 60.0 kd protein in intf-eaeh intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0290 b0290 Escherichia coli 562 -11536332 4000709274 yagw (de:hypothetical 60.0 kd protein in intf-eaeh intergenic region) (db:swissprot) YAGW_ECOLI P77694 ESCHERICHIA COLI 562 -11536332 7000687220 yagw yagw protein (db:pir2.dat) B64755 B64755 Escherichia coli 562 -11536332 7500896173 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:12972) (re:14615) (di:complement) ECU73857 U73857 g1657491 Escherichia coli 562 -11536332 239912 yagw putative receptor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completegenome.) (nt:f547; 24 pct identical (10 gaps) to 164 residues of) (le:9555) (re:11198) (di:complement) AE000136 AE000136 g1786483 Escherichia coli 562 -11536332 5000691486 (de:(ecoli_277) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_277 ECOLI_277 Escherichia coli 562 10122752

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869059	13085	35241	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869067	13086	35242	1524	508

Description

6500732475 yagx:b0291 hypothetical 91.2 kd protein in intf-eaeh intergenic region precursor (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0291 b0291 Escherichia coli 562 -11536333
 4000709275 yagx (de:hypothetical 91.2 kd protein in intf-eaeh intergenic region precursor) (db:swissprot) YAGX_ECOLI P77802 ESCHERICHIA COLI 562 -11536333 7000687221 yagx yagx protein (db:pir2.dat) C64755 C64755 Escherichia coli 562 -11536333 7500896174 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:14605) (re:17130) (di:complement) ECU73857 U73857 g1657492 Escherichia coli 562 -11536333 239913 yagx putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completgenome.) (nt:f841; 24 pct identical (69 gaps) to 641 residues of) (le:11188) (re:13713) (di:complement) AE000136 AE000136 g1786484 Escherichia coli 562 -11536333 5000691487 (de:(ecoli_278) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_278 ECOLI_278 Escherichia coli 562 10122753

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869080	13087	35243	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869104	13088	35244	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869116	13089	35245	1689	562

Description

6500732476 yagy:b0292 hypothetical 24.5 kd protein in intf-eaeh intergenic region precursor (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0292 b0292 Escherichia coli 562 -11536334 4000709276 yagy (de:hypothetical 24.5 kd protein in intf-eaeh intergenic region precursor) (db:swissprot) YAGY_ECOLI P77188 ESCHERICHIA COLI 562 -11536334 7000687222 yagy yagy protein (db:pir2.dat) D64755 D64755 Escherichia coli 562 -11536334 7500896175 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:17156) (re:17824) (di:complement) ECU73857 U73857 g1657493 Escherichia coli 562 -11536334 239914 yagy orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completengenome.) (nt:f222; 26 pct identical (9 gaps) to 132 residues of) (le:13739) (re:14407) (di:complement) AE000136 AE000136 g1786485 Escherichia coli 562 -11536334 5000691488 (de:(ecoli_279) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_279 ECOLI_279 Escherichia coli 562 10122754

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869118	13090	35246	588	195

Description

6500732477 yagz:b0293 hypothetical 20.1 kd protein in intf-eaeh intergenic region precursor (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0293 b0293 Escherichia coli 562 -11536335 4000709277 yagz (de:hypothetical 20.1 kd protein in intf-eaeh intergenic region precursor) (db:swissprot) YAGZ_ECOLI P77264 ESCHERICHIA COLI 562 -11536335 7000687223 yagz yagz protein (db:pir2.dat) E64755 E64755 Escherichia coli 562 -11536335 7500896176 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:17882) (re:18469) (di:complement) ECU73857 U73857 g1657494 Escherichia coli 562 -11536335 239915 yagz orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 26 of 400 of the completengenome.) (nt:f195; 24 pct identical (9 gaps) to 175 residues of) (le:14465) (re:15052) (di:complement) AE000136 AE000136 g1786486 Escherichia coli 562 -11536335 5000691489 (de:(ecoli_280) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_280 ECOLI_280 Escherichia coli 562 10122755

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869131	13091	35247	861	286

Description

GTC ORF with score 188 to: (sr:rattus norvegicus (strain:wistar) male liver dna, clone_lib:lambd) (db:genpept-rod) (ec:3.1.1.1) (de:rattus norvegicus gene for carboxylesterase precursor, exon12 andcomplete cds.) (le:ab010559:1:ab010560:152:ab010561:51)...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869148	13092	35248	1842	614

Description

6500732478 ykga:b0300 hypothetical transcriptional regulator in eaeh-beta intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0300 b0300 Escherichia coli 562 -11536336 4000708132 ykga (de:hypothetical transcriptional regulator in eaeh-beta intergenic region) (db:swissprot) YKGA_ECOLI P77601 ESCHERICHIA COLI 562 -11536336 7000688099 ykga probable transcription regulator ykga (db:pir2.dat) D64756 D64756 Escherichia coli 562 -11536336 7500938484 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to e. coli rob gene) (le:24248) (re:24967) (di:complement) ECU73857 U73857 g1657500 Escherichia coli 562 -11536336 239921 ykga putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:f239; 37 pct identical to 145 residues of the 289) (le:4066) (re:4785) (di:complement) AE000137 AE000137 g1786491 Escherichia coli 562 -11536336 5000691492 (de:(ecoli_284) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_284 ECOLI_284 Escherichia coli 562 10122758

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869168	13093	35249	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869171	13094	35250	300	99

Description

6500732479 ykgb:b0301 hypothetical 22.3 kd protein in eaeh-beta intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0301 b0301 Escherichia coli 562 -11536337 1500686252 ykgb (de:hypothetical 22.3 kd protein in eaeh-beta intergenic region) (db:swissprot) YKGB_ECOLI P75685 ESCHERICHIA COLI 562 -11536337 7000688100 ykgb membrane protein ykgb (cl:conserved hypothetical protein hi0219) (db:pir2.dat) E64756 E64756 Escherichia coli 562 -11536337 7500938485 ykgb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 27 of 400 of the completegenome.) (nt:f200; 49 pct identical (16 gaps) to 170 residues of) (le:5342) (re:5944) (di:complement) AE000137 AE000137 g1786492 Escherichia coli 562 -11536337 5000691493 (de:(ecoli_285) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_285 ECOLI_285 Escherichia coli 562 10060995

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869185	13095	35251	723	240

Description

6500732480 ykgc:b0304 probable pyridine nucleotide-disulfide oxidoreductase in eaeh-beta intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0304 b0304 Escherichia coli 562 -11536338 4000709571 ykgc (de:intergenic region) (db:swissprot) YKGC_ECOLI P77212 ESCHERICHIA COLI 562 -11536338 7000688101 ykgc probable mercury ii reductase::ykgc protein (ec:1.16.1.1) (db:pir2.dat) H64756 H64756 Escherichia coli 562 -11536338 7500938487 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to s. aureus mercury(ii) reductase) (le:26473) (re:27825) (di:complement) ECU73857 U73857 g1657503 Escherichia coli 562 -11536338 239924 ykgc putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 27 of 400 of the completegenome.) (nt:f450; 35 pct identical (29 gaps) to 430 residues of) (le:6292) (re:7644) (di:complement) AE000137 AE000137 g1786495 Escherichia coli 562 -11536338 5000691496 (de:(ecoli_288) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_288 ECOLI_288 Escherichia coli 562 10122761

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869193	13096	35252	642	214

Description

6500732481 ykgd:b0305 hypothetical transcriptional regulator in eaeh-beta intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0305 b0305 Escherichia coli 562 -11536339 4000708133 ykgd (de:hypothetical transcriptional regulator in eaeh-beta intergenic region) (db:swissprot) YKGD_ECOLI P77379 ESCHERICHIA COLI 562 -11536339 7000688102 ykgd ykgd protein (db:pir2.dat) A64757 A64757 Escherichia coli 562 -11536339 7500938488 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:28024) (re:28878) (di:direct) ECU73857 U73857 g1657504 Escherichia coli 562 -11536339 239925 ykgd putative arac-type regulatory protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:o284; residues 170-276 are 39 pct identical to aa) (le:7843) (re:8697) (di:direct) AE000137 AE000137 g1786496 Escherichia coli 562 -11536339 5000691497 (de:(ecoli_289) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_289 ECOLI_289 Escherichia coli 562 10122762

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869221	13097	35253	297	98

Description

GTC ORF with score 218 to: (sr:neurospora crassa (strain st. lawrence 74a (fgsc 262) dna) (db:genpept-pln1) (de:neurospora crassa alkaline phosphatase gene, complete cds.) (le:755:1354:1528:1677) (re:1280:1472:1616:1755) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869226	13098	35254	1092	364

Description

GTC ORF with score 1226 to: (sr:neurospora crassa (strain st. lawrence 74a (fgsc 262) dna) (db:genpept-pln1) (de:neurospora crassa alkaline phosphatase gene, complete cds.) (le:755:1354:1528:1677) (re:1280:1472:1616:1755) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869238	13099	35255	318	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869247	13100	35256	1002	333

Description

6500732482 ykge:b0306 hypothetical 26.0 kd protein in eaeh-beta intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0306 b0306 Escherichia coli 562 -11536340 4000709278 ykge (de:hypothetical 26.0 kd protein in eaeh-beta intergenic region) (db:swissprot) YKGE_ECOLI P77252 ESCHERICHIA COLI 562 -11536340 7000688103 ykge glycolate oxidase homolog ykge (cl:conserved hypothetical protein hp0139) (db:pir2.dat) B64757 B64757 Escherichia coli 562 -11536340 7500938489 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:29405) (re:30124) (di:direct) ECU73857 U73857 g1657505 Escherichia coli 562 -11536340 239926 ykge putative dehydrogenase subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:o239; 29 pct identical (12 gaps) to 179 residues of) (le:9224) (re:9943) (di:direct) AE000137 AE000137 g1786497 Escherichia coli 562 -11536340 5000691498 (de:(ecoli_290) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_290 ECOLI_290 Escherichia coli 562 10122763

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869253	13101	35257	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869260	13102	35258	714	237

Description

6500732483 ykgf:b0307 hypothetical 53.1 kd protein in eaeh-beta intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0307 b0307 Escherichia coli 562 -11536341 4000707936 ykgf (de:hypothetical 53.1 kd protein in eaeh-beta intergenic region) (db:swissprot) YKGF_ECOLI P77536 ESCHERICHIA COLI 562 -11536341 7000688104 ykgf probable iron-sulfur protein ykgf (cl:conserved hypothetical iron-sulfur protein hp0138) (db:pir2.dat) C64757 C64757 Escherichia coli 562 -11536341 7500938490 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:30135) (re:31562) (di:direct) ECU73857 U73857 g1657506 Escherichia coli 562 -11536341 239927 ykgf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:o475; 24 pct identical (9 gaps) to 163 residues of) (le:9954) (re:11381) (di:direct) AE000137 AE000137 g1786498 Escherichia coli 562 -11536341 5000691499 (de:(ecoli_291) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_291 ECOLI_291 Escherichia coli 562 10122764

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869261	13103	35259	855	284

Description

6500732484 ykkg:b0308 hypothetical 31.1 kd protein in eaeh-beta intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0308 b0308 Escherichia coli 562 -11536342 4000709279 ykkg (de:hypothetical 31.1 kd protein in eaeh-beta intergenic region) (db:swissprot) YKKG_ECOLI P77433 ESCHERICHIA COLI 562 -11536342 7000688105 ykkg ykkg protein (cl:ykkg protein) (db:pir2.dat) D64757 D64757 Escherichia coli 562 -11536342 7500938491 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:31402) (re:32250) (di:direct) ECU73857 U73857 g1657507 Escherichia coli 562 -11536342 239928 ykkg putative transporter (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:o282; 26 pct identical (2 gaps) to 97 residues of) (le:11221) (re:12069) (di:direct) AE000137 AE000137 g1786499 Escherichia coli 562 -11536342 5000691500 (de:(ecoli_292) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_292 ECOLI_292 Escherichia coli 562 10122765

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869263	13104	35260	309	102

Description

6500732485 ykgh:b0310 hypothetical 25.6 kd protein in eaeh-beta intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0310 b0310 Escherichia coli 562 -11536343 4000709280 ykgh (de:hypothetical 25.6 kd protein in eaeh-beta intergenic region) (db:swissprot) YKGH_ECOLI P77180 ESCHERICHIA COLI 562 -11536343 7000688106 ykgh membrane protein ykgh (db:pir2.dat) F64757 F64757 Escherichia coli 562 -11536343 7500938492 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical protein) (le:32493) (re:33161) (di:complement) ECU73857 U73857 g1657508 Escherichia coli 562 -11536343 239929 ykgh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 28 of 400 of the completegenome.) (nt:f222; phage stats; 25 pct identical (12 gaps) to) (le:68) (re:736) (di:complement) AE000138 AE000138 g1786502 Escherichia coli 562 -11536343 5000691502 (de:(ecoli_294) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_294 ECOLI_294 Escherichia coli 562 10122767

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869267	13105	35261	519	172

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869272	13106	35262	414	137

Description

6500732486 cynx:b0341 cyanate transport protein cynx (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0341 b0341 Escherichia coli 562 -11536344 67527 cynx (de:cyanate transport protein cynx) (db:swissprot) CYNX_ECOLI P17583 ESCHERICHIA COLI 562 -11536344 7000684963 cynx membrane protein cynx (cl:cynx protein) (db:pir1.dat) (mp:8 min) BVECCX E64761 Escherichia coli 562 -11536344 1500689805 cynx cyanate transport (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 31 of 400 of the completegenome.) (nt:o384; 98 pct identical to 335 residues of 350 aa) (le:2400) (re:3554) (di:direct) AE000141 AE000141 g1786536 Escherichia coli 562 -11536344 7500879861 cynx unknown (db:genpept-syn) (de:synthetic transposon tn5lac, complete sequence.) (le:6158) (re:7312) (di:complement) XXU90436 U90436 g2055401 synthetic construct 32630 -11536344 5000691524 (de:(ecoli_325) (pn:cyanate transport) (gn:cynx) (gtcfc:13.7:14.1) (ec:) (cynx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_325 ECOLI_325 Escherichia coli 562 10122784

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869292	13107	35263	294	97

Description

5000691549 yaih (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b0376 b0376 Escherichia coli 562 -11536345
7000691934 yaih yaih protein (db:pir2.dat) H64765 H64765 Escherichia coli
562 -11536345 7500960494 yaih putative enzyme (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 34 of
400 of the completegenome.) (nt:f385; 98 pct identical to 69 residues of
fragment) (le:4952) (re:6109) (di:complement) AE000144 AE000144 g1786574
Escherichia coli 562 -11536345 6500732487 yaih (gtcfc:14.2) (keggfc:14.2)
(rileyfc:5.9.0) (db:gtc-escherichia coli) b0376 b0376 Escherichia coli 562
-11536345

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869298	13108	35264	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869299	13109	35265	204	67

Description

6500732488 yaic:b0385 hypothetical 41.5 kd protein in psif-proc intergenic
region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli)
b0385 b0385 Escherichia coli 562 -11536346 109778 yaic (de:hypothetical
41.5 kd protein in psif-proc intergenic region) (db:swissprot) YAIC_ECOLI
P21830 ESCHERICHIA COLI 562 -11536346 7000687240 yaic membrane protein yaic
(db:pir2.dat) A64767 A64767 Escherichia coli 562 -11536346 7500896198 yaic
(db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:also
previously sequenced by another group, genbank) (le:111293) (re:112408)
(di:direct) ECU73857 U73857 g1657581 Escherichia coli 562 -11536346 240002
yaic orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 35 of 400 of the completegenome.)
(nt:o371; 100 pct identical to fragment yaic_ecoli) (le:2579) (re:3694)
(di:direct) AE000145 AE000145 g1786584 Escherichia coli 562 -11536346
5000691554 (de:(ecoli_369) (pn:hypothetical protein in
phoa:3"region:fragment) (gn:yaic) (gtcfc:13.7:14.1) (ec:) (yaic_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_369 ECOLI_369
Escherichia coli 562 10122809

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869302	13110	35266	402	133

Description

GTC ORF with score 128 to: (sr:human) (db:genpept-pri2) (de:homo sapiens hla class iii region containing tenascin x(tenascin-x) gene, partial cds; cytochrome p450 21-hydroxylase(cyp21b), complement component c4 (c4b) g11, helicase (ski2w), ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869303	13111	35267	615	204

Description

5000691555 yaii (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0387 b0387 Escherichia coli 562 -11536347
 7000691935 yaii yaii protein (cl:yaii protein) (db:pir2.dat) C64767 C64767 Escherichia coli 562 -11536347 7500960495 yaii orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completegenome.) (nt:o192; 100 pct identical to fragment gb:) (le:4520) (re:5098) (di:direct) AE000145 AE000145 g1786586 Escherichia coli 562 -11536347 6500732489 yaii (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0387 b0387 Escherichia coli 562 -11536347

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869315	13112	35268	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869335	13113	35269	456	152

Description

6500732490 yaie:b0391 hypothetical 10.2 kd protein in arom-araj intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0391 b0391 Escherichia coli 562 -11536348 109781 yaie (de:hypothetical 10.2 kd protein in arom-araj intergenic region) (db:swissprot) YAIE_ECOLI P36768 ESCHERICHIA COLI 562 -11536348 7000687241 yaie yaie protein (db:pir2.dat) G64767 G64767 Escherichia coli 562 -11536348 7500896201 yaie (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:hypothetical 10.7kd protein in araj-arom intergenic) (le:115767) (re:116051) (di:direct) ECU73857 U73857 g1657587 Escherichia coli 562 -11536348 240008 yaie orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completengenome.) (nt:o94; 100 pct identical to n-terminal 77 aa) (le:7053) (re:7337) (di:direct) AE000145 AE000145 g1786590 Escherichia coli 562 -11536348 5000691557 (de:(ecoli_375) (pn:hypothetical 10) (gn:yaie) (gtcfc:13.7:14.1) (ec:) (yaie_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_375 ECOLI_375 Escherichia coli 562 10122812

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869344	13114	35270	186	61

Description

6500732491 yaid:b0393 hypothetical 34.0 kd protein in arom-araj intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0393 b0393 Escherichia coli 562 -11536349 7500896199 yaid (de:hypothetical 34.0 kd protein in arom-araj intergenic region) (db:swissprot) YAIID_ECOLI P36767 ESCHERICHIA COLI 562 -11536349 163492 yaid yaid protein:conserved hypothetical protein 303 (db:pir2.dat) S41303 S41303 Escherichia coli 562 -11536349 5000691559 orf303 (db:genpept-bct1) (de:e.coli orf302, Orf303 and orf101 sequence.) (le:1042) (re:1953) (di:direct) ECORFABC X76979 g440403 Escherichia coli 562 -11536349 235754 yaid orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the completengenome.) (nt:f303; 100 pct identical to yaid_ecoli sw:) (le:7984) (re:8895) (di:complement) AE000145 AE000145 g1786592 Escherichia coli 562 -11536349 109779 yaid (de:hypothetical 34.0 kd protein in arom-araj intergenic region) (db:swissprot) YAIID_ECOLI P36767 ESCHERICHIA COLI 562 -11536349

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869352	13115	35271	384	127

Description

6500732492 yajb:b0404 hypothetical 23.0 kd protein in malz-quea intergenic region:orf 14 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0404 b0404 Escherichia coli 562 -11536350 109801 yajb (de:hypothetical 23.0 kd protein in malz-quea intergenic region (orf 14)) (db:swissprot) YAJB_ECOLI P21515 ESCHERICHIA COLI 562 -11536350 7000687249 yajb yajb protein (db:pir2.dat) D64769 D64769 Escherichia coli 562 -11536350 7500896228 yajb hypothetical 14.0 kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:3787) (re:4368) (di:complement) ECU82664 U82664 g1773088 Escherichia coli 562 -11536350 240181 yajb putative glycoprotein (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 37 of 400 of the completegenome.) (nt:f193; aa 1-70 are 100 pct identical to) (le:1930) (re:2511) (di:complement) AE000147 AE000147 g1786605 Escherichia coli 562 -11536350 5000691564 (de:(ecoli_388) (pn:hypothetical 14) (gn:yajb) (gtcfc:13.7:14.1) (ec:) (yajb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_388 ECOLI_388 Escherichia coli 562 10122818

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869353	13116	35272	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869354	13117	35273	198	65

Description

5000691566 yajd (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0410 b0410 Escherichia coli 562 -11536351 7000691936 yajd yajd protein (db:pir2.dat) B64770 B64770 Escherichia coli 562 -11536351 7500960496 yajd hypothetical 12.6kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:10055) (re:10402) (di:direct) ECU82664 U82664 g1773094 Escherichia coli 562 -11536351 240187 yajd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 37 of 400 of the completegenome.) (nt:o115; 100 pct identical to 108 residues of) (le:8198) (re:8545) (di:direct) AE000147 AE000147 g1786611 Escherichia coli 562 -11536351 6500732493 yajd (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0410 b0410 Escherichia coli 562 -11536351

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869364	13118	35274	312	103

Description

6500732494 yaji:b0412 hypothetical 21.8 kd protein in tsx-ribd intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0412 b0412 Escherichia coli 562 -11536352 7000687250 yaji yaji protein (db:pir2.dat) D64770 D64770 Escherichia coli 562 -11536352 240189 (db:genpept-bct1) (de:escherichia coli unknown orf, located between nusB gene and tsxgene, complete cds.) (nt:orf; spans region between the nusB gene, genbank) (le:102) (re:701) (di:direct) ECU31810 U31810 g969032 Escherichia coli 562 -11536352 7500896234 yaji (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:hypothetical protein) (le:11762) (re:12361) (di:complement) ECU82664 U82664 g1773096 Escherichia coli 562 -11536352 239428 yaji orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 37 of 400 of the completegenome.) (nt:f199; 100 pct identical to gb: ecu31810_1) (le:9905) (re:10504) (di:complement) AE000147 AE000147 g1786613 Escherichia coli 562 -11536352 109813 yaji (de:hypothetical 21.8 kd protein in tsx-ribd intergenic region) (db:swissprot) YAJI_ECOLI P46122 ESCHERICHIA COLI 562 -11536352 5000691567 (de:(ecoli_396) (pn:hypothetical 21) (gn:yaji) (gtcfc:13.7:14.1) (ec:) (yaji_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_396 ECOLI_396 Escherichia coli 562 10051545

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869367	13119	35275	336	112

Description

GTC ORF with score 496 to: (fn:suppressor of vegetative incompatibility) (db:genpept-pln1) (de:podospira anserina suppressor of vegetative incompatibility mod-e(mod-e) gene, complete cds.) (nt:an hsp90; heat shock protein) (le:886:1746:2247) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869372	13120	35276	399	132

Description

6500732495 apba:b0425 apba protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0:5.9.0) (db:gtc-escherichia coli) b0425 b0425 Escherichia coli 562 -11536353 120079 apba:pane (ec:1.1.1.169) (de:(kpa reductase)) (db:swissprot) APBA_ECOLI P77728 ESCHERICHIA COLI 562 -11536353 7000684587 apba ketopantoate reductase (db:pir2.dat) A64772 A64772 Escherichia coli 562 -11536353 7500876981 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to s. typhimurium apba) (le:23054) (re:23965) (di:complement) ECU82664 U82664 g1773109 Escherichia coli 562 -11536353 240202 apba involved in thiamin biosynthesis:alternative (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completgenome.) (nt:f303; 100 pct identical to fragment gb:) (le:10678) (re:11589) (di:complement) AE000148 AE000148 g1786627 Escherichia coli 562 -11536353 5000691575 (de:(ecoli_409) (pn:apba) (gn:apba) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_409 ECOLI_409 Escherichia coli 562 10062916

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869376	13121	35277	351	116

Description

GTC ORF with score 402 to: (fn:suppressor of vegetative incompatibility) (db:genpept-pln1) (de:podospora anserina suppressor of vegetative incompatibility mod-e(mod-e) gene, complete cds.) (nt:an hsp90; heat shock protein) (le:886:1746:2247) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869381	13122	35278	417	138

Description

6500732496 ybae:b0445 hypothetical 65.0 kd protein in hupb-cof intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0445 b0445 Escherichia coli 562 -11536354 110174 ybae (de:hypothetical 65.0 kd protein in hupb-cof intergenic region) (db:swissprot) YBAE_ECOLI P46890 ESCHERICHIA COLI 562 -11536354 7000687261 ybae probable membrane protein (db:pir2.dat) E64774 E64774 Escherichia coli 562 -11536354 222828 ybae ybae (sr:escherichia coli (strain:w3110) dna, clone_lib:kohara clone:3b) (db:genpept-bct1) (de:escherichia coli genes for beta-subunit of hu, ybau, ybav, ybaw,ybax, ybae, cof, ybao, complete cds, and for hupb, partial cds.) (nt:a hypothetical gene; similari... D82943 D82943 g1580716 Escherichia coli 562 -11536354 7500896533 ybae (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:hypothetical protein) (le:45062) (re:46762) (di:complement) ECU82664 U82664 g1773129 Escherichia coli 562 -11536354 240222 ybae orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 41 of 400 of the completegenome.) (nt:f566; 100 pct identical to fragment ybae_ecoli) (le:63) (re:1763) (di:complement) AE000151 AE000151 g1786650 Escherichia coli 562 -11536354 5000691583 (de:(ecoli_429) (pn:hypothetical protein in cof:3"region:fragment) (gn:ybae) (gtcfc:13.7:14.1) (ec:) (ybae_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_429 ECOLI_429 Escherichia coli 562 10119134

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869382	13123	35279	309	102

Description

6500732497 ybaj:b0461 hypothetical 14.6 kd protein in hha-acrb intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0461 b0461 Escherichia coli 562 -11536355 110175 ybaj (de:hypothetical 14.6 kd protein in hha-acrb intergenic region) (db:swissprot) YBAJ_ECOLI P37611 ESCHERICHIA COLI 562 -11536355 7000687262 ybaj ybaj protein (db:pir2.dat) D64776 D64776 Escherichia coli 562 -11536355 7500896534 ybaj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 42 of 400 of the completegenome.) (nt:f124; 100 pct identical to 72 aa of ybaj_ecoli) (le:3748) (re:4122) (di:complement) AE000152 AE000152 g1786666 Escherichia coli 562 -11536355 5000691594 (de:(ecoli_444) (pn:hypothetical 8) (gn:ybaj) (gtcfc:13.7:14.1) (ec:) (ybaj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_444 ECOLI_444 Escherichia coli 562 10122838

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869388	13124	35280	309	102

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869391	13125	35281	2535	844

Description

GTC ORF with score 207 to: (sr:homo sapiens male myeloblast cell-line kg-1 cdna to mrna) (db:genpept-pri2) (de:human mrna for kiaa0177 gene, partial cds.) (nt:similar to chicken poly(adp-ribose) synthase, has) (le:<1) (re:4898) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869446	13126	35282	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869447	13127	35283	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869448	13128	35284	390	129

Description

GTC ORF with score 105 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0637.) (nt:similar to saccharomyces cerevisiae) (le:<1) (re:1294) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869449	13129	35285	792	263

Description

6500732498 ybbd:b0500 hypothetical 10.1 kd protein in rhsd-gcl intergenic region:orf3 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0500 b0500 Escherichia coli 562 -11536356 110205 ybbd (de:hypothetical 10.1 kd protein in rhsd-gcl intergenic region (orf3)) (db:swissprot) YBBB_ECOLI P33669 ESCHERICHIA COLI 562 -11536356 7000687284 ybbd probable membrane protein ybbd (db:pir2.dat) C64781 C64781 Escherichia coli 562 -11536356 7500896567 ybbd hypothetical 9.2 kd protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:108088) (re:108348) (di:direct) ECU82664 U82664 g1773182 Escherichia coli 562 -11536356 240275 ybbd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 46 of 400 of the completegenome.) (nt:o86; 100 pct identical to 67 residues of) (le:5625) (re:5885) (di:direct) AE000156 AE000156 g1786709 Escherichia coli 562 -11536356 5000691622 (de:(ecoli_483) (pn:hypothetical 9) (gn:ybbd) (gtcfc:13.7:14.1) (ec:) (ybbd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_483 ECOLI_483 Escherichia coli 562 10122860

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869450	13130	35286	354	117

Description

6500732499 ybbb:b0503 hypothetical 41.1 kd protein in rhsd-gcl intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0503 b0503 Escherichia coli 562 -11536357 110201 ybbb (de:hypothetical 41.1 kd protein in rhsd-gcl intergenic region) (db:swissprot) YBBB_ECOLI P33667 ESCHERICHIA COLI 562 -11536357 7000687280 ybbb ybbb protein (db:pir2.dat) F64781 F64781 Escherichia coli 562 -11536357 7500896563 ybbb (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:hypothetical protein) (le:109580) (re:110674) (di:complement) ECU82664 U82664 g1773184 Escherichia coli 562 -11536357 240277 ybbb putative capsule anchoring protein (fn:phenotype; surface polysaccharides and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 46 of 400 of the completegenome.) (nt:f364; 100 pct identical to fragment ybbb_ecoli) (le:7117) (re:8211) (di:complement) AE000156 AE000156 g1786712 Escherichia coli 562 -11536357 5000691625 (de:(ecoli_486) (pn:hypothetical protein in rhsd:3"region:fragment) (gn:ybbb) (gtcfc:13.7:14.1) (ec:) (ybbb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_486 ECOLI_486 Escherichia coli 562 10122863

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869456	13131	35287	366	121

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869462	13132	35288	1326	442

Description

6500732500 ybbf:b0524 hypothetical 26.9 kd protein in pure-ppib intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0524 b0524 Escherichia coli 562 -11536358 110206 ybbf (de:hypothetical 26.9 kd protein in pure-ppib intergenic region) (db:swissprot) YBBF_ECOLI P43341 ESCHERICHIA COLI 562 -11536358 7000687285 ybbf ybbf protein (cl:hypothetical protein hi0735) (db:pir2.dat) C64784 C64784 Escherichia coli 562 -11536358 7500896568 (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (nt:similar to h. influenzae hi0735) (le:132667) (re:133389) (di:complement) ECU82664 U82664 g1773205 Escherichia coli 562 -11536358 240298 ybbf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 48 of 400 of the completegenome.) (nt:f240; 100 pct identical to fragment ybbf_ecoli) (le:6726) (re:7448) (di:complement) AE000158 AE000158 g1786735 Escherichia coli 562 -11536358 5000691643 (de:(ecoli_507) (pn:hypothetical protein in pure 5"region:fragment) (gn:ybbf) (gtcfc:13.7:14.1) (ec:) (ybbf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_507 ECOLI_507 Escherichia coli 562 10122877

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869471	13133	35289	327	108

Description

5000691671 ybch (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0567 b0567 Escherichia coli 562 -11536359 7000691937 ybch ybch protein (db:pir2.dat) E64789 E64789 Escherichia coli 562 -11536359 7500960497 ybch (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:27722) (re:28612) (di:complement) ECU82598 U82598 g1778482 Escherichia coli 562 -11536359 240078 ybch orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:f296; 99 pct identical to 130 aa of ybch_ecoli) (le:9980) (re:10870) (di:complement) AE000161 AE000161 g1786779 Escherichia coli 562 -11536359 6500732501 ybch hypothetical 16.8 kd protein in nfra 3region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #162) (db:genpept) (de:escherichia coli genomic dna. (12.6 - 12.9 min).) (nt:orf_id:o162#2; similar to swissprot accession) (le:1506) (re:2396) (di:complement) D90699 D90699 g4062193 Escherichia coli 562 -11536359

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869478	13134	35290	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869480	13135	35291	849	283

Description

6500732502 ybed:b0631 hypothetical 9.8 kd protein in lipb-daca intergenic region:orf1 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0631 b0631 Escherichia coli 562 -11536360 110246 ybed (de:hypothetical 9.8 kd protein in lipb-daca intergenic region (orf1)) (db:swissprot) YBED_ECOLI P30977 ESCHERICHIA COLI 562 -11536360 7000687322 ybed ybed protein (cl:ybed protein) (db:pir2.dat) E64797 E64797 Escherichia coli 562 -11536360 240144 (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohar) (db:genpept-bct1) (de:e.coli lipoic acid biosynthesis lipa, lipb, and orfs 1, 2 and 3genes, complete cds; daca gene, 3' end.) (nt:orf 1) (le:653) (re:916) (di:direct) ECOLIPAB L07636 g146621 Escherichia coli 562 -11536360 7500896665 ybed (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:103009) (re:103272) (di:complement) ECU82598 U82598 g1778548 Escherichia coli 562 -11536360 234983 ybed orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 58 of 400 of the completegenome.) (nt:f87; 98 pct identical to ybed_ecoli sw: p30977) (le:114) (re:377) (di:complement) AE000168 AE000168 g1786850 Escherichia coli 562 -11536360 5000691712 ybed hypothetical 9.8 kd protein in lipb-daca (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf_id:ol68#16; similar to swissprot accession) (le:13442) (re:13705) (di:complement) D90703 D90703 g4062252 Escherichia coli 562 -11536360

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869486	13136	35292	1413	471

Description

6500732503 ybea:b0636 hypothetical 17.3 kd protein in mrda-phpb intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0636 b0636 Escherichia coli 562 -11536361 240149 ybea (de:hypothetical 17.3 kd protein in mrda-phpb intergenic region) (db:swissprot) YBEA_ECOLI P05850 ESCHERICHIA COLI 562 -11536361 135170 ybea ybea protein (cl:conserved hypothetical protein hi0033) (db:pir1.dat) (mp:15 min) QQECP1 B24995 Escherichia coli 562 -11536361 5000691713 (db:genpept-bct1) (de:e. coli pbpa gene for penicillin-binding protein (pbp)2.) (nt:orf2 (aa 1-155)) (le:537) (re:1004) (di:direct) ECPBPA X04516 g581174 Escherichia coli 562 -11536361 7500896661 ybea (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:108878) (re:109345) (di:complement) ECU82598 U82598 g1778553 Escherichia coli 562 -11536361 237725 ybea orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 58 of 400 of the completegenome.) (nt:f155; 100 pct identical to ybea_ecoli sw: p05850) (le:5983) (re:6450) (di:complement) AE000168 AE000168 g1786855 Escherichia coli 562 -11536361 7502852280 ybea hypothetical 17k protein pbpa 5 region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:ol69#4; similar to pir accession number) (le:4496) (re:4963) (di:complement) D90704 D90704 g4062254 Escherichia coli 562 -11536361 110241 ybea (de:hypothetical 17.3 kd protein in mrda-phpb intergenic region) (db:swissprot) YBEA_ECOLI P05850 ESCHERICHIA COLI 562 -11536361

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869488	13137	35293	1284	427

Description

6500732504 ybel:b0643 hypothetical 18.8 kd protein in leus-gltl intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0643 b0643 Escherichia coli 562 -11536362 110256 ybel (de:hypothetical 18.8 kd protein in leus-gltl intergenic region) (db:swissprot) YBEL_ECOLI P46129 ESCHERICHIA COLI 562 -11536362 7000687327 ybel ybel protein (db:pir2.dat) A64799 A64799 Escherichia coli 562 -11536362 7500896670 ybel (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:115648) (re:116130) (di:direct) ECU82598 U82598 g1778561 Escherichia coli 562 -11536362 240157 ybel putative alpha helical protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:o160; 100 pct identical to fragment ybel_ecoli) (le:148) (re:630) (di:direct) AE000169 AE000169 g1786863 Escherichia coli 562 -11536362 5000691717 ybel hypothetical protein in leus 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:o169#11; similar to swissprot accession) (le:11266) (re:11748) (di:direct) D90704 D90704 g4062258 Escherichia coli 562 -11536362

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869489	13138	35294	294	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869494	13139	35295	417	138

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869519	13140	35296	549	183

Description

6500732505 ybek:b0651 hypothetical 33.8 kd protein in leus-gltl intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0651 b0651 Escherichia coli 562 -11536363 110255 ybek (de:hypothetical 33.8 kd protein in leus-gltl intergenic region) (db:swissprot) YBEK_ECOLI P41409 ESCHERICHIA COLI 562 -11536363 7000687326 ybek purine nucleosidase-related protein ybek (cl:yaaf protein) (db:pir2.dat) A64800 A64800 Escherichia coli 562 -11536363 7500896669 yaaf homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to e. coli yaaf) (le:124107) (re:125042) (di:complement) ECU82598 U82598 g1778569 Escherichia coli 562 -11536363 240165 ybek putative trna synthetase (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 59 of 400 of the completegenome.) (nt:f311; 100 pct identical to fragment ybek_ecoli) (le:8607) (re:9542) (di:complement) AE000169 AE000169 g1786871 Escherichia coli 562 -11536363 5000691725 ybek hypothetical protein in gltl 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #170) (db:genpept) (de:escherichia coli genomic dna. (14.6 - 14.9 min).) (nt:orf_id:o170#5; similar to swissprot accession) (le:5961) (re:6896) (di:complement) D90705 D90705 g4062271 Escherichia coli 562 -11536363

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869527	13141	35297	708	235

Description

6500732506 ybgg:b0732 ybgb:hypothetical 100.0 kd protein in hrsg-cyda intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0732 b0732 Escherichia coli 562 -11536364 110285 ybgg (de:hypothetical 100.0 kd protein in hrsg-cyda intergenic region) (db:swissprot) YBGG_ECOLI P54746 ESCHERICHIA COLI 562 -11536364 7000687348 ybgb ybgb protein (db:pir2.dat) C64809 C64809 Escherichia coli 562 -11536364 7500896743 ybgg putative sugar hydrolase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 66 of 400 of the completegenome.) (nt:o877) (le:5132) (re:7765) (di:direct) AE000176 AE000176 g1786952 Escherichia coli 562 -11536364 5000691768 ybgb hypothetical protein in hrsg 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept) (de:escherichia coli genomic dna. (16.5 - 16.9 min).) (nt:orf_id:o178#1; similar to swissprot accession) (le:1168) (re:3801) (di:direct) D90713 D90713 g4062319 Escherichia coli 562 -11536364

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869553	13142	35298	1659	552

Description

6500732507 ybge:b0735 10.9 kd protein in cydb-tolq intergenic region:orfd (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0735 b0735 Escherichia coli 562 -11536365 110289 ybge (de:10.9 kd protein in cydb-tolq intergenic region (orfd)) (db:swissprot) YBGE_ECOLI P37343 ESCHERICHIA COLI 562 -11536365 7000687346 ybge ybge protein (db:pir2.dat) F64809 F64809 Escherichia coli 562 -11536365 7500896741 ybge orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 67 of 400 of the completegenome.) (nt:o97; 100 pct identical to 97 residues of the 134) (le:94) (re:387) (di:direct) AE000177 AE000177 g1786956 Escherichia coli 562 -11536365 5000691769 ybge hypothetical protein in cydb-tolq intergenic (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept) (de:escherichia coli genomic dna. (16.5 - 16.9 min).) (nt:orf_id:ol78#4; similar to swissprot accession) (le:7499) (re:7792) (di:direct) D90713 D90713 g4062320 Escherichia coli 562 -11536365

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869565	13143	35299	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869601	13144	35300	297	98

Description

6500732508 ybgc:b0736 hypothetical 15.6 kd protein in cydb-tolq intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0736 b0736 Escherichia coli 562 -11536366 110286 ybgc (de:hypothetical 15.6 kd protein in cydb-tolq intergenic region) (db:swissprot) YBGC_ECOLI P08999 ESCHERICHIA COLI 562 -11536366 131571 ybgc ybgc protein (cl:15.5k protein (tolab operon 5' region)) (db:pir1.dat) (mp:17 min) WMEC15 A25980 Escherichia coli 562 -11536366 7500896738 (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli tolqra gene cluster dna.) (nt:orf 1; putative) (le:145) (re:549) (di:direct) ECOTOLQRA M16489 g1128977 Escherichia coli 562 -11536366 236120 ybgc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 67 of 400 of the completegenome.) (nt:ol34; 98 pct identical to ybgc_ecoli sw: p08999;gtg) (le:537) (re:941) (di:direct) AE000177 AE000177 g1786957 Escherichia coli 562 -11536366 5000691770 ybgc 15.5k protein tolal operon 5 region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #178) (db:genpept) (de:escherichia coli genomic dna. (16.5 - 16.9 min).) (nt:orf_id:ol78#5; similar to pir accession number) (le:7942) (re:8346) (di:direct) D90713 D90713 g4062321 Escherichia coli 562 -11536366

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869616	13145	35301	2652	883

Description

6500732509 mode:modr:b0761 molybdenum transport protein mode (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0761 b0761 Escherichia coli 562 -11536367 83992 mode:modr (de:molybdenum transport protein mode) (db:swissprot) MODE_ECOLI P46930 ESCHERICHIA COLI 562 -11536367 164504 mode repressor protein mode (cl:repressor protein mode) (db:pir2.dat) JC6037 JC6037 Escherichia coli 562 -11536367 239052 modr (db:genpept-bct1) (de:escherichia coli k12, substrain mc1000 molybdenum transport (modr), (moda), (modb), (modc), (modd), genes, complete cds.) (nt:regulatory gene) (le:1895) (re:2683) (di:complement) ECU07867 U07867 g1147816 Escherichia coli 562 -11536367 239441 mode mode (fn:repressor of modabcd operon) (db:genpept-bct1) (de:escherichia coli molybdate transport operon (moda, modb, modc, modd), mode (mode) and modf (modf) genes, complete cds.) (nt:the two operons (modabcd and mode) diverge.) (le:1594) (re:2382) (di:compl... ECU27192 U27192 g973218 Escherichia coli 562 -11536367 7500885753 molybdenum transport protein moda homolog (db:genpept-bct1) (de:escherichia coli molybdenum transport protein moda gene, completecds.) (nt:orf17.1; putative) (le:534) (re:1322) (di:complement) ECU34275 U34275 g1002825 Escherichia coli 562 -11536367 238536 mode molybdate uptake regulatory protein (fn:regulator; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 68 of 400 of the completegenome.) (nt:f262; 100 pct identical to mode_ecoli sw:) (le:9006) (re:9794) (di:complement) AE000178 AE000178 g1786976 Escherichia coli 562 -11536367 5000691775 mode molybdenum transport protein mode. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept) (de:escherichia coli genomic dna. (17.1 - 17.4 min).) (nt:orf_id:o180#1; similar to swissprot accession) (le:662) (re:1450) (di:complement) D90715 D90715 g4062331 Escherichia coli 562 -11536367

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869661	13146	35302	273	90

Description

6500732510 ybha:b0766 hypothetical 30.2 kd protein in modc-bioa intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0766 b0766 Escherichia coli 562 -11536368 110297 ybha (de:hypothetical 30.2 kd protein in modc-bioa intergenic region) (db:swissprot) YBHA_ECOLI P21829 ESCHERICHIA COLI 562 -11536368 7000687365 ybha ybha protein (db:pir2.dat) F64812 F64812 Escherichia coli 562 -11536368 7500896766 unknown (db:genpept-bct1) (de:escherichia coli molybdate transport operon (moda, modb, modc, modd), mode (mode) and modf (modf) genes, complete cds.) (le:5351) (re:6169) (di:complement) ECU27192 U27192 g973220 Escherichia coli 562 -11536368 239056 ybha putative phosphatase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 69 of 400 of the completegenome.) (nt:f272; 100 pct identical ybha_ecoli sw:) (le:2638) (re:3456) (di:complement) AE000179 AE000179 g1786982 Escherichia coli 562 -11536368 5000691777 ybha hypothetical 30.2 kd protein in modc 3region. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept) (de:escherichia coli genomic dna. (17.1 - 17.4 min).) (nt:orf_id:o180#6; similar to swissprot accession) (le:4419) (re:5237) (di:complement) D90715 D90715 g4062333 Escherichia coli 562 -11536368

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869662	13147	35303	609	202

Description

6500732511 ybhe:b0767 hypothetical 36.3 kd protein in modc-bioa intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0767 b0767 Escherichia coli 562 -11536369 110301 ybhe (de:hypothetical 36.3 kd protein in modc-bioa intergenic region) (db:swissprot) YBHE_ECOLI P52697 ESCHERICHIA COLI 562 -11536369 7000687369 ybhe ybhe protein (db:pir2.dat) G64812 G64812 Escherichia coli 562 -11536369 7500896769 ybhe putative isomerase (fn:orf; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 69 of 400 of the completegenome.) (nt:o331; 92 pct identical to the 333 aa) (le:3611) (re:4606) (di:direct) AE000179 AE000179 g1786983 Escherichia coli 562 -11536369 5000691778 ybhe hypothetical 30.2 kd protein in modc 3region. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180) (db:genpept) (de:escherichia coli genomic dna. (17.1 - 17.4 min).) (nt:orf_id:o180#7; similar to swissprot accession) (le:5392) (re:6387) (di:direct) D90715 D90715 g4062334 Escherichia coli 562 -11536369

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869669	13148	35304	2649	882

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869703	13149	35305	2910	969

Description

GTC ORF with score 618 to: (or:Arabidopsis thaliana) (sr:thale cress)
(db:genpept-pln2) (de:arabidopsis thaliana bac t14p8.) (nt:similar to
atpases associated with various cellular) (le:26974:27109:27262:27527)
(re:27029:27178:27441:27649) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869718	13150	35306	873	290

Description

6500732512 ybhd:b0768 hypothetical transcriptional regulator in modc-bioa
intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b0768 b0768 Escherichia coli 562 -11536370 110300
ybhd (de:hypothetical transcriptional regulator in modc-bioa intergenic
region) (db:swissprot) YBHD_ECOLI P52696 ESCHERICHIA COLI 562 -11536370
7000687368 ybhd ybhd protein (cl:hypothetical protein b2409) (db:pir2.dat)
H64812 H64812 Escherichia coli 562 -11536370 7500896768 ybhd putative
transcriptional regulator lysr-type (fn:putative regulator; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 69 of 400 of the
completegenome.) (nt:f338; last 108 residues are 100 pct identical to)
(le:4647) (re:5663) (di:complement) AE000179 AE000179 g1786984 Escherichia
coli 562 -11536370 5000691779 ybhd hypothetical transcriptional regulator
in modc (sr:escherichia coli(strain:k12) dna, clone:kohara clone #180)
(db:genpept) (de:escherichia coli genomic dna. (17.1 - 17.4 min).)
(nt:orf_id:o201#1; similar to swissprot accession) (le:6428) (re:7444)
(di:complement) D90715 D90715 g4062335 Escherichia coli 562 -11536370

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869722	13151	35307	1200	399

Description

6500732513 ycbe:b0933 hypothetical abc transporter atp-binding protein in pepn-pyrd intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0933 b0933 Escherichia coli 562 -11536371 110591 ssub (de:putative aliphatic sulfonates transport atp-binding protein ssub) (db:swissprot) SSUB_ECOLI P38053 ESCHERICHIA COLI 562 -11536371 7000687403 ycbe probable abc-type transport protein ycbe (cl:atp-binding cassette homology) (db:pir2.dat) D64833 D64833 Escherichia coli 562 -11536371

7500921569 ycbe putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 85 of 400 of the completegenome.) (nt:f255; 95 pct identical to fragment ycbe_ecoli) (le:10323) (re:11090) (di:complement) AE000195 AE000195 g1787164 Escherichia coli 562 -11536371 5000691885 ycbe hypothetical abc transporter atp-binding protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #219) (db:genpept) (de:escherichia coli genomic dna. (21.2 - 21.5 min).) (nt:orf_id:o221#1; similar to swissprot accession) (le:10430) (re:11197) (di:complement) D90731 D90731 g4062499 Escherichia coli 562 -11536371 7502852281 ycbe hypothetical abc transporter atp-binding protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #221) (db:genpept) (de:escherichia coli genomic dna. (21.4 - 21.8 min).) (nt:orf_id:o221#1; similar to swissprot accession) (le:1015) (re:1782) (di:complement) D90732 D90732 g4062501 Escherichia coli 562 -11536371

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869725	13152	35308	384	127

Description

6500732514 pqia:pqi5a:b0950 pqia:paraquat-inducible protein a (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0950 b0950
 Escherichia coli 562 -11536372 90837 pqia:pqi5a (de:paraquat-inducible protein a) (db:swissprot) PQIA_ECOLI P43670 ESCHERICHIA COLI 562 -11536372
 7000686169 pqia paraquat-inducible protein pqia (db:pir2.dat) E64835 E64835
 Escherichia coli 562 -11536372 223294 pqia paraquat-inducible protein a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept-bct1) (de:escherichia coli genomic dna. (21.6 - 22.0 min).) (le:5353) (re:6606) (di:direct) D90733 D90733 g1651462 Escherichia coli 562 -11536372 7500888382 pqia paraquat-inducible protein a (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 87 of 400 of the completegenome.) (nt:o417; this 417 aa orf is 94 pct identical (0 gaps)) (le:4309) (re:5562) (di:direct) AE000197 AE000197 g1787183
 Escherichia coli 562 -11536372 5000691901 pqi5a paraquat-inducible protein a. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna. (21.7 - 22.1 min).) (nt:orf_id:o222#3; similar to swissprot accession) (le:5353) (re:6606) (di:direct) D90733 D90733 g1651462 Escherichia coli 562 -11536372

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869726	13153	35309	1032	343

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869747	13154	35310	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869756	13155	35311	552	183

Description

6500732515 pqib:pqi5b:b0951 pqib:paraquat-inducible protein b (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0951 b0951 Escherichia coli 562 -11536373 90838 pqib:pqi5b (de:paraquat-inducible protein b) (db:swissprot) PQIB_ECOLI P43671 ESCHERICHIA COLI 562 -11536373 7000686170 pqib:pqi5b paraquat-inducible protein pqib (cl:pqib protein) (db:pir2.dat) F64835 F64835 Escherichia coli 562 -11536373 223295 pqib paraquat-inducible protein b (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept-bct1) (de:escherichia coli genomic dna. (21.6 - 22.0 min).) (le:6611) (re:8251) (di:direct) D90733 D90733 g1651463 Escherichia coli 562 -11536373 7500888383 pqib paraquat-inducible protein b (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 87 of 400 of the completegenome.) (nt:o546; 100 pct identical to 92 aa protein) (le:5567) (re:7207) (di:direct) AE000197 AE000197 g1787184 Escherichia coli 562 -11536373 5000691902 pqi5b paraquat-inducible protein b. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #222) (db:genpept) (de:escherichia coli genomic dna. (21.7 - 22.1 min).) (nt:orf_id:o222#4; similar to swissprot accession) (le:6611) (re:8251) (di:direct) D90733 D90733 g1651463 Escherichia coli 562 -11536373

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869763	13156	35312	420	139

Description

6500732516 yccg:b0963 hypothetical 17.3 kd protein in held-sert intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b0963 b0963 Escherichia coli 562 -11536374 7000691938 yccg:mgsa methylglyoxal synthase (cl:escherichia coli yccg protein) (ec:4.2.99.11) (db:pir2.dat) B64837 B64837 Escherichia coli 562 -11536374 7500960498 mgsa methylglyoxal synthase (fn:enzyme; central intermediary metabolism: pool,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 88 of 400 of the completegenome.) (nt:f155; formerly designated yccg) (le:8195) (re:8662) (di:complement) AE000198 AE000198 g1787197 Escherichia coli 562 -11536374 5000691909 yccg hypothetical protein in held 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #223) (db:genpept) (de:escherichia coli genomic dna. (22.0 - 22.3 min).) (nt:orf_id:o223#8; similar to swissprot accession) (le:8080) (re:8547) (di:complement) D90734 D90734 g4062530 Escherichia coli 562 -11536374

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869784	13157	35313	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869805	13158	35314	1659	553

Description

6500732517 dini:b1061 dna-damage-inducible protein i (gtcfc:14.2)
(keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1061 b1061
Escherichia coli 562 -11536375 120155 dini (de:dna-damage-inducible protein
i) (db:swissprot) DINI_ECOLI Q47143 ESCHERICHIA COLI 562 -11536375
7000685054 dini dna damage-inducible protein i:dini protein (db:pir2.dat)
B64849 B64849 Escherichia coli 562 -11536375 7500880326 dini dini
(sr:escherichia coli (strain:k-12, sub_strain:w3110) dna) (db:genpept-bct1)
(de:escherichia coli dini and sola genes for dini and sola, completecds.)
(le:867) (re:1112) (di:direct) ECODINI D31709 g1236736 Escherichia coli 562
-11536375 234152 dini damage-inducible protein i (fn:phenotype; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 97 of
400 of the completegenome.) (nt:f81; 100 pct identical to gb: ecodini_2)
(le:4578) (re:4823) (di:complement) AE000207 AE000207 g1787300 Escherichia
coli 562 -11536375 5000691979 (de:(ecoli_1023) (pn:function not assigned)
(gn:dini) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_1023 ECOLI_1023 Escherichia coli 562
10063029

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869807	13159	35315	504	167

Description

6500732518 mvim:b1068 virulence factor mvim homolog (gtcfc:14.2)
(keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1068 b1068
Escherichia coli 562 -11536376 1500686969 mvim (de:virulence factor mvim
homolog) (db:swissprot) MVIM_ECOLI P75931 ESCHERICHIA COLI 562 -11536376
7000685897 mvim probable virulence factor mvim (db:pir2.dat) A64850 A64850
Escherichia coli 562 -11536376 7500886174 mvim putative virulence factor
(fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli
k-12 mg1655 section 97 of 400 of the completegenome.) (nt:o307; 80 pct
identical to mvim_salty sw: p37168) (le:10142) (re:11065) (di:direct)
AE000207 AE000207 g1787307 Escherichia coli 562 -11536376 5000691983 mvim
mvim protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233)
(db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).)
(nt:orf_id:o233#16; similar to pir accession number) (le:13172) (re:14095)
(di:direct) D90743 D90743 g4062647 Escherichia coli 562 -11536376

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869813	13160	35316	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869814	13161	35317	405	134

Description

6500732519 mvin:b1069 virulence factor mvin homolog (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1069 b1069 Escherichia coli 562 -11536377 1500686970 mvin (de:virulence factor mvin homolog) (db:swissprot) MVIN_ECOLI P75932 ESCHERICHIA COLI 562 -11536377 7000685898 mvin probable virulence factor mvin (cl:mvin protein) (db:pir2.dat) B64850 B64850 Escherichia coli 562 -11536377 7500886175 mvin putative virulence factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.) (nt:o511; 94 pct identical to mvin_salty sw: p37169) (le:85) (re:1620) (di:direct) AE000208 AE000208 g1787309 Escherichia coli 562 -11536377 5000691984 mvin mvin protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia coli genomic dna. (24.1 - 24.5 min).) (nt:orf_id:o233#17; similar to pir accession number) (le:14205) (re:15740) (di:direct) D90743 D90743 g4062648 Escherichia coli 562 -11536377

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869816	13162	35318	453	150

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869843	13163	35319	2817	938

Description

6500732520 yceg:b1097 hypothetical 38.2 kd protein in pabc-holb intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1097 b1097 Escherichia coli 562 -11536378 110666 yceg (de:hypothetical 38.2 kd protein in pabc-holb intergenic region) (db:swissprot) YCEG_ECOLI P28306 ESCHERICHIA COLI 562 -11536378 7000687443 yceg yceg protein precursor (cl:yceg protein) (db:pir2.dat) F64853 F64853 Escherichia coli 562 -11536378 7500921682 yceg putative thymidylate kinase ec 2.7.4.9 (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 100 of 400 of the completegenome.) (nt:o340; 100 pct identical to fragment yceg_ecoli) (le:5417) (re:6439) (di:direct) AE000210 AE000210 g1787339 Escherichia coli 562 -11536378 5000691991 (de:(ecoli_1059) (pn:hypothetical protein in pabc-holb intergenic region:fragment) (gn:yceg) (gtcfc:13.7:14.1) (ec:) (yceg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1059 ECOLI_1059 Escherichia coli 562 10123158

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869850	13164	35320	468	155

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869852	13165	35321	351	116

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869856	13166	35322	627	208

Description

GTC ORF with score 152 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c19g12.) (nt:spac19g12.07c, putative splicing factor, len:604aa,) (le:11079:11379:11503) (re:11337:11456:11823) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869857	13167	35323	252	83

Description

GTC ORF with score 183 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c19g12.) (nt:spac19g12.07c, putative splicing factor, len:604aa,) (le:11079:11379:11503) (re:11337:11456:11823) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869858	13168	35324	294	97

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869861	13169	35325	459	152

Description

GTC ORF with score 315 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c19g12.) (nt:spac19g12.07c, putative splicing factor, len:604aa,) (le:11079:11379:11503) (re:11337:11456:11823) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869862	13170	35326	360	119

Description

GTC ORF with score 311 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c19g12.) (nt:spac19g12.07c, putative splicing factor, len:604aa,) (le:11079:11379:11503) (re:11337:11456:11823) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869877	13171	35327	1170	389

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869884	13172	35328	288	95

Description

6500732521 ycfj:b1110 hypothetical 18.9 kd protein in ndh-mfd intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1110 b1110 Escherichia coli 562 -11536379 110759 ycfj (de:hypothetical 18.9 kd protein in ndh-mfd intergenic region) (db:swissprot) YCFJ_ECOLI P37796 ESCHERICHIA COLI 562 -11536379 7000687452 ycfj ycfj protein (db:pir2.dat) C64855 C64855 Escherichia coli 562 -11536379 7500921732 ycfj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 101 of 400 of the completegenome.) (nt:o179; 100 pct identical to 63 aa fragment of) (le:5911) (re:6450) (di:direct) AE000211 AE000211 g1787353 Escherichia coli 562 -11536379 5000691999 ycfj hypothetical protein in ndh 3region . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #237) (db:genpept) (de:escherichia coli genomic dna. (25.0 - 25.4 min).) (nt:orf_id:o237#9; similar to swissprot accession) (le:9540) (re:10079) (di:direct) D90746 D90746 g4062679 Escherichia coli 562 -11536379

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869887	13173	35329	1086	361

Description

6500732522 ycfa:b1156 hypothetical 21.7 kd protein in inte-pin intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1156 b1156 Escherichia coli 562 -11536380 110746 ycfa (de:hypothetical 21.7 kd protein in inte-pin intergenic region) (db:swissprot) YCFA_ECOLI P09153 ESCHERICHIA COLI 562 -11536380 7000687448 ycfa ycfa protein (cl:phage t4 tail fiber assembly protein gp38) (db:pir2.dat) (mp:25 min) A64861 A64861 Escherichia coli 562 -11536380 7500921725 ycfa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 104 of 400 of the completegenome.) (nt:f200; 100 pct identical to 199 aa of ycfa_ecoli) (le:11927) (re:12529) (di:complement) AE000214 AE000214 g1787402 Escherichia coli 562 -11536380 5000692034 (de:(ecoli_1118) (pn:hypothetical 32) (gn:ycfa) (gtcfc:13.7:14.1) (ec:)) (ycfa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1118 ECOLI_1118 Escherichia coli 562 10123200

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869895	13174	35330	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869924	13175	35331	537	178

Description

6500732523 hnr:b1235 hnr protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0:5.9.0) (db:gtc-escherichia coli) b1235 b1235 Escherichia coli 562 -11536381 301353 hnr (de:hnr protein) (db:swissprot) HNR_ECOLI P37055 ESCHERICHIA COLI 562 -11536381 162621 hnr:hrn 37k regulator response protein homolog:hnr protein (cl:response regulator homology) (db:pir2.dat) (mp:28 min) A36871 A36871 Escherichia coli 562 -11536381 223436 hnr regulator response protein homolog:37.3k (sr:escherichia coli(strain:k12) dna, clone:kohara clone #249) (db:genpept-bct1) (de:escherichia coli genomic dna(27.5-27.8 min).) (le:11581) (re:12594) (di:direct) D90758 D90758 g1651626 Escherichia coli 562 -11536381 223444 hnr regulator response protein homolog:37.3k (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept-bct1) (de:escherichia coli genomic dna (27.6-28.0 min).) (le:7238) (re:8251) (di:direct) D90759 D90759 g1651635 Escherichia coli 562 -11536381 224713 hrn 37k regulator response protein homolog (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #251(27.7-28.2 min).) (nt:orf_id:o249#11; similar to (pir accession number) (le:7238) (re:8251) (di:direct) D90852 D90852 g1805512 Escherichia coli 562 -11536381 5000692082 hnr (db:genpept-bct1) (de:e.coli (k12) hnr gene.) (le:40) (re:1053) (di:direct) ECHNRG X66003 g41734 Escherichia coli 562 -11536381 233128 hnr hnr protein (fn:regulator; basic proteins - synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 112 of 400 of the completegenome.) (nt:o337; 100 pct identical to hnr_ecoli sw: p37055) (le:76) (re:1089) (di:direct) AE000222 AE000222 g1787487 Escherichia coli 562 -11536381 7502852282 hrn 37k regulator response protein homolog (sr:escherichia coli(strain:k12) dna, clone:kohara clone #249) (db:genpept) (de:escherichia coli genomic dna. (27.6 - 27.9 min).) (nt:orf_id:o251#1; similar to pir accession number) (le:11581) (re:12594) (di:direct) D90758 D90758 g1651626 Escherichia coli 562 -11536381 7502852283 hrn 37k regulator response protein homolog (sr:escherichia coli(strain:k12) dna, clone:kohara clone #250) (db:genpept) (de:escherichia coli genomic dna. (27.7 - 28.1 min).) (nt:orf_id:o251#1; similar to pir accession number) (le:7238) (re:8251) (di:direct) D90759 D90759 g1651635 Escherichia coli 562 -11536381 77435 hnr (de:hnr protein) (db:swissprot) HNR_ECOLI P37055 ESCHERICHIA COLI 562 -11536381

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869932	13176	35332	285	94

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869941	13177	35333	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869959	13178	35334	417	138

Description

6500732524 ycin:b1273 hypothetical 9.4 kd protein in soh-b-topa intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1273 b1273 Escherichia coli 562 -11536382 110823 ycin (de:hypothetical 9.4 kd protein in soh-b-topa intergenic region) (db:swissprot) YCIN_ECOLI P46132 ESCHERICHIA COLI 562 -11536382 7000687473 ycin ycin protein (db:pir2.dat) D64875 D64875 Escherichia coli 562 -11536382 223484 ycin (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #253(28.4-28.7 min.)) (nt:orf_id:o253#13; similar to (swissprot accession) (le:13037) (re:13288) (di:complement) D90764 D90764 g1742068 Escherichia coli 562 -11536382 300302 ycin (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf_id:o253#13; similar to (swissprot accession) (le:10543) (re:10794) (di:complement) D90765 D90765 g1742084 Escherichia coli 562 -11536382 300287 ycin orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 115 of 400 of the completegenome.) (nt:f83; 100 pct identical to 42 aa of ycin_ecoli) (le:3701) (re:3952) (di:complement) AE000225 AE000225 g1787528 Escherichia coli 562 -11536382 223499 ycin (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #254(28.4-28.9 min.)) (nt:orf_id:o253#13; similar to (swissprot accession) (le:10543) (re:10794) (di:complement) D90765 D90765 g1742084 Escherichia coli 562 -11536382 5000692100 (de:(ecoli_1233) (pn:hypothetical 5) (gn:ycin) (gtcfc:13.7:14.1) (ec:) (ycin_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1233 ECOLI_1233 Escherichia coli 562 10119495

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501869964	13179	35335	2022	674

Description

6500732525 ycjc:b1299 hypothetical 20.1 kd protein in sapa-aldh intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1299 b1299 Escherichia coli 562 -11536383 110828 ycjc (de:hypothetical 20.1 kd protein in sapa-aldh intergenic region) (db:swissprot) YCJC_ECOLI P38522 ESCHERICHIA COLI 562 -11536383 7000687477 ycjc aldehyde dehydrogenase-related protein ycjc:ycjc protein (db:pir2.dat) F64878 F64878 Escherichia coli 562 -11536383 223541 ycjc immunity repressor protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf_id:o257#8; similar to (swissprot accession) (le:9281) (re:9838) (di:direct) D90768 D90768 g1742129 Escherichia coli 562 -11536383 300331 ycjc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 118 of 400 of the completegenome.) (nt:o185; 100 pct identical to 121 aa) (le:2576) (re:3133) (di:direct) AE000228 AE000228 g1787557 Escherichia coli 562 -11536383 5000692116 (de:(ecoli_1259) (pn:hypothetical protein in aldh 5"region:fragment) (gn:ycjc) (gtcfc:13.7:14.1) (ec:) (ycjc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1259 ECOLI_1259 Escherichia coli 562 10119511

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869971	13180	35336	489	162

Description

6500732526 ydaa:b1333 35.6 kd protein in tpx-fnr intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1333 b1333 Escherichia coli 562 -11536384 7000691939 ydaa membrane protein ydaa (cl:ydaa protein) (db:pir1.dat) QQECX H64882 Escherichia coli 562 -11536384 223599 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #260(29.8-30.2 min.)) (nt:orf_id:o261#5; similar to (swissprot accession) (le:16145) (re:17095) (di:complement) D90771 D90771 g1742190 Escherichia coli 562 -11536384 300382 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.)) (nt:orf_id:o261#5; similar to (swissprot accession) (le:6210) (re:7160) (di:complement) D90772 D90772 g1742201 Escherichia coli 562 -11536384 300372 ydaa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 121 of 400 of the completegenome.) (nt:f316; genex of j01608; this 316 aa orf is 50 pct) (le:5774) (re:6724) (di:complement) AE000231 AE000231 g1787594 Escherichia coli 562 -11536384 223609 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #261(30.0-30.3 min.)) (nt:orf_id:o261#5; similar to (swissprot accession) (le:6210) (re:7160) (di:complement) D90772 D90772 g1742201 Escherichia coli 562 -11536384 5000692146 (de:(ecoli_1293) (pn:hypothetical protein in fnr 5"region:fragment) (gn:ydaa) (gtcfc:13.7:14.1) (ec:) (ydaa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1293 ECOLI_1293 Escherichia coli 562 10119538

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869972	13181	35337	801	266

Description

5000692160 sieb (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1353 b1353 Escherichia coli 562 -11536385 7000691914 sieb superinfection exclusion protein b (db:pir2.dat) D64885 D64885 Escherichia coli 562 -11536385 7500960457 sieb phage superinfection exclusion protein (fn:phenotype; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 123 of 400 of the completegenome.) (nt:o203; 97 pct identical to 84 aa of sieb_ecoli) (le:1141) (re:1752) (di:direct) AE000233 AE000233 g1787616 Escherichia coli 562 -11536385 6500732527 sieb (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1353 b1353 Escherichia coli 562 -11536385

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869973	13182	35338	363	120

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869979	13183	35339	249	82

Description

5000692207 ydba_2 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b1405 b1405 Escherichia coli 562 -11536386
7500960499 ydba_2 split orf (fn:orf; unknown function) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 127 of 400 of the completegenome.)
(nt:o1107; 100 pct identical to 1106 aa of) (le:7232) (re:10555) (di:direct)
AE000237 AE000237 g1787672 Escherichia coli 562 -11536386 7000691940 ydba_2
ydba_2 protein interrupted (db:pir) H64891 H64891 Escherichia coli 562
-11536386 6500732528 ydba_2 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b1405 b1405 Escherichia coli 562 -11536386

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501869981	13184	35340	630	209

Description

6500732529 ydcd:b1457 hypothetical 18.9 kd protein in rhse-narv intergenic region:orf-e2 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1457 b1457 Escherichia coli 562 -11536387 7500922192 ydcd (de:hypothetical 18.9 kd protein in rhse-narv intergenic region (orf-e2)) (db:swissprot) YDCD_ECOLI P31991 ESCHERICHIA COLI 562 -11536387 7000691941 ydcd ydcd protein (db:pir2.dat) D64898 D64898 Escherichia coli 562 -11536387 223764 ydcd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #274(32.7-33.0 min.)) (nt:orf_id:o274#6; similar to (swissprot accession) (le:12158) (re:12640) (di:direct) D90785 D90785 g1742369 Escherichia coli 562 -11536387 223783 ydcd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #275(32.8-33.2 min.)) (nt:orf_id:o274#6; similar to (swissprot accession) (le:6226) (re:6708) (di:direct) D90786 D90786 g1742377 Escherichia coli 562 -11536387 300535 ydcd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #276(33.0-33.3 min.)) (nt:orf_id:o274#6; similar to (swissprot accession) (le:152) (re:634) (di:direct) D90787 D90787 g1742390 Escherichia coli 562 -11536387 300529 (db:genpept-bct1) (de:escherichia coli rhse genetic element; defective rhse core protein,complete cds; complete orf-e2; h-rpt subelement; complete orf-h.) (nt:orfe2) (le:2031) (re:2513) (di:direct) ECORHSEX L19083 g1786179 Escherichia coli 562 -11536387 299930 ydcd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 132 of 400 of the completegenome.) (nt:o160; 98 pct identical to ydcd_ecoli sw:) (le:11062) (re:11544) (di:direct) AE000242 AE000242 g1787729 Escherichia coli 562 -11536387 223771 ydcd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #274(32.7-33.0 min.)) (nt:orf_id:o274#6; similar to (swissprot accession) (le:12158) (re:12640) (di:direct) D90785 D90785 g1742369 Escherichia coli 562 -11536387 235829 ydcd (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #276(33.0-33.3 min.)) (nt:orf_id:o274#6; similar to (swissprot accession) (le:152) (re:634) (di:direct) D90787 D90787 g1742390 Escherichia coli 562 -11536387 5000692251 (de:(ecoli_1417) (pn:hypothetical 18) (gn:ydcd) (gtcfc:13.7:14.1) (ec:) (ydcd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1417 ECOLI_1417 Escherichia coli 562 10119619

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501869986	13185	35341	483	160

Description

6500732530 ydde:b1464 hypothetical 32.3 kd protein in rhse-narv intergenic region:orfb (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1464 b1464 Escherichia coli 562 -11536388 111271 ydde (de:hypothetical 32.3 kd protein in rhse-narv intergenic region (orfb)) (db:swissprot) YDDE_ECOLI P37757 ESCHERICHIA COLI 562 -11536388 7000687523 ydde ydde protein (db:pir2.dat) C64899 C64899 Escherichia coli 562 -11536388 223777 ydde (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #275(32.8-33.2 min.)) (nt:orf_id:o276#3; similar to (pir accession number) (le:11269) (re:12162) (di:complement) D90786 D90786 g1742383 Escherichia coli 562 -11536388 223789 ydde (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #276(33.0-33.3 min.)) (nt:orf_id:o276#3; similar to (pir accession number) (le:5195) (re:6088) (di:complement) D90787 D90787 g1742396 Escherichia coli 562 -11536388 300541 ydde orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 133 of 400 of the completegenome.) (nt:f297; 100 pct identical to fragment ydde_ecoli) (le:4500) (re:5393) (di:complement) AE000243 AE000243 g1787737 Escherichia coli 562 -11536388 5000692258 (de:(ecoli_1424) (pn:hypothetical protein in rhse-narv intergenic region:orfb:fragment) (gn:ydde) (gtcfc:13.7:14.1) (ec:) (ydde_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1424 ECOLI_1424 Escherichia coli 562 10119623

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501869993	13186	35342	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870018	13187	35343	663	220

Description

5000692263 yddg (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b1473 b1473 Escherichia coli 562 -11536389
7000691942 yddg membrane protein yddg (db:pir2.dat) D64900 D64900
Escherichia coli 562 -11536389 7500960500 yddg orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
134 of 400 of the completegenome.) (nt:f293; 100 pct identical to fragment
yddg_ecoli) (le:3687) (re:4568) (di:complement) AE000244 AE000244 g1787747
Escherichia coli 562 -11536389 6500732531 yddg orf:hypothetical protein
(fn:orf; unknown) (db:genpept) (de:escherichia coli k-12 mg1655 section 134
of 400 of the completegenome.) (nt:f293; 100 pct identical to fragment
yddg_ecoli) (le:3687) (re:4568) (di:complement) AE000244 AE000244 g1787747
Escherichia coli 562 -11536389

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870020	13188	35344	342	113

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870026	13189	35345	861	286

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870027	13190	35346	429	143

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870045	13191	35347	249	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870057	13192	35348	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870067	13193	35349	384	127

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870070	13194	35350	789	262

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870087	13195	35351	855	284

Description

6500732532 xasa:acsa:gadc:b1492 xasa:amino acid antiporter:extreme acid sensitivity protein (gtcfc:12.1) (keggfc:14.2) (rileyfc:5.8.0:5.9.0) (db:gtc-escherichia coli) b1492 b1492 Escherichia coli 562 -11536390 108073 xasa:acsa:gadc (de:amino acid antiporter (extreme acid sensitivity protein)) (db:swissprot) XASA_ECOLI P39183 ESCHERICHIA COLI 562 -11536390 7000687021 xasa:gadc extreme acid resistance protein xasa:probable permease xasa (db:pir2.dat) G64902 G64902 Escherichia coli 562 -11536390 7500894433 xasa acid sensitivity protein:putative transporter (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 136 of 400 of the completegenome.) (nt:f511; 100 pct identical to fragment xasa_ecoli) (le:5811) (re:7346) (di:complement) AE000246 AE000246 g1787768 Escherichia coli 562 -11536390 5000692276 (de:(ecoli_1452) (pn:extreme acid sensitivity protein) (gn:xasa) (gtcfc:13.7:14.1) (ec:) (xasa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1452 ECOLI_1452 Escherichia coli 562 10123351

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870091	13196	35352	462	153
<u>Description</u>				
6500732533 pqq1:b1494 yddc:probable zinc protease pqq1 (gtcfc:10.11:14.2) (ec:3.4.99.-) (keggfc:14.1) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1494 b1494 Escherichia coli 562 -11536391 111268 pqq1 (ec:3.4.99.-) (de:probable zinc protease pqq1,) (db:swissprot) PQQ1_ECOLI P31828 ESCHERICHIA COLI 562 -11536391 7000686171 yddc:pqq1 probable zinc proteinase yddc (ec:3.4.99.-) (db:pir2.dat) A64903 A64903 Escherichia coli 562 -11536391 7500888385 pqq1 putative peptidase (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:3.4.99.-) (de:escherichia coli k-12 mg1655 section 136 of 400 of the completegenome.) (nt:f931; formerly 2 orfs designated yddc and yddd) (le:9264) (re:12059) (di:complement) AE000246 AE000246 g1787770 Escherichia coli 562 -11536391 5000692277 (de:(ecoli_1454) (pn:hypothetical 80) (gn:yddc) (gtcfc:13.7:14.1) (ec:3.4.99.-) (yddc_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1454 ECOLI_1454 Escherichia coli 562 10123352				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870095	13197	35353	252	83
<u>Description</u>				
6500732534 yddb:b1495 hypothetical 89.3 kd protein in pqq1-hipa intergenic region:cds103 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1495 b1495 Escherichia coli 562 -11536392 111266 yddb (de:hypothetical 89.3 kd protein in pqq1-hipa intergenic region (cds103)) (db:swissprot) YDDB_ECOLI P31827 ESCHERICHIA COLI 562 -11536392 7000687522 yddb yddb protein precursor:cds103 protein (db:pir2.dat) B64903 B64903 Escherichia coli 562 -11536392 223842 yddb (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #280(33.7-34.1 min.).) (nt:orf_id:o280#4; similar to (swissprot accession) (le:12884) (re:15256) (di:complement) D90791 D90791 g1742453 Escherichia coli 562 -11536392 300579 yddb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 136 of 400 of the completegenome.) (nt:f790; this 790 aa orf is 96 pct identical (3 gaps)) (le:12104) (re:14476) (di:complement) AE000246 AE000246 g1787771 Escherichia coli 562 -11536392 5000692278 (de:(ecoli_1455) (pn:hypothetical 86) (gn:yddb) (gtcfc:13.7:14.1) (ec:) (yddb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1455 ECOLI_1455 Escherichia coli 562 10119654				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870098	13198	35354	477	158
<u>Description</u>				
5000692312 ydeh (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)				
(db:gtc-escherichia coli) b1535 b1535 Escherichia coli 562 -11536393				
7500922248 ydeh (de:hypothetical 33.9 kd protein in marb-dcp intergenic region) (db:swissprot) YDEH_ECOLI P31129 ESCHERICHIA COLI 562 -11536393				
7000691943 ydeh ydeh protein (db:pir2.dat) B64908 B64908 Escherichia coli 562 -11536393 7500922250 ydeh orf:hypothetical protein (fn:orf; unknown)				
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 141 of 400 of the completegenome.) (nt:f296; residues 1-175 are 100 pct identical to)				
(le:1775) (re:2665) (di:complement) AE000251 AE000251 g1787816 Escherichia coli 562 -11536393 6500732535 ydeh (gtcfc:14.2) (keggfc:14.2)				
(rileyfc:5.9.0) (db:gtc-escherichia coli) b1535 b1535 Escherichia coli 562 -11536393				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870101	13199	35355	801	266
<u>Description</u>				
6500732536 ydfg:b1539 hypothetical oxidoreductase in dcp-noha intergenic region (gtcfc:14.2) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.9.0)				
(db:gtc-escherichia coli) b1539 b1539 Escherichia coli 562 -11536394 111324 ydfg (ec:1.-.-.-) (de:probable oxidoreductase in dcp-noha intergenic region,) (db:swissprot) YDFG_ECOLI P39831 ESCHERICHIA COLI 562 -11536394				
7000687534 ydfg probable dehydrogenase:ydfg (cl:short-chain alcohol dehydrogenase homology) (ec:1.1.1.-) (db:pir2.dat) F64908 F64908 Escherichia coli 562 -11536394 223919 ydfg 3-oxoacyl-acyl-carrier protein reductase				
(ec) (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #306(34.8-35.1 min.)) (nt:orf_id:o306#11; similar to (swissprot accession) (le:10113)				
(re:10859) (di:direct) D90797 D90797 g1742536 Escherichia coli 562 -11536394 300638 ydfg putative oxidoreductase (fn:putative enzyme; not classified)				
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 141 of 400 of the completegenome.) (nt:o248; 93 pct identical to fragment ydfg_ecoli)				
(le:6332) (re:7078) (di:direct) AE000251 AE000251 g1787820 Escherichia coli 562 -11536394 5000692315 (de:ecoli_1499) (pn:hypothetical oxidoreductase in dcp:3"region:fragment) (gn:ydfg) (gtcfc:13.7:14.1) (ec:1.-.-.-)				
(ydfg_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli))				
ECOLI_1499 ECOLI_1499 Escherichia coli 562 10119689				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870103	13200	35356	678	225
<u>Description</u>				
5000692346 ydfe (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1577 b1577 Escherichia coli 562 -11536395 163505 ydfe ydfe protein (db:pir2.dat) S03698 S03698 Escherichia coli 562 -11536395 7500960501 (db:genpept-bct1) (de:e. coli genes dica, dicb, dicc and dicf.) (nt:put. orf6 (35kd)) (le:2497) (re:3417) (di:direct) ECDICABC X07465 g41282 Escherichia coli 562 -11536395 232683 ydfe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 143 of 400 of the completegenome.) (nt:o306; 100 pct identical to pir: s03698; residues) (le:7830) (re:8750) (di:direct) AE000253 AE000253 g1787859 Escherichia coli 562 -11536395 6500732537 ydfe (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1577 b1577 Escherichia coli 562 -11536395				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870117	13201	35357	276	91
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870127	13202	35358	750	249
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870128	13203	35359	282	93
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870134	13204	35360	270	89
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870143	13205	35361	285	94
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870147	13206	35362	642	213

Description

5000692364 asr (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b1597 b1597 Escherichia coli 562 -11536396 60425
asr (de:acid shock protein) (db:swissprot) ASR_ECOLI P36560 ESCHERICHIA COLI
562 -11536396 7000684650 asr asr protein (db:pir2.dat) G64915 G64915
Escherichia coli 562 -11536396 224009 asr acid shock protein.
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #311(35.7-36.1
min.)) (nt:orf_id:o311#11; similar to (swissprot accession) (le:14003)
(re:14338) (di:direct) D90802 D90802 g1742631 Escherichia coli 562 -11536396
300717 asr acid shock protein (fn:phenotype; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 145 of 400 of the
completegenome.) (nt:o111; residues 1-68 are 100 pct identical) (le:6192)
(re:6527) (di:direct) AE000255 AE000255 g1787881 Escherichia coli 562
-11536396 6500732538 asr (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b1597 b1597 Escherichia coli 562 -11536396

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870148	13207	35363	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870149	13208	35364	1794	597

Description

6500732539 ydhc:b1660 hypothetical 43.4 kd protein in purr-cfa intergenic
region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli)
b1660 b1660 Escherichia coli 562 -11536397 111350 ydhc (de:hypothetical
43.4 kd protein in purr-cfa intergenic region) (db:swissprot) YDHC_ECOLI
P37597 ESCHERICHIA COLI 562 -11536397 7000687550 ydhc ydhc protein
(cl:bicyclomycin resistance protein) (db:pir2.dat) F64923 F64923 Escherichia
coli 562 -11536397 7500922318 ydhc putative transport protein (fn:putative
transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 151 of 400 of the completegenome.) (nt:o403; this 403 aa orf
is 90 pct identical (7 gaps)) (le:4627) (re:5838) (di:direct) AE000261
AE000261 g1787950 Escherichia coli 562 -11536397 5000692407
(de:(ecoli_1619) (pn:hypothetical 43) (gn:ydhc) (gtcfc:13.7:14.1) (ec:)
(ydhc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_1619 ECOLI_1619 Escherichia coli 562 10123412

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870160	13209	35365	1509	502

Description

GTC ORF with score 103 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid f35c5, complete sequence.) (nt:cdna est yk207f10.3 comes from this gene; cdna est) (le:10256:10369:10501:10605) (re:10321:10455:10557:11249) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870192	13210	35366	396	131

Description

6500732540 ydib:b1692 hypothetical 31.2 kd protein in lpp-arod intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1692 b1692 Escherichia coli 562 -11536398 111359 ydib (de:hypothetical 31.2 kd protein in lpp-arod intergenic region) (db:swissprot) YDIB_ECOLI P28244 ESCHERICHIA COLI 562 -11536398 7000687557 ydib ydib protein (cl:shikimate dehydrogenase:shikimate dehydrogenase homology) (db:pir2.dat) D64927 D64927 Escherichia coli 562 -11536398 224127 ydib shikimate 5-dehydrogenase ec 1.1.1.25 . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #320(37.9-38.3 min.)) (nt:orf_id:o320#4; similar to (swissprot accession) (le:2893) (re:3759) (di:complement) D90811 D90811 g1742758 Escherichia coli 562 -11536398 300796 ydib putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 154 of 400 of the completegenome.) (nt:o288; 92 pct identical (1 gap) to 222 residues) (le:5035) (re:5901) (di:direct) AE000264 AE000264 g1787983 Escherichia coli 562 -11536398 5000692433 (de:(ecoli_1649) (pn:hypothetical protein in arod 5"region:fragment) (gn:ydib) (gtcfc:13.7:14.1) (ec:) (ydib_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1649 ECOLI_1649 Escherichia coli 562 10119766

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870193	13211	35367	1350	449

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870204	13212	35368	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870219	13213	35369	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870220	13214	35370	807	268

Description

5000692434 ydif (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b1694 b1694 Escherichia coli 562 -11536399
7000691944 ydif ydif protein (db:pir2.dat) F64927 F64927 Escherichia coli
562 -11536399 7500960504 ydif putative enzyme (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 154
of 400 of the completegenome.) (nt:o531; 100 pct identical to fragment
ydif_ecoli) (le:6833) (re:8428) (di:direct) AE000264 AE000264 g1787985
Escherichia coli 562 -11536399 6500732541 ydif (gtcfc:14.2) (keggfc:14.2)
(rileyfc:5.9.0) (db:gtc-escherichia coli) b1694 b1694 Escherichia coli 562
-11536399

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870222	13215	35371	393	130

Description

6500732542 ydid:b1701 hypothetical 62.8 kd protein in arod-ppsa intergenic
region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli)
b1701 b1701 Escherichia coli 562 -11536400 7000687559 ydid ydid protein
(cl:acetate--coa ligase homology) (db:pir2.dat) E64928 E64928 Escherichia
coli 562 -11536400 7500960503 ydid putative ligase/synthetase (fn:putative
enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
section 155 of 400 of the completegenome.) (nt:o566; this 566 aa orf is 84
pct identical (2 gaps)) (le:3596) (re:5296) (di:direct) AE000265 AE000265
g1787993 Escherichia coli 562 -11536400 111361 ydid_ecoli (de:hypothetical
protein in ppsa 3'region (fragment).) P38135 P38135 Escherichia coli 562
-11536400 5000692441 (de:(ecoli_1658) (pn:hypothetical protein in
ppsa:3'region:fragment) (gn:ydid) (gtcfc:13.7:14.1) (ec:) (ydif_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1658
ECOLI_1658 Escherichia coli 562 10123429

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870227	13216	35372	489	162

Description

5000692457 ydjc (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b1733 b1733 Escherichia coli 562 -11536401
7500922380 ydjc (de:hypothetical 27.8 kd protein in celf-kate intergenic
region) (db:swissprot) YDJC_ECOLI P37794 ESCHERICHIA COLI 562 -11536401
7000691945 ydjc ydjc protein (cl:cellobiose phosphotransferase system celc)
(db:pir2.dat) E64932 E64932 Escherichia coli 562 -11536401 224194 ydjc
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #325(38.9-39.2
min.)) (nt:orf_id:o326#2; similar to (swissprot accession) (le:8975)
(re:9724) (di:complement) D90816 D90816 g1742830 Escherichia coli 562
-11536401 300844 ydjc (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #326(39.1-39.4 min.)) (nt:orf_id:o326#2; similar to (swissprot
accession) (le:1746) (re:2495) (di:complement) D90817 D90817 g1742839
Escherichia coli 562 -11536401 7500922382 ydjc orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
158 of 400 of the completegenome.) (nt:f249; 87 pct identical to ydjc_ecoli
sw: p37794;) (le:6293) (re:7042) (di:complement) AE000268 AE000268 g1788028
Escherichia coli 562 -11536401 224202 ydjc (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #325(38.9-39.2 min.))
(nt:orf_id:o326#2; similar to (swissprot accession) (le:8975) (re:9724)
(di:complement) D90816 D90816 g1742830 Escherichia coli 562 -11536401
6500732543 ydjc (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b1733 b1733 Escherichia coli 562 -11536401

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870229	13217	35373	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870235	13218	35374	414	137

Description

6500732544 yeca:b1908 hypothetical 25.0 kd protein in tyrp-leuz intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1908 b1908 Escherichia coli 562 -11536402 111505 yeca (de:hypothetical 25.0 kd protein in tyrp-leuz intergenic region) (db:swissprot) YECA_ECOLI P06979 ESCHERICHIA COLI 562 -11536402 7000687598 yeca yeca protein (cl:yeca protein) (db:pir1.dat) (mp:42 min) QQECW7 D64954 Escherichia coli 562 -11536402 224414 yeca preprotein translocase seca subunit. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf_id:o341#8; similar to (swissprot accession) (le:7484) (re:8149) (di:complement) D90832 D90832 g1736570 Escherichia coli 562 -11536402 301054 yeca orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:f221; residues 1-74 are 100 pct identical) (le:2982) (re:3647) (di:complement) AE000284 AE000284 g1788219 Escherichia coli 562 -11536402 5000692576 (de:(ecoli_1865) (pn:hypothetical 8) (gn:yeca) (gtcfc:13.7:14.1) (ec:) (yeca_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1865 ECOLI_1865 Escherichia coli 562 10119905

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870238	13219	35375	900	299

Description

5000692578 yecf (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1915 b1915 Escherichia coli 562 -11536403 7500922935 yecf (de:hypothetical 8.2 kd protein in uvry-sdia intergenic region) (db:swissprot) YECF_ECOLI P46120 ESCHERICHIA COLI 562 -11536403 7000691947 yecf yecf protein (db:pir2.dat) H64954 H64954 Escherichia coli 562 -11536403 224418 yecf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf_id:o341#12; similar to (swissprot accession) (le:12348) (re:12572) (di:direct) D90832 D90832 g1736574 Escherichia coli 562 -11536403 7500922937 yecf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:o74; residues 1-37 are 100 pct identical to aa) (le:7846) (re:8070) (di:direct) AE000284 AE000284 g1788223 Escherichia coli 562 -11536403 301058 yecf (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf_id:o341#12; similar to (swissprot accession) (le:12348) (re:12572) (di:direct) D90832 D90832 g1736574 Escherichia coli 562 -11536403 6500732545 yecf (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1915 b1915 Escherichia coli 562 -11536403

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870246	13220	35376	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870273	13221	35377	213	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870274	13222	35378	468	155

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870281	13223	35379	2391	796

Description

GTC ORF with score 498 to: (or:Homo sapiens) (fn:peripheral proteins believed to act as) (sr:human) (db:genpept-pril) (de:human ankyrin g (ank-3) mrna, complete cds.) (nt:480 kda; antibodies that recognize this sequence) (le:193) (re:13326) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870284	13224	35380	570	189

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870289	13225	35381	1581	526

Description

GTC ORF with score 1224 to: (de:(yer125w) (pn:rsp5 protein:ubiquitin-protein ligase) (gn:npl1:sygp-orf41:rsp5) (gtcfc:5.9) (ec:6.3.2.-) (rsp5_yeast) (keggfc:5.9) (sgdfc:3.4.0:6.3.0:6.5.1:9.1.0:11.1.0) (db:gtc-saccharomyces cerevisiae))

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870290	13226	35382	510	169

Description

GTC ORF with score 583 to: (de:(yer125w) (pn:rsp5 protein:ubiquitin-protein ligase) (gn:npl1:sygp-orf41:rsp5) (gtcfc:5.9) (ec:6.3.2.-) (rsp5_yeast) (keggfc:5.9) (sgdfc:3.4.0:6.3.0:6.5.1:9.1.0:11.1.0) (db:gtc-saccharomyces cerevisiae))

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870294	13227	35383	228	75

Description

5000692580 yecc (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1918 b1918 Escherichia coli 562 -11536404
 7500922954 yecc (de:hypothetical amino-acid abc transporter permease protein yecc) (db:swissprot) YECS_ECOLI P76315 ESCHERICHIA COLI 562 -11536404 7000691946 yecc yecc protein (cl:histidine permease protein m) (db:pir2.dat) C64955 C64955 Escherichia coli 562 -11536404 224421 octopine transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf_id:o341#15; similar to (swissprot accession) (le:14341) (re:15009) (di:complement) D90832 D90832 g1736577 Escherichia coli 562 -11536404 7500922956 yecc putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:f222; this 222 aa orf is 48 pct identical (0 gaps)) (le:9839) (re:10507) (di:complement) AE000284 AE000284 g1788226 Escherichia coli 562 -11536404 301061 octopine transport system permease protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf_id:o341#15; similar to (swissprot accession) (le:14341) (re:15009) (di:complement) D90832 D90832 g1736577 Escherichia coli 562 -11536404 6500732546 yecc (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1918 b1918 Escherichia coli 562 -11536404

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870296	13228	35384	378	125

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870297	13229	35385	252	83

Description

6500732547 yedk:b1931 yedg:hypothetical 24.5 kd protein in amya-flie intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b1931 b1931 Escherichia coli 562 -11536405
 1500686259 yedk (de:hypothetical 24.5 kd protein in amya-flie intergenic region) (db:swissprot) YEDK_ECOLI P76318 ESCHERICHIA COLI 562 -11536405
 7000687610 yedg yedg protein (db:pir2.dat) H64956 H64956 Escherichia coli 562 -11536405 7500922961 yedk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 175 of 400 of the completegenome.) (nt:o217; this 217 aa orf is 36 pct identical (1 gap)) (le:9422) (re:10075) (di:direct) AE000285 AE000285 gl788240 Escherichia coli 562 -11536405 5000692587 (de:(ecoli_1885) (pn:hypothetical 8) (gn:yedg) (gtcfc:13.7:14.1) (ec:) (yedg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1885 ECOLI_1885 Escherichia coli 562 10061009

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870299	13230	35386	318	105

Description

GTC ORF with score 457 to: (de:(yer125w) (pn:rsp5 protein:ubiquitin-protein ligase) (gn:npl1:sygp-orf41:rsp5) (gtcfc:5.9) (ec:6.3.2.-) (rsp5_yeast) (keggfc:5.9) (sgdfc:3.4.0:6.3.0:6.5.1:9.1.0:11.1.0) (db:gtc-saccharomyces cerevisiae))

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870320	13231	35387	432	143

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870324	13232	35388	309	102

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870334	13233	35389	675	224

Description

6500732548 dsrb:b1952 dsrb protein (gtcfc:14.3) (keggfc:14.2)
(rileyfc:5.8.0:5.9.0) (db:gtc-escherichia coli) b1952 b1952 Escherichia coli
562 -11536406 69338 dsrb (de:dsrb protein) (db:swissprot) DSRB_ECOLI P40678
ESCHERICHIA COLI 562 -11536406 162971 dsrb dsrb protein (db:pir2.dat)
I59352 I59352 Escherichia coli 562 -11536406 224460 dsrb dsrb protein.
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #343(43.3-43.6
min.)) (nt:orf_id:o343#17; similar to (swissprot accession) (le:14015)
(re:14203) (di:complement) D90834 D90834 g1736618 Escherichia coli 562
-11536406 301106 dsrb dsrb protein. (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #344(43.5-43.9 min.)) (nt:orf_id:o343#17; similar to
(swissprot accession) (le:3040) (re:3228) (di:complement) D90835 D90835
g1736625 Escherichia coli 562 -11536406 301100 dsrb dsrb (fn:unknown)
(db:genpept-bct1) (de:escherichia coli dsrb (dsrb) gene, complete cds, and
rcsaanti-silencer rna (dsra) gene, complete sequence.) (le:1390) (re:1578)
(di:direct) ECU17136 U17136 g595988 Escherichia coli 562 -11536406 238726
dsrb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 177 of 400 of the completegenome.)
(nt:f62; 100 pct identical to dsrb_ecoli sw: p40678) (le:3133) (re:3321)
(di:complement) AE000287 AE000287 g1788263 Escherichia coli 562 -11536406
224466 dsrb dsrb protein. (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #344(43.5-43.9 min.)) (nt:orf_id:o343#17; similar to
(swissprot accession) (le:3040) (re:3228) (di:complement) D90835 D90835
g1736625 Escherichia coli 562 -11536406 5000692593 (de:(ecoli_1906)
(pn:dsrb protein) (gn:dsrb) (gtcfc:13.7:14.1) (ec:) (dsrb_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1906
ECOLI_1906 Escherichia coli 562 10011921

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870335	13234	35390	555	184

Description

6500732549 cbl:b1987 transcriptional regulator (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0:5.9.0) (db:gtc-escherichia coli) b1987 b1987 Escherichia coli 562 -11536407 1500686215 cbl (de:transcriptional regulator cbl) (db:swissprot) CBL_ECOLI Q47083 ESCHERICHIA COLI 562 -11536407 7000684761 cbl cbl protein (cl:regulatory protein lysr) (db:pir2.dat) C64963 C64963 Escherichia coli 562 -11536407 224488 cys regulon transcriptional activator. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #347(44.2-44.5 min.)) (nt:orf_id:o347#6; similar to (swissprot accession) (le:8752) (re:9702) (di:complement) D90837 D90837 g1736649 Escherichia coli 562 -11536407 301128 cbl transcriptional regulator cys regulon:accessory (fn:regulator; amino acid biosynthesis: cysteine) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 180 of 400 of the completegenome.) (nt:f316; 99 pct identical to pir: i41150) (le:7849) (re:8799) (di:complement) AE000290 AE000290 g1788296 Escherichia coli 562 -11536407 5000692620 (de:(ecoli_1936) (pn:cbl protein) (gn:cbl) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1936 ECOLI_1936 Escherichia coli 562 10119940

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870336	13235	35391	696	231

Description

6500732550 yeea:b2008 hypothetical 40.0 kd protein in cobu-sbcb intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2008 b2008 Escherichia coli 562 -11536408 111533 yeea (de:hypothetical 40.0 kd protein in cobu-sbmc intergenic region) (db:swissprot) YEEA_ECOLI P33011 ESCHERICHIA COLI 562 -11536408 7000687615 yeea yeea protein (db:pir2.dat) G64965 G64965 Escherichia coli 562 -11536408 224512 yeea (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o348#20; similar to (swissprot accession) (le:15099) (re:16157) (di:complement) D90838 D90838 g1736674 Escherichia coli 562 -11536408 301159 yeea (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #349(44.6-45.0 min.)) (nt:orf_id:o348#20; similar to (swissprot accession) (le:8185) (re:9243) (di:complement) D90839 D90839 g1736682 Escherichia coli 562 -11536408 301152 yeea orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 182 of 400 of the completegenome.) (nt:f352; 100 pct identical to fragment yeea_ecoli) (le:4848) (re:5906) (di:complement) AE000292 AE000292 g1788318 Escherichia coli 562 -11536408 224519 yeea (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #349(44.6-45.0 min.)) (nt:orf_id:o348#20; similar to (swissprot accession) (le:8185) (re:9243) (di:complement) D90839 D90839 g1736682 Escherichia coli 562 -11536408 5000692639 (de:(ecoli_1956) (pn:hypothetical 16) (gn:yeea) (gtcfc:13.7:14.1) (ec:) (yeea_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1956 ECOLI_1956 Escherichia coli 562 10119953

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870341	13236	35392	651	216

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870342	13237	35393	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870343	13238	35394	360	120

Description

6500732551 yeec:phse:b2010 yeec:probable penicillin-binding protein (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2010 b2010 Escherichia coli 562 -11536409 7000684977 dacd:yeec:phse serine-type d-ala-d-ala carboxypeptidase:dacd precursor:penicillin-binding protein 6b (cl:penicillin-binding protein 5) (ec:3.4.16.4) (db:pir2.dat) A64966 A64966 Escherichia coli 562 -11536409 301161 phse probable penicillin-binding protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #349(44.6-45.0 min.)) (nt:orf_id:o349#1; similar to (swissprot accession) (le:10033) (re:11205) (di:complement) D90839 D90839 g1736684 Escherichia coli 562 -11536409 224521 dacd penicillin binding protein 6b (fn:putative enzyme; murein sacculus,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 182 of 400 of the completegenome.) (nt:f390; 100 pct identical to phse_ecoli sw:) (le:6696) (re:7868) (di:complement) AE000292 AE000292 g1788320 Escherichia coli 562 -11536409 89695 phse_ecoli (de:probable penicillin-binding protein.) P33013 P33013 Escherichia coli 562 -11536409 5000692640 (de:(ecoli_1958) (pn:probable penicillin-binding protein) (gn:yeec) (gtcfc:13.7:14.1) (ec:) (phse_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1958 ECOLI_1958 Escherichia coli 562 10031817

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870364	13239	35395	798	265

Description

5000692646 yefm (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2017 b2017 Escherichia coli 562 -11536410 7000691948 yefm yefm protein (db:pir2.dat) H64966 H64966 Escherichia coli 562 -11536410 7500960505 yefm orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 183 of 400 of the completegenome.) (nt:f92; this 92 aa orf is 96 pct identical (0 gaps)) (le:3878) (re:4156) (di:complement) AE000293 AE000293 g1788328 Escherichia coli 562 -11536410 6500732552 yefm (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2017 b2017 Escherichia coli 562 -11536410

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501870368	13240	35396	186	61

Description

5000692651 yefh (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b2033 b2033 Escherichia coli 562 -11536411
7000690845 wbbj (ec:2.3.1.-) (de:(ec 2.3.1.-)) (db:swissprot) WBBJ_ECOLI
P37750 ESCHERICHIA COLI 562 -11536411 7000690844 yefh acetyl coa
acetyltransferase (cl:galactoside acetyltransferase) (db:pir2.dat) (mp:45
min) H64968 H64968 Escherichia coli 562 -11536411 224558 yefh galactoside
acetyltransferase ec 2.3.1.18 (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #351(45.1-45.5 min.)) (nt:orf_id:o351#9; similar to (swissprot
accession) (le:10794) (re:11384) (di:complement) D90841 D90841 g1736723
Escherichia coli 562 -11536411 224570 yefh galactoside acetyltransferase ec
2.3.1.18 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#352(45.3-45.7 min.)) (nt:orf_id:o351#9; similar to (swissprot accession)
(le:1583) (re:2173) (di:complement) D90842 D90842 g1736736 Escherichia coli
562 -11536411 7502852284 wbbj putative o-acetyl transferase
(db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose 4,6-dehydratase
(rmlb),dtdp-6-deoxy-1-mannose-dehydrogenase (rmla),
glucose-1-phosphatethymidylyltransferase (rmlc), putative o-antigen transporter (... ECU09876 U09876
g2665493 Escherichia coli 562 -11536411 301198 wbbj putative o-acetyl
transferase (fn:putative enzyme; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 184 of 400 of the completgenome.)
(nt:f196; formerly designated yefh) (le:7251) (re:7841) (di:complement)
AE000294 AE000294 g1788345 Escherichia coli 562 -11536411 301210 wbbj
putative o-acetyl transferase (db:genpept-bct1) (de:escherichia coli k-12
dtdp-d-glucose 4,6-dehydratase (rmlb),dtdp-6-deoxy-1-mannose-dehydrogenase
(rmla), glucose-1-phosphatethymidylyltransferase (rmlc), putative o-antigen transporter
(... ECU09876 U09876 g2665493 Escherichia coli 562 -11536411 6500732553
yefh (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli)
b2033 b2033 Escherichia coli 562 -11536411

1c542 U.S. PTO
09/417507
10/14/99

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501870370	13241	35397	360	119

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501870391	13242	35398	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870425	13243	35399	201	66
<u>Description</u>				
6500732554 asma:b2064 yega:asma protein precursor (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2064 b2064 Escherichia coli 562 -11536412 111562 asma (de:asma protein precursor) (db:swissprot) ASMA_ECOLI P28249 ESCHERICHIA COLI 562 -11536412 7000684644 yega:asma yega protein precursor (db:pir2.dat) G64972 G64972 Escherichia coli 562 -11536412 224600 yega (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #355(45.9-46.2 min.)) (nt:orf_id:o355#3; similar to (swissprot accession) (le:6383) (re:8236) (di:complement) D90844 D90844 g1736768 Escherichia coli 562 -11536412 301240 asma suppressor of ompf assembly mutants (fn:phenotype; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 186 of 400 of the completegenome.) (nt:f617; formerly designated yega) (le:6346) (re:8199) (di:complement) AE000296 AE000296 g1788378 Escherichia coli 562 -11536412 5000692674 (de:(ecoli_2012) (pn:hypothetical in dcd:3"region:fragment) (gn:yega) (gtcfc:13.7:14.1) (ec:) (yega_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2012 ECOLI_2012 Escherichia coli 562 10119982				

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501870427	13244	35400	270	89

Description

6500732555 yege:b2067 hypothetical 123.9 kd protein in udk-alka intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2067 b2067 Escherichia coli 562 -11536413 111565 yege (de:hypothetical 123.9 kd protein in udk-alka intergenic region) (db:swissprot) YEGE_ECOLI P38097 ESCHERICHIA COLI 562 -11536413 7000687622 yege yege protein (db:pir2.dat) B64973 B64973 Escherichia coli 562 -11536413 224603 yege nodulation protein v ec 2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #355(45.9-46.2 min.)) (nt:orf_id:o355#6; similar to (swissprot accession) (le:9890) (re:13207) (di:direct) D90844 D90844 g1736771 Escherichia coli 562 -11536413 301248 yege nodulation protein v ec 2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #356(46.1-46.5 min.)) (nt:orf_id:o355#6; similar to (swissprot accession) (le:1987) (re:5304) (di:direct) D90845 D90845 g1736777 Escherichia coli 562 -11536413 301243 yege putative sensor-type protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 186 of 400 of the completegenome.) (nt:o1105; 100 pct identical to fragment yege_ecoli) (le:9853) (re:13170) (di:direct) AE000296 AE000296 g1788381 Escherichia coli 562 -11536413 224608 yege nodulation protein v ec 2.7.3.-. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #356(46.1-46.5 min.)) (nt:orf_id:o355#6; similar to (swissprot accession) (le:1987) (re:5304) (di:direct) D90845 D90845 g1736777 Escherichia coli 562 -11536413 5000692675 (de:(ecoli_2015) (pn:hypothetical protein in alka:3"region:fragment) (gn:yege) (gtcfc:13.7:14.1) (ec:) (yege_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2015 ECOLI_2015 Escherichia coli 562 10119983

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501870430	13245	35401	1131	376

Description

GTC ORF with score 1034 to: (sr:c.albicans (strain b792, atcc 11651) dna) (db:genpept-pln1) (de:c.albicans thymidylate synthase (ts) gene, complete cds.) (nt:thymidylate synthase precursor (ec 2.1.1.45)) (le:415) (re:1362) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870431	13246	35402	375	124

Description

5000692676 yegd (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b2069 b2069 Escherichia coli 562 -11536414
7000691949 yegd yegd protein (db:pir2.dat) D64973 D64973 Escherichia coli
562 -11536414 7500960506 yegd putative heat shock protein (fn:putative
regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 187 of 400 of the completegenome.) (nt:o471; uug start; 99
pct identical to) (le:1004) (re:2419) (di:direct) AE000297 AE000297 g1788384
Escherichia coli 562 -11536414 6500732556 yegd (gtcfc:14.2) (keggfc:14.2)
(rileyfc:5.9.0) (db:gtc-escherichia coli) b2069 b2069 Escherichia coli 562
-11536414

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870432	13247	35403	453	150

Description

6500732557 yeht:b2125 hypothetical 27.9 kd protein in molr-bglx intergenic
region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0:5.9.0) (db:gtc-escherichia
coli) b2125 b2125 Escherichia coli 562 -11536415 111586 yeht
(de:hypothetical 27.9 kd protein in molr-bglx intergenic region)
(db:swissprot) YEHT_ECOLI P33356 ESCHERICHIA COLI 562 -11536415 7000687637
yeht yeht protein (cl:yeht protein:response regulator homology)
(db:pir2.dat) D64980 D64980 Escherichia coli 562 -11536415 7500923031 yeht
(sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome
region of e.coli k12 bhb2600.) (nt:belongs to uhpA family of
transcriptional) (le:25012) (re:25746) (di:complement) ECOHU47 U00007
g405856 Escherichia coli 562 -11536415 234735 yeht orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
191 of 400 of the completegenome.) (nt:f244; 100 pct identical to yeht_ecoli
sw:) (le:8053) (re:8787) (di:complement) AE000301 AE000301 g2367130
Escherichia coli 562 -11536415

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870434	13248	35404	198	65

Description

6500732558 yehy:b2130 hypothetical abc transporter permease protein yehy (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2130 b2130 Escherichia coli 562 -11536416 111591 yehy (de:hypothetical abc transporter permease protein yehy) (db:swissprot) YEHY_ECOLI P33361 ESCHERICHIA COLI 562 -11536416 7000687642 yehy yehy protein (db:pir2.dat) A64981 A64981 Escherichia coli 562 -11536416 7500923036 yehy putative transport system permease protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 192 of 400 of the completegenome.) (nt:f385; residues 51-345 are 100 pct identical to) (le:2675) (re:3832) (di:complement) AE000302 AE000302 g1788451 Escherichia coli 562 -11536416 5000692720 (de:(ecoli_2079) (pn:hypothetical 31) (gn:yehy) (gtcfc:13.7:14.1) (ec:) (yehy_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2079 ECOLI_2079 Escherichia coli 562 10123577

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870456	13249	35405	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870467	13250	35406	348	115

Description

6500732559 yohf:b2137 hypothetical oxidoreductase in pbpg-cdd intergenic region (gtcfc:14.2) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2137 b2137 Escherichia coli 562 -11536417 115244 yohf (ec:1.-.-.-) (de:(ec 1.-.-.-)) (db:swissprot) YOHF_ECOLI P33368 ESCHERICHIA COLI 562 -11536417 7000688176 yohf yohf protein (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase homology) (db:pir2.dat) H64981 H64981 Escherichia coli 562 -11536417 7500952099 yohf putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:f253; 100 pct identical to yohf_ecoli sw: p33368) (le:1578) (re:2339) (di:complement) AE000303 AE000303 g1788459 Escherichia coli 562 -11536417 5000692725 (de:(ecoli_2086) (pn:hypothetical oxidoreductase in pbpg-cdd intergenic region) (gn:yohf) (gtcfc:13.7:14.1) (ec:1.-.-.-) (yohf_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2086 ECOLI_2086 Escherichia coli 562 10123579

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870468	13251	35407	516	171

Description

6500732560 yohj:b2141 hypothetical 14.6 kd protein in pbpg-cdd intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2141 b2141 Escherichia coli 562 -11536418 115249 yohj (de:hypothetical 14.6 kd protein in pbpg-cdd intergenic region) (db:swissprot) YOHJ_ECOLI P33372 ESCHERICHIA COLI 562 -11536418 7000688180 yohj yohj protein (cl:conserved hypothetical protein h1297) (db:pir2.dat) D64982 D64982 Escherichia coli 562 -11536418 7500952104 yohj (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (le:43394) (re:43792) (di:direct) ECOHU47 U00007 g405872 Escherichia coli 562 -11536418 234752 yohj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:ol32; 100 pct identical to yohj_ecoli sw: p33372) (le:5693) (re:6091) (di:direct) AE000303 AE000303 g1788463 Escherichia coli 562 -11536418 5000692729 (de:(ecoli_2090) (pn:hypothetical 14) (gn:yohj) (gtcfc:13.7:14.1) (ec:) (yohj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2090 ECOLI_2090 Escherichia coli 562 10056974

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870472	13252	35408	639	212

Description

GTC ORF with score 123 to: (sr:porphyridium purpureum (strain:iam-r1) cdna to mrna) (db:genpept-pln1) (ec:4.2.1.1) (de:porphyridium purpureum mrna for carbonic anhydrase, complete cds.) (nt:n-terminal half and c-terminal half of the putative) (le:91) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870480	13253	35409	351	116

Description

6500732561 yohk:b2142 hypothetical 24.5 kd protein in pbpg-cdd intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2142 b2142 Escherichia coli 562 -11536419 115251 yohk (de:hypothetical 24.5 kd protein in pbpg-cdd intergenic region) (db:swissprot) YOHK_ECOLI P33373 ESCHERICHIA COLI 562 -11536419 7000688181 yohk yohk protein (cl:yohk protein) (db:pir2.dat) E64982 E64982 Escherichia coli 562 -11536419

7500952106 yohk putative serotonin transporter (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:o231; residues 10295 are 100 pct identical to) (le:6088) (re:6783) (di:direct) AE000303 AE000303 g1788464 Escherichia coli 562 -11536419 5000692730 (de:(ecoli_2091) (pn:hypothetical 24) (gn:yohk) (gtcfc:13.7:14.1) (ec:) (yohk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2091 ECOLI_2091 Escherichia coli 562 10056976

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870484	13254	35410	606	201

Description

6500732562 sana:b2144 sana protein (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2144 b2144 Escherichia coli 562 -11536420 97893 sana (de:sana protein) (db:swissprot) SANA_ECOLI P33017 ESCHERICHIA COLI 562 -11536420 7000686553 sana sana protein (cl:conserved hypothetical protein hi1262) (db:pir2.dat) G64982 G64982 Escherichia coli 562 -11536420 7500891298 sana vancomycin sensitivity (fn:transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:o239; 100 pct identical to fragment yeif_ecoli) (le:7947) (re:8666) (di:direct) AE000303 AE000303 g1788466 Escherichia coli 562 -11536420 5000692731 (de:(ecoli_2093) (pn:sana protein) (gn:sana) (gtcfc:13.7:14.1) (ec:) (sana_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2093 ECOLI_2093 Escherichia coli 562 10123580

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870496	13255	35411	294	97

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870502	13256	35412	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870509	13257	35413	363	120

Description

GTC ORF with score 154 to: (fn:catalyzesf the conversion of sterigmatocystin) (sr:aspergillus parasiticus (strain srrc 143) (library: un1-zap) cdn) (db:genpept-pln1) (de:aspergillus parastieus o-methyltransferase (omt-1) mrna, completecds.) (le:12) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870511	13258	35414	840	279

Description

6500732563 yeia:b2147 hypothetical 45.3 kd protein in cdd-mglc intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2147 b2147 Escherichia coli 562 -11536421 7000687644 yeia yeia protein (db:pir2.dat) B64983 B64983 Escherichia coli 562 -11536421 7500960508 yeia putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 193 of 400 of the completegenome.) (nt:o413; residues 315-390 are 100 pct identical to) (le:10328) (re:11569) (di:direct) AE000303 AE000303 g1788469 Escherichia coli 562 -11536421 111600 yeia_ecoli (de:hypothetical protein in cdd-mglc intergenic region (fragment).) P25889 P25889 Escherichia coli 562 -11536421 5000692734 (de:(ecoli_2096) (pn:hypothetical protein in cdd-mglc intergenic region:fragment) (gn:yeia) (gtcfc:13.7:14.1) (ec:) (yeia_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2096 ECOLI_2096 Escherichia coli 562 10123583

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870544	13259	35415	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870571	13260	35416	399	132

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870572	13261	35417	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870580	13262	35418	630	209

Description

GTC ORF with score 447 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870581	13263	35419	507	168

Description

GTC ORF with score 357 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870582	13264	35420	288	95

Description

6500732564 yeii:b2160 hypothetical 39.7 kd protein in nfo-frua intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2160 b2160 Escherichia coli 562 -11536422 111607 yeii (de:hypothetical sugar kinase in nfo-frua intergenic region) (db:swissprot) YEII_ECOLI P33020 ESCHERICHIA COLI 562 -11536422 7000687650 yeii yeii protein (cl:yeii protein) (db:pir2.dat) G64984 G64984 Escherichia coli 562 -11536422 7500923049 yeii putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 195 of 400 of the completegenome.) (nt:o362; this 362 aa orf is 100 pct identical (0 gaps)) (le:4814) (re:5902) (di:direct) AE000305 AE000305 g1788484 Escherichia coli 562 -11536422 5000692739 (de:(ecoli_2109) (pn:hypothetical 38) (gn:yeii) (gtcfc:13.7:14.1) (ec:) (yeii_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2109 ECOLI_2109 Escherichia coli 562 10123590

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870583	13265	35421	573	190

Description

GTC ORF with score 142 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870622	13266	35422	1323	440

Description

6500732565 yeir:b2173 hypothetical 36.1 kd protein in frub-rtn intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2173 b2173 Escherichia coli 562 -11536423 111618 yeir (de:hypothetical 36.1 kd protein in frub-spr intergenic region) (db:swissprot) YEIR_ECOLI P33030 ESCHERICHIA COLI 562 -11536423 7000687659 yeir yeir protein (db:pir2.dat) D64986 D64986 Escherichia coli 562 -11536423 7500923057 yeir orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 197 of 400 of the completegenome.) (nt:o328; 100 pct identical to 102 residues of) (le:89) (re:1075) (di:direct) AE000307 AE000307 g1788499 Escherichia coli 562 -11536423 5000692749 (de:(ecoli_2122) (pn:hypothetical protein in frub 5"region:fragment) (gn:yeir) (gtcfc:13.7:14.1) (ec:) (yeir_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2122 ECOLI_2122 Escherichia coli 562 10123591

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870624	13267	35423	381	126

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870631	13268	35424	186	61

Description

6500732566 yejh:b2184 hypothetical 66.4 kd protein in rsua-rply intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2184 b2184 Escherichia coli 562 -11536424 111630 yejh (de:hypothetical 66.4 kd protein in rsua-rply intergenic region) (db:swissprot) YEJH_ECOLI P33919 ESCHERICHIA COLI 562 -11536424 7000687666 yejh yejh protein (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) G64987 G64987 Escherichia coli 562 -11536424 7500923064 yejh putative atp-dependent helicase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 198 of 400 of the completegenome.) (nt:o586; residues 1-396 are 100 pct identical to 396) (le:2259) (re:4019) (di:direct) AE000308 AE000308 g1788511 Escherichia coli 562 -11536424 5000692759 (de:(ecoli_2133) (pn:hypothetical 45) (gn:yejh) (gtcfc:13.7:14.1) (ec:) (yejh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2133 ECOLI_2133 Escherichia coli 562 10123595

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870656	13269	35425	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870657	13270	35426	1197	398

Description

5000692763 yejo (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2190 b2190 Escherichia coli 562 -11536425 7000691950 yejo yejo protein (db:pir2.dat) D64988 D64988 Escherichia coli 562 -11536425 7500960509 yejo putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 198 of 400 of the completegenome.) (nt:f836; this 836 aa orf is 99 pct identical to) (le:8017) (re:10527) (di:complement) AE000308 AE000308 g1788516 Escherichia coli 562 -11536425 6500732567 yejo (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2190 b2190 Escherichia coli 562 -11536425

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870686	13271	35427	960	319

Description

6500732568 yojh:b2210 hypothetical 60.2 kd protein in eco-alkb intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2210 b2210 Escherichia coli 562 -11536426 115263 yojh (ec:1.1.99.16) (de:dehydrogenase (acceptor)) (mqo)) (db:swissprot) MQO_ECOLI P33940 ESCHERICHIA COLI 562 -11536426 7000688183 yojh yojh protein (db:pir2.dat) H64990 H64990 Escherichia coli 562 -11536426 224677 yojh (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #373(49.5-49.9 min.)) (nt:orf_id:o372#5; similar to (swissprot accession) (le:4626) (re:6272) (di:complement) D90850 D90850 g1736851 Escherichia coli 562 -11536426 301317 yojh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 200 of 400 of the completegenome.) (nt:f548; this 548 aa orf is 100 pct identical to) (le:1428) (re:3074) (di:complement) AE000310 AE000310 g1788539 Escherichia coli 562 -11536426 5000692780 (de:(ecoli_2159) (pn:hypothetical 54) (gn:yojh) (gtcfc:13.7:14.1) (ec:) (yojh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2159 ECOLI_2159 Escherichia coli 562 10120024

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870689	13272	35428	879	292

Description

6500732569 yojl:b2214 hypothetical 38.5 kd protein in ada-ompc intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2214 b2214 Escherichia coli 562 -11536427 115268 apbe (de:thiamine biosynthesis lipoprotein apbe precursor) (db:swissprot) APBE_ECOLI P33944 ESCHERICHIA COLI 562 -11536427 7000688185 yojl yojl protein (cl:hypothetical protein hi0172) (db:pir2.dat) D64991 D64991 Escherichia coli 562 -11536427 7500952114 yojl orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 200 of 400 of the completegenome.) (nt:f351; residues 1-121 are 100 pct identical) (le:6799) (re:7854) (di:complement) AE000310 AE000310 g1788543 Escherichia coli 562 -11536427 5000692782 (de:(ecoli_2163) (pn:hypothetical 13) (gn:yojl) (gtcfc:13.7:14.1) (ec:) (yojl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2163 ECOLI_2163 Escherichia coli 562 10123601

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870697	13273	35429	642	213

Description

6500732570 yojn:b2216 probable sensor protein yojn (gtcfc:14.2) (ec:2.7.3.-) (keggfc:14.1) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2216 b2216 Escherichia coli 562 -11536428 115269 yojn (ec:2.7.3.-) (de:probable sensor protein yojn,) (db:swissprot) YOJN_ECOLI P39838 ESCHERICHIA COLI 562 -11536428 7000688186 yojn yojn protein (db:pir2.dat) F64991 F64991 Escherichia coli 562 -11536428 224683 yojq (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #373(49.5-49.9 min.).) (nt:orf_id:o373#6; similar to (swissprot accession) (le:13011) (re:15683) (di:direct) D90850 D90850 g1736857 Escherichia coli 562 -11536428 301323 yojn putative 2-component sensor protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 200 of 400 of the completegenome.) (nt:o890; residues 502-701 are 99 pct identical) (le:9808) (re:12480) (di:direct) AE000310 AE000310 g1788545 Escherichia coli 562 -11536428 5000692783 (de:(ecoli_2165) (pn:hypothetical 25) (gn:yojn) (gtcfc:13.7:14.1) (ec:) (yojn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2165 ECOLI_2165 Escherichia coli 562 10120025

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870701	13274	35430	702	234

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870717	13275	35431	390	129

Description

GTC ORF with score 98 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid d1014.) (nt:coded for by c. elegans cdna cemse31f; similar to) (le:12157:12681:13492:13697) (re:12471:13337:13647:14056) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870722	13276	35432	543	180

Description

6500732571 atoe:atob:b2223 short-chain fatty acids transporter (gtcfc::12.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2223 b2223
 Escherichia coli 562 -11536429 1500686891 atoe (de:short-chain fatty acids transporter) (db:swissprot) ATOE_ECOLI P76460 ESCHERICHIA COLI 562 -11536429
 7000684661 atob atob protein (cl:conserved hypothetical integral membrane protein hp0693) (db:pir2.dat) E64992 E64992 Escherichia coli 562 -11536429
 224703 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #374(49.8-50.1 min.)) (nt:orf_id:o374#6; similar to (swissprot accession) (le:10664) (re:11986) (di:direct) D90851 D90851 g1736878 Escherichia coli 562 -11536429 301343 atoe short chain fatty acid transporter (fn:transport; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 201 of 400 of the completegenome.) (nt:o440; this 440 aa orf is 74 pct identical (7 gaps)) (le:7859) (re:9181) (di:direct) AE000311 AE000311 g1788553 Escherichia coli 562 -11536429 5000692787 (de:(ecoli_2172) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2172 ECOLI_2172 Escherichia coli 562 10062936

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870724	13277	35433	210	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870742	13278	35434	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870745	13279	35435	219	72

Description

6500732572 yfaa:b2230 hypothetical 64.5 kd protein in atob-gyra intergenic region:pufy (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2230 b2230 Escherichia coli 562 -11536430 111797 yfaa:pufy (de:hypothetical 64.5 kd protein in atob-gyra intergenic region) (db:swissprot) YFAA_ECOLI P17994 ESCHERICHIA COLI 562 -11536430 7000687672 yfaa yfaa protein (db:pir2.dat) D64993 D64993 Escherichia coli 562 -11536430 7500923314 yfaa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 202 of 400 of the completengenome.) (nt:f578; this 578 aa orf is 100 pct identical to) (le:7656) (re:9392) (di:complement) AE000312 AE000312 g1788561 Escherichia coli 562 -11536430 5000692794 (de:(ecoli_2179) (pn:hypothetical protein in gyra 5"region:pufy:fragment) (gn:yfaa) (gtcfc:13.7:14.1) (ec:) (yfaa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2179 ECOLI_2179 Escherichia coli 562 10123608

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870749	13280	35436	762	253

Description

6500732573 yfal:b2233 hypothetical 131.2 kd protein in ubig-nrda intergenic region precursor (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2233 b2233 Escherichia coli 562 -11536431 111805 yfal (de:precursor) (db:swissprot) YFAL_ECOLI P45508 ESCHERICHIA COLI 562 -11536431 7000687676 yfal yfal protein (db:pir2.dat) G64993 G64993 Escherichia coli 562 -11536431 7500923319 yfal putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 203 of 400 of the completengenome.) (nt:f1251; residues 70-229 are 100 pct identical to) (le:954) (re:4706) (di:complement) AE000313 AE000313 g1788565 Escherichia coli 562 -11536431 5000692795 (de:(ecoli_2182) (pn:hypothetical 36) (gn:yfal) (gtcfc:13.7:14.1) (ec:) (yfal_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2182 ECOLI_2182 Escherichia coli 562 10123609

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870752	13281	35437	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870764	13282	35438	291	96

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870780	13283	35439	312	103

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870782	13284	35440	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870783	13285	35441	714	237

Description

5000692815 yfbb (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b2263 b2263 Escherichia coli 562 -11536432
7000691951 yfbb yfbb protein (cl:hypothetical protein hi0282) (db:pir2.dat)
E64997 E64997 Escherichia coli 562 -11536432 7500960510 yfbb putative
enzyme (fn:putative enzyme; not classified) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 206 of 400 of the completegenome.)
(nt:f252; 97 pct identical (0 gaps) to 149 residues of) (le:3256) (re:4014)
(di:complement) AE000316 AE000316 g1788598 Escherichia coli 562 -11536432
6500732574 yfbb (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b2263 b2263 Escherichia coli 562 -11536432

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870788	13286	35442	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870799	13287	35443	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870800	13288	35444	477	158

Description

5000692908 yfea (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
 (db:gtc-escherichia coli) b2395 b2395 Escherichia coli 562 -11536433
 7000691952 yfea yfea protein (db:pir2.dat) H65013 H65013 Escherichia coli
 562 -11536433 7500960511 yfea orf:hypothetical protein (fn:orf; unknown)
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 217 of 400 of the
 completengenome.) (nt:f768; 100 pct identical to 131 residues of) (le:7322)
 (re:9628) (di:complement) AE000327 AE000327 g1788739 Escherichia coli 562
 -11536433 6500732575 yfea (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
 (db:gtc-escherichia coli) b2395 b2395 Escherichia coli 562 -11536433

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870803	13289	35445	300	100

Description

5000692909 yfec (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
 (db:gtc-escherichia coli) b2398 b2398 Escherichia coli 562 -11536434
 7000691953 yfec yfec protein (cl:yfec protein) (db:pir2.dat) A65014 A65014
 Escherichia coli 562 -11536434 7500960512 yfec orf:hypothetical protein
 (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
 218 of 400 of the completengenome.) (nt:ol19; residues 6-44 and 82-115 are
 100 pct) (le:141) (re:500) (di:direct) AE000328 AE000328 g1788741
 Escherichia coli 562 -11536434 6500732576 yfec (gtcfc:14.2) (keggfc:14.2)
 (rileyfc:5.9.0) (db:gtc-escherichia coli) b2398 b2398 Escherichia coli 562
 -11536434

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870812	13290	35446	369	122

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870815	13291	35447	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870821	13292	35448	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870825	13293	35449	648	216

Description

GTC ORF with score 118 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone c1241.) (nt:similar to h.sapience cellular apoptosis) (le:36648) (re:38000) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870826	13294	35450	426	141

Description

6500732577 yfeh:b2410 hypothetical 36.4 kd protein in xapb-lig intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2410 b2410 Escherichia coli 562 -11536435 111856 yfeh (de:hypothetical 36.4 kd protein in xapb-lig intergenic region) (db:swissprot) YFEH_ECOLI P39836 ESCHERICHIA COLI 562 -11536435 7000687698 yfeh yfeh protein (db:pir2.dat) A65015 A65015 Escherichia coli 562 -11536435 7500923411 yfeh putative cytochrome oxidase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 218 of 400 of the completengenome.) (nt:o332; 100 pct identical to 231 residues of) (le:8635) (re:9633) (di:direct) AE000328 AE000328 g1788749 Escherichia coli 562 -11536435 5000692914 (de:(ecoli_2351) (pn:hypothetical protein in xapb-lig intergenic region:fragment) (gn:yfeh) (gtcfc:13.7:14.1) (ec:) (yfeh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2351 ECOLI_2351 Escherichia coli 562 10123672

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870827	13295	35451	420	139

Description

6500732578 cchb:b2456 cchb protein (gtcfc:14.2) (keggfc:14.2)
 (rileyfc:5.9.0) (db:gtc-escherichia coli) b2456 b2456 Escherichia coli 562
 -11536436 500685108 cchb (de:cchb protein) (db:swissprot) CCHB_ECOLI P77633
 ESCHERICHIA COLI 562 -11536436 7000684767 cchb cchb protein (cl:carbon
 dioxide concentrating mechanism protein ccml) (db:pir2.dat) G65020 G65020
 Escherichia coli 562 -11536436 225022 cchb cchb protein. (sr:escherichia
 coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
 (de:e.coli genomic dna, kohara clone #421(55.1-55.5 min.)) (nt:similar to
 (swissprot accession number p41792)) (le:11807) (re:12094) (di:complement)
 D90874 D90874 g1799882 Escherichia coli 562 -11536436 7500878349 cchb detox
 protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia
 coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:f95; 91 pct
 identical to 95 residues of) (le:8446) (re:8733) (di:complement) AE000332
 AE000332 g1788798 Escherichia coli 562 -11536436 5000692945
 (de:(ecoli_2396) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)
 (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2396
 ECOLI_2396 Escherichia coli 562 10062963

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870828	13296	35452	507	168

Description

GTC ORF with score 267 to: (sr:schizosaccharomyces pombe (strain:972 h-)
 dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38
 kb genomic dna, clone c1241.) (nt:similar to h.sapience cellular apoptosis)
 (le:36648) (re:38000) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870831	13297	35453	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870832	13298	35454	1308	435

Description

5000692946 ccha (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b2457 b2457 Escherichia coli 562 -11536437
7000690861 ccha ccha protein (db:pir2.dat) H65020 H65020 Escherichia coli
562 -11536437 225023 ccha ccha protein precursor. (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #421(55.1-55.5 min.)) (nt:similar to
(swissprot accession number p41791)) (le:12201) (re:12536) (di:complement)
D90874 D90874 g1799883 Escherichia coli 562 -11536437 7500959707 ccha detox
protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia
coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:f111; 96 pct
identical to ccha_salty sw: p41791) (le:8840) (re:9175) (di:complement)
AE000332 AE000332 g1788799 Escherichia coli 562 -11536437 6500732579 ccha
(gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2457
b2457 Escherichia coli 562 -11536437

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870840	13299	35455	294	97

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870845	13300	35456	435	144

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870850	13301	35457	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870851	13302	35458	456	151

Description

6500732580 yffh:b2467 hypothetical 21.7 kd protein in tkfb-narq intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2467 b2467 Escherichia coli 562 -11536438 111879 yffh (de:hypothetical 21.7 kd protein in tkfb-narq intergenic region) (db:swissprot) YFFH_ECOLI P37128 ESCHERICHIA COLI 562 -11536438 7000687704 yffh yffh protein (cl:yffh protein:mutt domain homology) (db:pir2.dat) B65022 B65022 Escherichia coli 562 -11536438 225029 yffh (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #422(55.5-55.8 min.)) (nt:similar to (swissprot accession number p37128)) (le:5996) (re:6571) (di:complement) D90875 D90875 g1799890 Escherichia coli 562 -11536438 7500923435 yffh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 223 of 400 of the completegenome.) (nt:f192; 100 pct identical to fragment yffh_ecoli) (le:6946) (re:7521) (di:complement) AE000333 AE000333 g1788810 Escherichia coli 562 -11536438 5000692955 (de:(ecoli_2407) (pn:hypothetical protein in narq 5"region:fragment) (gn:yffh) (gtcfc:13.7:14.1) (ec:) (yffh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2407 ECOLI_2407 Escherichia coli 562 10120211

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870852	13303	35459	633	210

Description

6500732581 yffg:b2468 hypothetical 71.8 kd protein in tkfb-narq intergenic region:aeg53.0 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2468 b2468 Escherichia coli 562 -11536439 111878 aega (de:aega protein) (db:swissprot) AEGA_ECOLI P37127 ESCHERICHIA COLI 562 -11536439 7000687703 yffg yffg protein (db:pir2.dat) C65022 C65022 Escherichia coli 562 -11536439 7500876630 yffg putative oxidoreductase:fe-s subunit (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 223 of 400 of the completegenome.) (nt:f659; 99 pct identical to 555 residues) (le:7589) (re:9568) (di:complement) AE000333 AE000333 g1788811 Escherichia coli 562 -11536439 5000692956 (de:(ecoli_2408) (pn:hypothetical 71) (gn:yffg) (gtcfc:13.7:14.1) (ec:) (yffg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2408 ECOLI_2408 Escherichia coli 562 10123701

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870853	13304	35460	492	164

Description

6500732582 acrd:b2470 acriflavin resistance protein d (gtcfc:11.1:13.3)
(keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2470 b2470
Escherichia coli 562 -11536440 58293 acrd (de:acriflavin resistance protein
d) (db:swissprot) ACRD_ECOLI P24177 ESCHERICHIA COLI 562 -11536440
7000684505 acrd acriflavin resistance protein acrd (cl:acriflavin
resistance protein) (db:pir2.dat) E65022 E65022 Escherichia coli 562
-11536440 225032 envd gene product homolog (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #422(55.5-55.8 min.)) (nt:similar to
(pir accession number c42959)) (le:10688) (re:13801) (di:direct) D90875
D90875 g1799893 Escherichia coli 562 -11536440 7500876374 acrd sensitivity
to acriflavine:integral membrane (fn:putative transport; drug/analog
sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 224
of 400 of the completegenome.) (nt:o1037; 1027 residues are 99 pct identical
(1 gap)) (le:112) (re:3225) (di:direct) AE000334 AE000334 g1788814
Escherichia coli 562 -11536440 5000692957 (de:(ecoli_2410) (pn:sensitivity
to acriflavine, integral membrane protein, possible efflux pump) (gn:acrd)
(gtcfc:13.7:14.1) (ec:) (acrd_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2410 ECOLI_2410 Escherichia coli 562
10120213

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870859	13305	35461	432	143

Description

5000692962 gcvr (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b2479 b2479 Escherichia coli 562 -11536441
7000690888 gcvr gcvr protein (db:pir2.dat) F65023 F65023 Escherichia coli
562 -11536441 225044 gcvr gcv operon transcriptional regulator.
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #423(55.7-56.1
min.)) (nt:similar to (swissprot accession number p23483)) (le:10790)
(re:11428) (di:direct) D90876 D90876 g1799906 Escherichia coli 562 -11536441
225054 gcvr gcv operon transcriptional regulator. (sr:escherichia coli
(strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #424(55.9-56.3 min.)) (nt:similar to
(swissprot accession number p23483)) (le:3530) (re:4168) (di:direct) D90877
D90877 g1805537 Escherichia coli 562 -11536441 7500959744 gcvr
transcriptional regulation of gcv operon (fn:regulator; central intermediary
metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225
of 400 of the completegenome.) (nt:o212; residues 37-174 are 100 pct
identical) (le:2146) (re:2784) (di:direct) AE000335 AE000335 g1788824
Escherichia coli 562 -11536441 6500732583 gcvr (gtcfc:14.2) (keggfc:14.2)
(rileyfc:5.9.0) (db:gtc-escherichia coli) b2479 b2479 Escherichia coli 562
-11536441

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870860	13306	35462	255	84

Description

6500732584 yfia:b2597 12.7 kd protein in sfhb-pheI intergenic region:urf1:orfs54 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2597 b2597 Escherichia coli 562 -11536442 163239 yfia hypothetical 13k protein pheA 5 region:yfia protein (db:pir2.dat) (mp:57 min) Q5ECPA A30275 Escherichia coli 562 -11536442 225171 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #437(58.6-59.0 min.)) (nt:similar to (pir accession number a30275)) (le:15305) (re:15646) (di:direct) D90887 D90887 g1800000 Escherichia coli 562 -11536442 225173 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #438(58.9-59.3 min.)) (nt:similar to (pir accession number a30275)) (le:37) (re:378) (di:direct) D90888 D90888 g1800003 Escherichia coli 562 -11536442 235405 urf1 orfs54 (fn:probable sigma-54 modulation protein) (db:genpept-bct1) (de:e.coli genes for unknown protein, leader peptide and urf1.) (le:883) (re:1224) (di:direct) ECLPURF1 Z70523 g1246515 Escherichia coli 562 -11536442 7500959782 (sr:e.coli k12 dna, clone pmul000) (db:genpept-bct1) (de:e.coli phe and tyr operons: pheA and phe genes coding forchorismate mutase/prephenate dehydratase and phe leader peptide;and arof and tyra genes encoding dhap synthetase and chorismatemutase/prep... ECOPHEAB M10431 g147173 Escherichia coli 562 -11536442 233326 yfia putative yhbh sigma 54 modulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:ol113; 100 pct identical to yfia_ecoli sw:) (le:2946) (re:3287) (di:direct) AE000346 AE000346 g1788949 Escherichia coli 562 -11536442 5000693044 (de:(ecoli_2533) (pn:12) (gn:yfia) (gtcfc:13.7:14.1) (ec:) (yfia_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2533 ECOLI_2533 Escherichia coli 562 10086823

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870864	13307	35463	522	173

Description

6500732585 yfjb:b2615 hypothetical 32.6 kd protein in grpe-recn intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2615 b2615 Escherichia coli 562 -11536443 7000691954 yfjb yfjb protein (cl:conserved hypothetical protein hi0072) (db:pir2.dat) B65040 B65040 Escherichia coli 562 -11536443 225190 yfjb (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #438(58.9-59.3 min.)) (nt:similar to (swissprot accession number p37768)) (le:13715) (re:14593) (di:direct) D90888 D90888 g1800020 Escherichia coli 562 -11536443 7500960513 yfjb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the completegenome.) (nt:o292; residues 1-119 are 99 pct identical to) (le:4553) (re:5431) (di:direct) AE000347 AE000347 g1788968 Escherichia coli 562 -11536443 5000693053 (de:(ecoli_2551) (pn:hypothetical 32) (gn:yfjb) (gtcfc:13.7:14.1) (ec:)) (yfjb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2551 ECOLI_2551 Escherichia coli 562 10120294

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870868	13308	35464	540	179

Description

6500732586 ygac:b2671 hypothetical 13.1 kd protein in stpa-nrde intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2671 b2671 Escherichia coli 562 -11536444 112249 ygac (de:hypothetical 13.1 kd protein in stpa-nrde intergenic region) (db:swissprot) YGAC_ECOLI P36931 ESCHERICHIA COLI 562 -11536444 7000687764 ygac ygac protein (db:pir2.dat) H65046 H65046 Escherichia coli 562 -11536444 7500923999 ygac orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 242 of 400 of the completegenome.) (nt:f114; alternate name ygac; orf of u07823; 97 pct) (le:851) (re:1195) (di:complement) AE000352 AE000352 g1789026 Escherichia coli 562 -11536444 5000693099 (de:(ecoli_2604) (pn:hypothetical 12) (gn:ygac) (gtcfc:13.7:14.1) (ec:)) (ygac_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2604 ECOLI_2604 Escherichia coli 562 10123775

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870874	13309	35465	270	89

Description

6500732587 srlr:gutrb2707 srlr:glucitol operon repressor (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2707 b2707 Escherichia coli 562 -11536445 234599 srlr:gutrb2707 (de:glucitol operon repressor) (db:swissprot) SRLR_ECOLI P15082 ESCHERICHIA COLI 562 -11536445 164469 srlr:gutrb2707 regulatory protein gutr:glucitol operon protein r:srlr protein (cl:regulatory protein gutr) (db:pir2.dat) S01832 S01832 Escherichia coli 562 -11536445 5000693113 (db:genpept-bct1) (de:escherichia coli gutm gene and gutr gene for activator and repressor proteins.) (nt:gutr r protein (aa 1-257)) (le:779) (re:1552) (di:direct) ECGUTMR X13463 g41630 Escherichia coli 562 -11536445 239280 (db:genpept-bct1) (de:e.coli glucitol (gut) operon: glucitol-specific enzyme ii (guta), and iii (gutb), glucitol-6-phosphate dehydrogenase (gutd), activator (gutm) and repressor (gutrb) genes, complete cds.) (nt:gutr operon repressor (gutrb)) (le:3748) (re:... ECOGUT J02708 g146282 Escherichia coli 562 -11536445 7500892078 gutrb (fn:glucitol operon repressor) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:cg site no. 152; alternate gene name srlr) (le:1350) (re:2123) (di:direct) ECU29579 U29579 g882599 Escherichia coli 562 -11536445 233045 srlr regulator for gut srl:glucitol operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 244 of 400 of the complete genome.) (nt:o257; 100 pct identical to srlr_ecoli sw: p15082;) (le:7003) (re:7776) (di:direct) AE000354 AE000354 g1789059 Escherichia coli 562 -11536445 99472 srlr:gutrb2707 (de:glucitol operon repressor) (db:swissprot) SRLR_ECOLI P15082 ESCHERICHIA COLI 562 -11536445

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870878	13310	35466	276	91

Description

6500732588 gutq:srlq:b2708 gutq:gutq protein (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2708 b2708 Escherichia coli 562 -11536446 75116 gutq:srlq (de:gutq protein) (db:swissprot) GUTQ_ECOLI P17115 ESCHERICHIA COLI 562 -11536446 7000685479 gutq probable atp-binding protein gutq (cl:probable atp-binding protein gutq) (db:pir2.dat) (mp:58 min) H65050 H65050 Escherichia coli 562 -11536446 7500882858 gutq (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (nt:alternate gene name srlq) (le:2155) (re:3081) (di:direct) ECU29579 U29579 g882600 Escherichia coli 562 -11536446 239281 gutq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 244 of 400 of the completegenome.) (nt:o308; 100 pct identical to gb: ecu29579_4) (le:7808) (re:8734) (di:direct) AE000354 AE000354 g1789060 Escherichia coli 562 -11536446 5000693114 (de:(ecoli_2636) (pn:gutq protein) (gn:gutq) (gtcfc:13.7:14.1) (ec:)) (gutq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2636 ECOLI_2636 Escherichia coli 562 10123784

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870879	13311	35467	465	154

Description

6500732589 ygaa:b2709 hypothetical sigma-54-dependent transcriptional regulator in gutq-hypf intergenic region (gtcfc:10.2:14.1) (keggfc:14.2) (rileyfc:5.9.0:5.9.0) (db:gtc-escherichia coli) b2709 b2709 Escherichia coli 562 -11536447 112247 ygaa (de:intergenic region) (db:swissprot) YGAA_ECOLI P37013 ESCHERICHIA COLI 562 -11536447 7000687763 ygaa ygaa protein (cl:rna polymerase sigma factor interaction domain homology) (db:pir2.dat) A65051 A65051 Escherichia coli 562 -11536447 7500923998 (db:genpept-bct1) (de:escherichia coli k12 putative tripartite transcription factor(orf529 and orf504) genes, complete cds, and (orf60) gene, partialcds.) (nt:putative orf 529aa; orf529) (le:265) (re:1854) (di:direct) ECU03846 U03846 g434587 Escherichia coli 562 -11536447 238458 ygaa putative 2-component transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 244 of 400 of the completegenome.) (nt:f529; joins 2 orfs from earlier version; now) (le:8731) (re:10320) (di:complement) AE000354 AE000354 g2367150 Escherichia coli 562 -11536447

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870888	13312	35468	492	163

Description

6500732590 hypf:hyda:b2712 transcriptional regulatory protein hypf (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2712 b2712 Escherichia coli 562 -11536448 78488 hypf:hyda (de:transcriptional regulatory protein hypf) (db:swissprot) HYPF_ECOLI P30131 ESCHERICHIA COLI 562 -11536448 7000685599 hypf hypf protein (cl:probabe transcription regulator hypf) (db:pir2.dat) D65051 D65051 Escherichia coli 562 -11536448 7500883744 hypf transcriptional regulatory protein (fn:regulator; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 245 of 400 of the completegenome.) (nt:f750; 96 pct identical (1 gap) to hypf_ecoli) (le:2783) (re:5035) (di:complement) AE000355 AE000355 g2367152 Escherichia coli 562 -11536448

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870891	13313	35469	993	330

Description

6500732591 hyci:b2717 hydrogenase 3 maturation protease (gtcfc:10.11:14.2) (ec:3.-.-.-) (keggfc:14.1) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2717 b2717 Escherichia coli 562 -11536449 205532 hyci hydrogenase 3 hyci (cl:hydrogenase 3 hyci) (db:pir2.dat) S67469 S67469 Escherichia coli 562 -11536449 233179 hyci (db:genpept-bct1) (de:e.coli hyc operon hyca,b,c,d,e,f,g,h,i genes.) (le:7604) (re:8074) (di:direct) ECHYC X17506 g1136794 Escherichia coli 562 -11536449 239291 hyci (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 61 to 62 minutes.) (le:14877) (re:15347) (di:complement) ECU29579 U29579 g882610 Escherichia coli 562 -11536449 7500959765 hyci protease involved in processing c-terminal end (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 246 of 400 of the completegenome.) (nt:f156; 100 pct identical to gb: echyc_9) (le:110) (re:580) (di:complement) AE000356 AE000356 g1789072 Escherichia coli 562 -11536449 500684957 hyci_ecoli (de:) Q57451 Q57451 Escherichia coli 562 -11536449 5000693120 (de:(ecoli_2646) (pn:function not assigned) (gn:hyci) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2646 ECOLI_2646 Escherichia coli 562 10060950

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870919	13314	35470	621	207

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870924	13315	35471	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870928	13316	35472	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870940	13317	35473	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870941	13318	35474	1089	362

Description

6500732592 ygce:b2776 hypothetical sugar kinase in cysj-eno intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2776 b2776 Escherichia coli 562 -11536450 112283 ygce (de:hypothetical sugar kinase in cysj-eno intergenic region) (db:swissprot) YGCE_ECOLI P55138 ESCHERICHIA COLI 562 -11536450 7000687781 ygce ygce protein (db:pir2.dat) D65059 D65059 Escherichia coli 562 -11536450 7500924060 ygce putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 251 of 400 of the completegenome.) (nt:o492; this 374 aa orf is 100 pct identical (0 gaps)) (le:2473) (re:3951) (di:direct) AE000361 AE000361 g1789138 Escherichia coli 562 -11536450 5000693156 (de:(ecoli_2707) (pn:hypothetical 41) (gn:ygce) (gtcfc:13.7:14.1) (ec:) (ygce_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2707 ECOLI_2707 Escherichia coli 562 10123828

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870952	13319	35475	1038	345

Description

6500732593 mazg:b2781 mazg protein (gtcfc:14.2) (keggfc:14.2)
(rileyfc:5.9.0) (db:gtc-escherichia coli) b2781 b2781 Escherichia coli 562
-11536451 83079 mazg (de:mazg protein) (db:swissprot) MAZG_ECOLI P33646
ESCHERICHIA COLI 562 -11536451 7000685791 mazg mazg protein
(cl:beta-lactamase regulatory protein:beta-lactamase regulatory protein
homology) (db:pir2.dat) A65060 A65060 Escherichia coli 562 -11536451
7500885351 mazg (db:genpept-bct1) (de:escherichia coli k-12 genome;
approximately 62 minute region.) (nt:cg site no. 33299) (le:7759) (re:8550)
(di:complement) ECU29580 U29580 g882675 Escherichia coli 562 -11536451
239355 mazg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 252 of 400 of the completegenome.)
(nt:f263; 99 pct identical (1 gap) to mazg_ecoli) (le:144) (re:935)
(di:complement) AE000362 AE000362 g1789144 Escherichia coli 562 -11536451
5000693159 (de:(ecoli_2712) (pn:mazg protein) (gn:mazg) (gtcfc:13.7:14.1)
(ec:) (mazg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_2712 ECOLI_2712 Escherichia coli 562 10025298

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501870954	13320	35476	2340	779

Description

6500732594 syd:ydr:b2793 syd:syd protein (gtcfc:14.3) (keggfc:14.2)
(rileyfc:5.8.0:5.9.0) (db:gtc-escherichia coli) b2793 b2793 Escherichia coli
562 -11536452 100003 syd:ydr (de:syd protein) (db:swissprot) SYDP_ECOLI
P43526 ESCHERICHIA COLI 562 -11536452 164674 syd syd protein (db:pir2.dat)
A55944 A55944 Escherichia coli 562 -11536452 239367 syd syd protein
(fn:interacts with secy protein in vivo) (sr:escherichia coli (strain:k-12)
dna) (db:genpept-bct1) (de:escherichia coli syd gene for syd protein,
complete cds.) (nt:identified as a multicopy suppressor of a dominant)
(le:554) (re:1099) (di:direct) ECOSYDP D38520 g780114 Escherichia coli 562
-11536452 7500892345 (db:genpept-bct1) (de:escherichia coli k-12 genome;
approximately 63 to 64 minutes.) (nt:gtg start) (le:6290) (re:6835)
(di:complement) ECU29581 U29581 g882688 Escherichia coli 562 -11536452
236058 syd interacts with secy (fn:orf; unknown function) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 253 of 400 of the completegenome.)
(nt:f181; 100 pct identical to sydp_ecoli sw:) (le:2448) (re:2993)
(di:complement) AE000363 AE000363 g1789157 Escherichia coli 562 -11536452
5000693168 (de:(ecoli_2724) (pn:protein) (gn:syd) (gtcfc:13.7:14.1) (ec:)
(sydp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_2724 ECOLI_2724 Escherichia coli 562 10041857

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870956	13321	35477	240	79

Description

6500732595 bgla:b2901 6-phospho-beta-glucosidase bgla (gtcfc:14.2) (ec:3.2.1.86) (keggfc:14.1) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2901 b2901 Escherichia coli 562 -11536453 1500686130 bgla (ec:3.2.1.86) (de:6-phospho-beta-glucosidase bgla,) (db:swissprot) BGLA_ECOLI Q46829 ESCHERICHIA COLI 562 -11536453 7000684701 bgla bgla protein (cl:agrobacterium beta-glucosidase) (db:pir2.dat) E65074 E65074 Escherichia coli 562 -11536453 7500877784 bgla 6-phospho-beta-glucosidase a:cryptic (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.) (nt:o479; this 479 aa orf is 66 pct identical (4 gaps)) (le:7365) (re:8804) (di:direct) AE000373 AE000373 g2367174 Escherichia coli 562 -11536453

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870957	13322	35478	225	74

Description

GTC ORF with score 176 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid t22d1.) (nt:highly similar to human tumor necrosis factor type) (le:15814:15952:16139) (re:15902:16093:16249) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870959	13323	35479	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870979	13324	35480	309	102

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870989	13325	35481	561	186

Description

6500732596 visc:b2906 visc protein (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b2906 b2906 Escherichia coli 562 -11536454 7000691931 visc visc protein (cl:ubih protein) (db:pir2.dat) (mp:63 min) B65075 B65075 Escherichia coli 562 -11536454 7500953724 visc (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f400) (le:5506) (re:6708) (di:complement) ECU28377 U28377 g882436 Escherichia coli 562 -11536454 239120 visc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 264 of 400 of the completegenome.) (nt:f400; 99 pct identical to visc_ecoli sw: p25535) (le:2045) (re:3247) (di:complement) AE000374 AE000374 g1789273 Escherichia coli 562 -11536454 5000693242 (de:(ecoli_2829) (pn:visc protein) (gn:visc) (gtcfc:13.7:14.1) (ec:) (visc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2829 ECOLI_2829 Escherichia coli 562 10123904

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501870994	13326	35482	516	171

Description

6500732597 icc:b3032 icc protein (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3032 b3032 Escherichia coli 562 -11536455 78690 icc (de:icc protein) (db:swissprot) ICC_ECOLI P36650 ESCHERICHIA COLI 562 -11536455 7000685604 cpda:icc 3:5-cyclic-nucleotide phosphodiesterase:cpda:icc protein (cl:3',5'-cyclic-nucleotide phosphodiesterase cpda:3',5'-cyclic-nucleotide phosphodiesterase cpda homology:phosphoesterase core homology) (ec:3.1.4.17) (db:pir1.dat) (mp:68.4 min) F65090 F65090 Escherichia coli 562 -11536455 7500883790 icc icc (fn:affect the expression of the lacz gene) (sr:escherichia coli (strain k12, isolate w3110) dna) (db:genpept-bct1) (de:e. coli dna for icc protein, complete cds.) (le:985) (re:1812) (di:direct) ECOICC D16557 g453396 Escherichia coli 562 -11536455 234833 icc regulator of lacz (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 275 of 400 of the completegenome.) (nt:f275; 100 pct identical to icc_ecoli sw: p36650;) (le:3666) (re:4493) (di:complement) AE000385 AE000385 g1789410 Escherichia coli 562 -11536455 5000693326 (de:(ecoli_2955) (pn:affects the expression of the lacz gene) (gn:icc) (gtcfc:13.7:14.1) (ec:) (icc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2955 ECOLI_2955 Escherichia coli 562 10021028

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871000	13327	35483	465	154

Description

6500732598 ygid:b3039 hypothetical 29.9 kd protein in tolC-ribB intergenic region:orfC:f271 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3039 b3039 Escherichia coli 562 -11536456 112389 ygid (de:(f271)) (db:swissprot) YGID_ECOLI P24197 ESCHERICHIA COLI 562 -11536456 7000687855 ygid ygid protein (cl:ygid protein) (db:pir2.dat) E65091 E65091 Escherichia coli 562 -11536456 7500924254 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f271; alternate_name ygid; orfC of m77129) (le:136007) (re:136822) (di:complement) ECU28377 U28377 g882569 Escherichia coli 562 -11536456 239253 ygid orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 275 of 400 of the completegenome.) (nt:f271; 100 pct identical 242 residues from) (le:9279) (re:10094) (di:complement) AE000385 AE000385 g1789417 Escherichia coli 562 -11536456 5000693332 (de:(ecoli_2962) (pn:hypothetical 29) (gn:ygid) (gtcfc:13.7:14.1) (ec:) (ygid_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2962 ECOLI_2962 Escherichia coli 562 10054117

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871003	13328	35484	369	122

Description

6500732599 ygif:b3054 hypothetical 48.4 kd protein in glne-cca intergenic region:orfX (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3054 b3054 Escherichia coli 562 -11536457 304599 ygif (de:hypothetical 48.4 kd protein in glne-cca intergenic region (orfX)) (db:swissprot) YGIF_ECOLI P30871 ESCHERICHIA COLI 562 -11536457 163893 ygif ygif protein (db:pir2.dat) S37754 S37754 Escherichia coli 562 -11536457 5000693342 orfX (db:genpept-bct1) (de:e.coli orfX gene.) (nt:open reading frame upstream glne) (le:63) (re:1364) (di:direct) ECORFXEA Z21844 g49399 Escherichia coli 562 -11536457 235782 ygif orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 277 of 400 of the completegenome.) (nt:f433) (le:4584) (re:5885) (di:complement) AE000387 AE000387 g1789434 Escherichia coli 562 -11536457 7502852285 orfX (db:genpept) (de:e.coli orfX gene.) (nt:open reading frame upstream glne) (le:63) (re:1364) (di:direct) ECORFXEA Z21844 g49399 Escherichia coli 562 -11536457 112391 ygif (de:hypothetical 48.4 kd protein in glne-cca intergenic region (orfX)) (db:swissprot) YGIF_ECOLI P30871 ESCHERICHIA COLI 562 -11536457

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871004	13329	35485	630	209

Description

6500732600 ygig:b3058 hypothetical 13.6 kd protein in baca-ttda intergenic region:f123 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3058 b3058 Escherichia coli 562 -11536458 7000691956 ygig probable dihydroneopterin aldolase (cl:dihydroneopterin aldolase fola:dihydroneopterin aldolase homology) (ec:4.1.2.25) (db:pir2.dat) H65093 H65093 Escherichia coli 562 -11536458 7500960515 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:alternate name ygig; orf_f123) (le:9016) (re:9387) (di:complement) ECU28379 U28379 g882580 Escherichia coli 562 -11536458 239263 ygig putative kinase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 277 of 400 of the completegenome.) (nt:f123; this 123 aa orf is 95 pct identical (0 gaps)) (le:9141) (re:9512) (di:complement) AE000387 AE000387 g1789438 Escherichia coli 562 -11536458 5000693344 (de:(ecoli_2981) (pn:hypothetical 13) (gn:ygig) (gtcfc:13.7:14.1) (ec:)) (ygig_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2981 ECOLI_2981 Escherichia coli 562 10123963

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871006	13330	35486	816	271

Description

6500732601 ygih:b3059 hypothetical 22.2 kd protein in baca-ttda intergenic region:o205 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3059 b3059 Escherichia coli 562 -11536459 112395 ygih (de:hypothetical 22.2 kd protein in baca-ttda intergenic region (o205)) (db:swissprot) YGIH_ECOLI P31056 ESCHERICHIA COLI 562 -11536459 7000687856 ygih ygih protein (cl:escherichia coli ygih protein) (db:pir2.dat) A65094 A65094 Escherichia coli 562 -11536459 7500924257 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:alternate name ygih; orf_o205) (le:9489) (re:10106) (di:direct) ECU28379 U28379 g882581 Escherichia coli 562 -11536459 239264 ygih orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 277 of 400 of the completegenome.) (nt:o205; n-ter of this 205 aa orf is 100 pct identical) (le:9614) (re:10231) (di:direct) AE000387 AE000387 g1789439 Escherichia coli 562 -11536459 5000693345 (de:(ecoli_2982) (pn:hypothetical 22) (gn:ygih) (gtcfc:13.7:14.1) (ec:)) (ygih_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2982 ECOLI_2982 Escherichia coli 562 10054123

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871016	13331	35487	417	138

Description

6500732602 ygje:b3063 hypothetical 52.9 kd protein in ttldb-rpsu intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3063 b3063 Escherichia coli 562 -11536460 112417 ygje (de:antiporter) (db:swissprot) TTDT_ECOLI P39414 ESCHERICHIA COLI 562 -11536460 7000687866 ygje ygje protein (cl:2-oxoglutarate/malate translocator) (db:pir1.dat) (mp:67 min) QQECSR E65094 Escherichia coli 562 -11536460 7500924293 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:alternate name ygje; orf_o487) (le:12819) (re:14282) (di:direct) ECU28379 U28379 g882586 Escherichia coli 562 -11536460 239268 ygje orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 278 of 400 of the completegenome.) (nt:o487) (le:1695) (re:3158) (di:direct) AE000388 AE000388 g1789444 Escherichia coli 562 -11536460 5000693347 (de:(ecoli_2986) (pn:hypothetical 32) (gn:ygje) (gtcfc:13.7:14.1) (ec:) (ygje_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2986 ECOLI_2986 Escherichia coli 562 10123966

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871023	13332	35488	894	297

Description

6500732603 ygjr (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0:5.9.0) (db:gtc-escherichia coli) b3087 b3087 Escherichia coli 562 -11536461 7000691957 ygjr ygjr protein (cl:escherichia coli ygjr protein) (db:pir2.dat) D65097 D65097 Escherichia coli 562 -11536461 7500924306 ygjr orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 280 of 400 of the completegenome.) (nt:o334; sequence change joins orfs ygjr and ygjs from) (le:9589) (re:10593) (di:direct) AE000390 AE000390 g2367190 Escherichia coli 562 -11536461 7500924304 ygjr (de:hypothetical 37.0 kd protein in ebgc-uxaa intergenic region) (db:swissprot) YGJR_ECOLI P42599 ESCHERICHIA COLI 562 -11536461

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871027	13333	35489	519	172

Description

5000693451 yhc (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b3217 b3217 Escherichia coli 562 -11536462
7000691958 yhc yhc protein (db:pir2.dat) C65113 C65113 Escherichia coli
562 -11536462 7500960516 (db:genpept-bct1) (de:escherichia coli k-12
chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o159; 2nd start)
(le:145930) (re:146409) (di:direct) ECOUW67 U18997 g606156 Escherichia coli
562 -11536462 236455 yhc orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 291 of 400 of the
completegenome.) (nt:o159; this 159 aa orf is 96 pct identical (0 gaps))
(le:4472) (re:4951) (di:direct) AE000401 AE000401 g1789611 Escherichia coli
562 -11536462 6500732604 yhc (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b3217 b3217 Escherichia coli 562 -11536462

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871034	13334	35490	468	155

Description

6500732605 yhdh:b3253 hypothetical 34.7 kd protein in mreB-acbB intergenic
region:orf1:o324 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b3253 b3253 Escherichia coli 562 -11536463 112722
yhdh (de:hypothetical 34.7 kd protein in mreB-acbB intergenic region (orf1))
(db:swissprot) YHDH_ECOLI P26646 ESCHERICHIA COLI 562 -11536463 163276 yhdh
hypothetical 35k protein fabE 5 region:yhdh protein (cl:bacillus subtilis
conserved hypothetical protein yhfP) (db:pir2.dat) JS0688 JS0688 Escherichia
coli 562 -11536463 236492 35 kda protein (fn:unknown) (sr:escherichia coli
(strain k-12) f- dna) (db:genpept-bct1) (de:e.coli biotin carboxylase and
biotin carboxyl carrier protein(fabE) and orf1 35 kda protein genes,
complete cds.) (nt:gene not essential for cell growth; orf1; putative)
(le:... ECOACOAC M80458 g145173 Escherichia coli 562 -11536463 7500936839
yhdh (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from
67.4 to 76.0 minutes.) (nt:orf_o324; orf of ecoacoac) (le:184229)
(re:185203) (di:direct) ECOUW67 U18997 g606193 Escherichia coli 562
-11536463 233712 yhdh putative dehydrogenase (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 294
of 400 of the completegenome.) (nt:o324) (le:7222) (re:8196) (di:direct)
AE000404 AE000404 g1789651 Escherichia coli 562 -11536463 5000693476
(de:(ecoli_3177) (pn:hypothetical 34) (gn:yhdh) (gtcfc:13.7:14.1) (ec:)
(yhdh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_3177 ECOLI_3177 Escherichia coli 562 10054450

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871054	13335	35491	393	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871068	13336	35492	336	111

Description

6500732606 acrf:envd:b3266 acrf:acriflavin resistance protein f:envd protein (gtcfc:11.1:13.3) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3266 b3266 Escherichia coli 562 -11536464 233720 acrf:envd (de:acriflavin resistance protein f (envd protein)) (db:swissprot) ACRF_ECOLI P24181 ESCHERICHIA COLI 562 -11536464 7000684507 acrf:envd acriflavin resistance protein acrf:envd protein (cl:acriflavin resistance protein) (db:pir2.dat) D65119 D65119 Escherichia coli 562 -11536464 5000693484 envd (fn:cell division) (db:genpept-bct1) (de:e.coli envc, envd and envr genes.) (le:3604) (re:6708) (di:direct) ECENVCD X57948 g510830 Escherichia coli 562 -11536464 7500876376 acrf acriflavine resistance protein (fn:resistance to acriflavine, hydrophobic) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:e. coli acriflavine resistant proteins (acre and acrf) genes, complete cds.) (le:1371) (re:4475) (di:direct) ECOACREF M96848 g290409 Escherichia coli 562 -11536464 232771 acrf integral transmembrane protein:acridine (fn:membrane; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 295 of 400 of the complete genome.) (nt:o1034; alternate name envd, has different start) (le:4829) (re:7933) (di:direct) AE000405 AE000405 g1789666 Escherichia coli 562 -11536464 58295 acrf:envd (de:acriflavin resistance protein f (envd protein)) (db:swissprot) ACRF_ECOLI P24181 ESCHERICHIA COLI 562 -11536464

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871073	13337	35493	345	115

Description

6500732607 smg:b3284 smg protein (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.8.0:5.9.0) (db:gtc-escherichia coli) b3284 b3284 Escherichia coli 562 -11536465 98675 smg (de:smg protein) (db:swissprot) SMG_ECOLI P30853 ESCHERICHIA COLI 562 -11536465 7000686611 smg smg protein (db:pir2.dat) G65120 G65120 Escherichia coli 562 -11536465 7500891725 smg (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f157; geneplot suggests ecmfsmg orf is wrong) (le:212739) (re:213212) (di:complement) ECOUW67 U18997 g606218 Escherichia coli 562 -11536465 236517 smg orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 297 of 400 of the completegenome.) (nt:f157; 100 pct identical to smg_ecoli sw: p30853) (le:62) (re:535) (di:complement) AE000407 AE000407 g1789679 Escherichia coli 562 -11536465 5000693494 (de:(ecoli_3202) (pn:protein) (gn:smg) (gtcfc:13.7:14.1) (ec:) (smg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3202 ECOLI_3202 Escherichia coli 562 10040550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871083	13338	35494	432	143

Description

5000693495 smf (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3285 b3285 Escherichia coli 562 -11536466 7000691918 smf smf protein (db:pir2.dat) H65120 H65120 Escherichia coli 562 -11536466 7500960464 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f102; orf created by difference between our) (le:213184) (re:213492) (di:complement) ECOUW67 U18997 g606219 Escherichia coli 562 -11536466 236518 smf_2 orf:fragment 2 (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 297 of 400 of the completegenome.) (nt:f102; 99 pct identical to 102 residues of 374) (le:507) (re:815) (di:complement) AE000407 AE000407 g1789680 Escherichia coli 562 -11536466 6500732608 smf (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3285 b3285 Escherichia coli 562 -11536466

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871085	13339	35495	714	237
<u>Description</u>				
6500732609 sun:fmv:fmv:b3289 fmu:sun protein:fmv protein (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3289 b3289 Escherichia coli 562 -11536467 72203 sun:fmv:fmv:rsmb (de:sun protein (fmu protein)) (db:swissprot) SUN_ECOLI P36929 ESCHERICHIA COLI 562 -11536467 7000686699 fmu fmu protein (cl:hypothetical protein hi0624) (db:pir2.dat) D65121 D65121 Escherichia coli 562 -11536467 306532 sun (db:genpept-bct1) (de:e.coli fmt, sun and trka genes.) (le:516) (re:1805) (di:direct) ECFMSTUNT Y10307 g1772512 Escherichia coli 562 -11536467 232897 sun orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 297 of 400 of the completegenome.) (nt:o429; joins orfs fmu and fmv) (le:3277) (re:4566) (di:direct) AE000407 AE000407 g2367212 Escherichia coli 562 -11536467				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871088	13340	35496	999	332
<u>Description</u>				
6500732610 yhea:b3337 hypothetical 7.4 kd protein in bfr-tufa intergenic region:gen64:f64 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3337 b3337 Escherichia coli 562 -11536468 112751 bfd (de:bacterioferritin-associated ferredoxin) (db:swissprot) BFD_ECOLI P13655 ESCHERICHIA COLI 562 -11536468 135187 yhea yhea protein (cl:yhea protein) (db:pir1.dat) (mp:73 min) QQECB7 JV0033 Escherichia coli 562 -11536468 236570 gen64 glycoprotein 64 (db:genpept-bct1) (de:e. coli (clones lambda-(g206,9h3), subclones pgs-(275,277,280,281)) glycoprotein 24' (gen24) gene, 3' end; glycoprotein 64(gen64) and bacterioferritin (bfr) genes, complete cds; type 4prepilin-like protein specific leader peptidas... ECOBFR M27176 g145408 Escherichia coli 562 -11536468 7500936873 yhea (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f64) (le:247545) (re:247739) (di:complement) ECOUW67 U18997 g606271 Escherichia coli 562 -11536468 233897 yhea orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 300 of 400 of the completegenome.) (nt:f64) (le:66) (re:260) (di:complement) AE000410 AE000410 g1789735 Escherichia coli 562 -11536468 5000693514 (de:(ecoli_3255) (pn:hypothetical 7) (gn:yhea) (gtcfc:13.7:14.1) (ec:) (yhea_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3255 ECOLI_3255 Escherichia coli 562 10054479				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871092	13341	35497	471	156

Description

6500732611 slyx:b3348 slyx protein (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3348 b3348 Escherichia coli 562 -11536469 98641 slyx (de:slyx protein) (db:swissprot) SLYX_ECOLI P30857 ESCHERICHIA COLI 562 -11536469 163515 slyx slyx protein (db:pir2.dat) A49988 A49988 Escherichia coli 562 -11536469 236581 (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli slyd gene, complete cds.) (nt:orf72) (le:70) (re:288) (di:direct) ECOSLYDX L13261 g290468 Escherichia coli 562 -11536469 7500891710 slyd (fn:host gene required for lysis of phix174) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:258388) (re:258606) (di:direct) ECOUW67 U18997 g606282 Escherichia coli 562 -11536469 235996 slyx host factor for lysis of phix174 infection (fn:orf; unknown function) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 301 of 400 of the completgenome.) (nt:o72; 100 pct identical amino acid sequence and) (le:141) (re:359) (di:direct) AE000411 AE000411 g1789747 Escherichia coli 562 -11536469 5000693521 (de:(ecoli_3266) (pn:slyx protein) (gn:slyx) (gtcfc:13.7:14.1) (ec:) (slyx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3266 ECOLI_3266 Escherichia coli 562 10040516

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871100	13342	35498	324	107

Description

6500732612 yhgf:b3407 hypothetical 81.4 kd protein in greb-feoa intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3407 b3407 Escherichia coli 562 -11536470 112803 yhgf (de:hypothetical 81.4 kd protein in greb-feoa intergenic region) (db:swissprot) YHGF_ECOLI P46837 ESCHERICHIA COLI 562 -11536470 7000687990 yhgf yhgf protein (cl:hypothetical protein ydci) (db:pir2.dat) B65136 B65136 Escherichia coli 562 -11536470 7500936935 yhgf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 306 of 400 of the completgenome.) (nt:o740; 100 pct identical to 740 aa) (le:4741) (re:6963) (di:direct) AE000416 AE000416 g1789811 Escherichia coli 562 -11536470 5000693556 (de:(ecoli_3325) (pn:hypothetical 81) (gn:yhgf) (gtcfc:13.7:14.1) (ec:) (yhgf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3325 ECOLI_3325 Escherichia coli 562 10124025

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871107	13343	35499	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871123	13344	35500	585	194

Description

5000693567 gntu_2 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b3435 b3435 Escherichia coli 562 -11536471
7000690899 gntu_2 gluconate permease component gntu2 (cl:d-serine permease)
(db:pir2.dat) F65139 F65139 Escherichia coli 562 -11536471 7500959756
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to
76.0 minutes.) (nt:orf_f111) (le:356460) (re:356795) (di:complement) ECOUW67
U18997 g606370 Escherichia coli 562 -11536471 236669 gntu_2 low-affinity
gluconate transport permease (fn:transport; transport of small molecules:)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the
completeness.) (nt:f111; 100 pct identical to 111 residues of 446 aa)
(le:2113) (re:2448) (di:complement) AE000420 AE000420 g1789843 Escherichia
coli 562 -11536471 6500732613 gntu_2 (gtcfc:14.2) (keggfc:14.2)
(rileyfc:5.9.0) (db:gtc-escherichia coli) b3435 b3435 Escherichia coli 562
-11536471

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871129	13345	35501	1521	506

Description

5000693568 gntu_1 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b3436 b3436 Escherichia coli 562 -11536472
7000690898 gntu_1 gluconate permease component gntu1 (cl:d-serine permease)
(db:pir2.dat) G65139 G65139 Escherichia coli 562 -11536472 7500959755
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to
76.0 minutes.) (nt:orf_f332) (le:356801) (re:357799) (di:complement) ECOUW67
U18997 g606371 Escherichia coli 562 -11536472 236670 gntu_1 low-affinity
gluconate transport permease (fn:transport; transport of small molecules:)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the
completeness.) (nt:f332; 100 pct identical to n-terminal 331 residues)
(le:2454) (re:3452) (di:complement) AE000420 AE000420 g1789844 Escherichia
coli 562 -11536472 6500732614 gntu_1 (gtcfc:14.2) (keggfc:14.2)
(rileyfc:5.9.0) (db:gtc-escherichia coli) b3436 b3436 Escherichia coli 562
-11536472

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871150	13346	35502	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871153	13347	35503	975	324

Description

6500732615 yhha:b3448 hypothetical 16.6 kd protein in ggt-ugp_q intergenic region precursor:ol46a:orf_q (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3448 b3448 Escherichia coli 562 -11536473
7500936946 yhha (de:(ol46a) (orf_q)) (db:swissprot) YHHA_ECOLI P23850
ESCHERICHIA COLI 562 -11536473 163354 yhha yhha protein (db:pir2.dat) S47667 S47667 Escherichia coli 562 -11536473 240336 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yhha) (le:1205) (re:1645) (di:direct) ECOUW76 U00039 g466584 Escherichia coli 562 -11536473 5000693575 orf::q (db:genpept-bct1) (de:e. coli ug_{pq} gene for glycerophosphoryl diester phosphodiesterase(cytoplasmic) and orf_q.) (le:758) (re:1198) (di:complement) ECUGPQQ X56908 g43254 Escherichia coli 562 -11536473 236683 yhha orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 311 of 400 of the completegenome.) (nt:ol46; 100 pct identical to yhha_ecoli sw: p23850;) (le:2496) (re:2936) (di:direct) AE000421 AE000421 g1789857 Escherichia coli 562 -11536473 112817 yhha (de:(ol46a) (orf_q)) (db:swissprot) YHHA_ECOLI P23850 ESCHERICHIA COLI 562 -11536473

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871154	13348	35504	525	175

Description

5000693589 yhhh (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3483 b3483 Escherichia coli 562 -11536474 164849 yhhh yhhh protein (cl:yhhh protein) (db:pir2.dat) S47702 S47702 Escherichia coli 562 -11536474 7500960517 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:possible upstream start for ol27; alternate gene) (le:37676) (re:38044) (di:direct) ECOUW76 U00039 g466619 Escherichia coli 562 -11536474 236718 yhhh orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 314 of 400 of the completegenome.) (nt:ol22; this 122 aa orf is 100 pct identical to) (le:4287) (re:4655) (di:direct) AE000424 AE000424 g1789895 Escherichia coli 562 -11536474 6500732616 yhhh (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3483 b3483 Escherichia coli 562 -11536474

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871158	13349	35505	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871183	13350	35506	660	219

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871194	13351	35507	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871197	13352	35508	483	160

Description

5000693608 slp (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b3506 b3506 Escherichia coli 562 -11536475 164623
slp outer-membrane lipoprotein (cl:rnd protein) (db:pir2.dat) S47726 S47726
Escherichia coli 562 -11536475 7500960403 slp (sr:escherichia coli
(sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e.
coli chromosomal region from 76.0 to 81.5 minutes.) (le:68187) (re:68786)
(di:direct) ECOUW76 U00039 g466643 Escherichia coli 562 -11536475 236742
slp outer membrane protein induced after carbon (fn:membrane; outer membrane
constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 317
of 400 of the completegenome.) (nt:ol99) (le:3045) (re:3644) (di:direct)
AE000427 AE000427 g1789922 Escherichia coli 562 -11536475 6500732617 slp
(gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3506
b3506 Escherichia coli 562 -11536475

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871209	13353	35509	258	85

Description

6500732618 yiay:b3589 hypothetical 40.2 kd protein in avta-selb intergenic region:f382 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3589 b3589 Escherichia coli 562 -11536476 136323 yiay probable alcohol dehydrogenase::orf f382 (cl:lactaldehyde reductase:lactaldehyde reductase homology) (ec:1.1.1.1) (db:pir1.dat) (mp:76-81.5 minutes) S47810 S47810 Escherichia coli 562 -11536476 7500953175 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:170929) (re:172077) (di:complement) ECOUW76 U00039 g466727 Escherichia coli 562 -11536476 236826 yiay putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 326 of 400 of the completegenome.) (nt:f382; n-ter of this 382 aa orf is 99 pct identical) (le:5752) (re:6900) (di:complement) AE000436 AE000436 gl790015 Escherichia coli 562 -11536476 5000693672 (de:(ecoli_3509) (pn:hypothetical 40) (gn:yiay) (gtcfc:13.7:14.1) (ec:) (yiay_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3509 ECOLI_3509 Escherichia coli 562 10065521

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871217	13354	35510	1005	334

Description

6500732619 yibk:b3606 hypothetical 17.7 kd protein in lctd-cyse intergenic region:o157b (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3606 b3606 Escherichia coli 562 -11536477 113165 yibk (ec:2.1.1.-) (de:hypothetical trna/rrna methyltransferase yibk,) (db:swissprot) YIBK_ECOLI P33899 ESCHERICHIA COLI 562 -11536477 163444 yibk yibk protein:hypothetical protein 157b (db:pir2.dat) S47827 S47827 Escherichia coli 562 -11536477 7500937321 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yibk) (le:195465) (re:195938) (di:direct) ECOUW76 U00039 g466744 Escherichia coli 562 -11536477 236843 yibk orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 328 of 400 of the completegenome.) (nt:o157) (le:9011) (re:9484) (di:direct) AE000438 AE000438 gl790034 Escherichia coli 562 -11536477 5000693682 (de:(ecoli_3526) (pn:hypothetical 17) (gn:yibk) (gtcfc:13.7:14.1) (ec:) (yibk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3526 ECOLI_3526 Escherichia coli 562 10054893

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871223	13355	35511	270	89

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871242	13356	35512	297	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871257	13357	35513	1200	399

Description

6500732620 ttk:b3641 ttk protein (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.8.0:5.9.0) (db:gtc-escherichia coli) b3641 b3641 Escherichia coli 562 -11536478 102705 ttk (de:ttk protein) (db:swissprot) TTK_ECOLI P06969 ESCHERICHIA COLI 562 -11536478 7000686837 ttk ttk protein (cl:hypothetical protein hi0955) (db:pir2.dat) C65165 C65165 Escherichia coli 562 -11536478 7500893570 ttk 23 kd protein (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:3844) (re:4482) (di:direct) ECOUW82 L10328 g290491 Escherichia coli 562 -11536478 236879 ttk putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:o212; 100 pct identical amino acid sequence and) (le:6347) (re:6985) (di:direct) AE000441 AE000441 g1790072 Escherichia coli 562 -11536478 5000693689 (de:(ecoli_3561) (pn:protein) (gn:ttk) (gtcfc:13.7:14.1) (ec:) (ttk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3561 ECOLI_3561 Escherichia coli 562 10044523

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871268	13358	35514	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871270	13359	35515	2697	898

Description

6500732621 yidi:b3677 hypothetical 15.7 kd protein in emrd-glvlg intergenic region:ol49 (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3677 b3677 Escherichia coli 562 -11536479 113214 yidi (de:hypothetical 15.7 kd protein in emrd-glvlg intergenic region) (db:swissprot) YIDI_ECOLI P31446 ESCHERICHIA COLI 562 -11536479 7000688023 ol49 ol49 protein (db:pir2.dat) F65169 F65169 Escherichia coli 562 -11536479 7500937368 ol49 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:45809) (re:46258) (di:direct) ECOUW82 L10328 g290526 Escherichia coli 562 -11536479 236914 yidi orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (le:3590) (re:4039) (di:direct) AE000445 AE000445 g1790111 Escherichia coli 562 -11536479 5000693707 (de:(ecoli_3596) (pn:hypothetical 15) (gn:ol49) (gtcfc:13.7:14.1) (ec:)) (yidi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3596 ECOLI_3596 Escherichia coli 562 10054942

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871283	13360	35516	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871289	13361	35517	498	165

Description

6500732622 ibpb:hs1s:htpe:b3686 hs1s:16 kd heat shock protein b (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3686 b3686 Escherichia coli 562 -11536480 7000689505 hs1s heat shock protein ibpb (cl:heat shock protein ibpa) (db:pir2.dat) G65170 G65170 Escherichia coli 562 -11536480 7500955807 hs1s (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:heat shock inducible; alternate gene name ibpb) (le:55863) (re:56297) (di:complement) ECOUW82 L10328 g290535 Escherichia coli 562 -11536480 236923 ibpb heat shock protein (fn:factor; adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:f144; heat shock inducible; alternate gene name) (le:13644) (re:14078) (di:complement) AE000445 AE000445 g1790120 Escherichia coli 562 -11536480 5000693713 (de:(ecoli_3605) (pn:16 kd heat shock protein b; belongs to the small heat shock:hsp20 family) (gn:hs1s) (gtcfc:13.7:14.1) (ec:)) (ibpb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3605 ECOLI_3605 Escherichia coli 562 10124068

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871294	13362	35518	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871296	13363	35519	390	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871297	13364	35520	774	257

Description

6500732623 ibpa:hslt:htpn:b3687 hslt:16 kd heat shock protein a (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3687 b3687 Escherichia coli 562 -11536481 78662 ibpa:hslt:htpn (de:16 kd heat shock protein a) (db:swissprot) IBPA_ECOLI P29209 ESCHERICHIA COLI 562 -11536481 163168 hslt heat shock protein ibpa:hslt protein (cl:heat shock protein ibpa) (db:pir2.dat) A45245 A45245 Escherichia coli 562 -11536481 236924 ibpa (sr:escherichia coli (sub_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli ibpa and ibpb genes, complete cds.) (nt:putative) (le:670) (re:1083) (di:direct) ECOPROTS M94104 g147369 Escherichia coli 562 -11536481 7500883788 hslt (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:heat shock inducible; alternate gene name ibpa) (le:56403) (re:56816) (di:complement) ECOUW82 L10328 g290536 Escherichia coli 562 -11536481 235563 ibpa heat shock protein (fn:factor; adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completegenome.) (nt:f137; heat shock inducible; alternate gene name) (le:83) (re:496) (di:complement) AE000446 AE000446 g1790122 Escherichia coli 562 -11536481 5000693714 (de:(ecoli_3606) (pn:16 kd heat shock protein a; belongs to the small heat shock:hsp20 family) (gn:hslt) (gtcfc:13.7:14.1) (ec:) (ibpa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3606 ECOLI_3606 Escherichia coli 562 10021000

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871306	13365	35521	1308	436

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871315	13366	35522	810	269

Description

6500732624 yidq:b3688 o135:hypothetical 14.8 kd protein in ibpa-gyrb intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3688 b3688 Escherichia coli 562 -11536482 113219 yidq (de:hypothetical 14.8 kd protein in ibpa-gyrb intergenic region) (db:swissprot) YIDQ_ECOLI P31454 ESCHERICHIA COLI 562 -11536482 7000688028 o135 o135 protein (db:pir2.dat) A65171 A65171 Escherichia coli 562 -11536482 7500937373 o135 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:57047) (re:57454) (di:direct) ECOUW82 L10328 g290537 Escherichia coli 562 -11536482 236925 yidq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 336 of 400 of the completegenome.) (le:727) (re:1134) (di:direct) AE000446 AE000446 g1790123 Escherichia coli 562 -11536482 5000693715 (de:(ecoli_3607) (pn:hypothetical 14) (gn:o135) (gtcfc:13.7:14.1) (ec:)) (yidq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3607 ECOLI_3607 Escherichia coli 562 10054947

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871318	13367	35523	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871325	13368	35524	339	112

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871329	13369	35525	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871337	13370	35526	711	236

Description

5000693757 yige (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b3815 b3815 Escherichia coli 562 -11536483
7000691960 yige yige protein (db:pir2.dat) H65185 H65185 Escherichia coli
562 -11536483 7500960519 f161 (fn:unknown) (db:genpept-bct1) (de:e. coli
genomic sequence of the region from 84.5 to 86.5 minutes.) (le:53682)
(re:54167) (di:complement) ECOUW85 M87049 g148214 Escherichia coli 562
-11536483 237039 yige orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 347 of 400 of the
completegenome.) (nt:f161; this 161 aa orf is 96 pct identical (0 gaps))
(le:6202) (re:6687) (di:complement) AE000457 AE000457 g1790248 Escherichia
coli 562 -11536483 6500732625 yige (gtcfc:14.2) (keggfc:14.2)
(rileyfc:5.9.0) (db:gtc-escherichia coli) b3815 b3815 Escherichia coli 562
-11536483

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871339	13371	35527	480	159

Description

6500732626 rard:b3819 rard protein (gtcfc:14.2) (keggfc:14.2)
(rileyfc:5.9.0) (db:gtc-escherichia coli) b3819 b3819 Escherichia coli 562
-11536484 163627 rard rard protein (cl:escherichia coli rard protein)
(db:pir2.dat) S30709 S30709 Escherichia coli 562 -11536484 7500955843 f300
(fn:unknown) (db:genpept-bct1) (de:e. coli genomic sequence of the region
from 84.5 to 86.5 minutes.) (le:56398) (re:57300) (di:complement) ECOUW85
M87049 g148218 Escherichia coli 562 -11536484 237043 rard orf:hypothetical
protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
section 347 of 400 of the completegenome.) (nt:f300; this 300 aa orf is 96
pct identical to) (le:8919) (re:9821) (di:complement) AE000457 AE000457
g1790252 Escherichia coli 562 -11536484 5000693760 (de:(ecoli_3725)
(pn:rard protein) (gn:rard) (gtcfc:13.7:14.1) (ec:) (rard_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) ECOLI_3725
ECOLI_3725 Escherichia coli 562 10087014

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871340	13372	35528	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871360	13373	35529	501	166

Description

5000693764 yigl (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b3826 b3826 Escherichia coli 562 -11536485
7000691961 yigl yigl protein:hypothetical protein o171 (db:pir2.dat) C65187
C65187 Escherichia coli 562 -11536485 7500960520 o171 (fn:unknown)
(db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to
86.5 minutes.) (le:63414) (re:63929) (di:direct) ECOUW85 M87049 g148225
Escherichia coli 562 -11536485 237050 yigl orf:hypothetical protein
(fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
348 of 400 of the completegenome.) (nt:o171; this 171 aa orf is 99 pct
identical to) (le:5526) (re:6041) (di:direct) AE000458 AE000458 g1790260
Escherichia coli 562 -11536485 6500732627 yigl (gtcfc:14.2) (keggfc:14.2)
(rileyfc:5.9.0) (db:gtc-escherichia coli) b3826 b3826 Escherichia coli 562
-11536485

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871361	13374	35530	870	290

Description

6500732628 yigu:b3839 hypothetical 29.0 kd protein in udp-rfah intergenic
region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0:5.9.0) (db:gtc-escherichia
coli) b3839 b3839 Escherichia coli 562 -11536486 7500937459 tatc:mttb
(de:sec-independent protein translocase protein tatc) (db:swissprot)
TATC_ECOLI P27857 ESCHERICHIA COLI 562 -11536486 7000691962 yigu yigu
protein (cl:conserved hypothetical protein hi0188) (db:pir2.dat) H65188
H65188 Escherichia coli 562 -11536486 7500937461 mttb mttb (fn:involved in
folded protein translocation and) (db:genpept-bct1) (de:escherichia coli
mtta1 (mtta1), mttb (mttb), andmttc (mttc) genes, complete
cds.) (nt:membrane protein; tatc; yigu) (le:1475) (re:2251) (di:direct)
AF067848 AF067848 g3193219 Escherichia coli 562 -11536486 7500937463 tatc
tatc protein (fn:sec-independent protein translocase) (db:genpept-bct1)
(de:escherichia coli tatabcd operon.) (nt:alternative gene names: yigu,
mttb) (le:847) (re:1623) (di:direct) ECO5830 AJ005830 g3123498 Escherichia
coli 562 -11536486 7500937462 yigu orf:hypothetical protein (fn:orf;
unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 349 of
400 of the completegenome.) (nt:o258; sequence change joins two orfs
relative) (le:6475) (re:7251) (di:direct) AE000459 AE000459 g2367313
Escherichia coli 562 -11536486

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871362	13375	35531	267	88

Description

5000693774 yigw (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b3840 b3840 Escherichia coli 562 -11536487
7000691963 yigw yigw protein:hypothetical protein o206 (db:pir2.dat) A65189
A65189 Escherichia coli 562 -11536487 7500960521 yigw_1 orf:hypothetical
protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
section 349 of 400 of the completegenome.) (nt:o206; 98 pct identical to
n-terminal 184 residues) (le:7281) (re:7901) (di:direct) AE000459 AE000459
g1790274 Escherichia coli 562 -11536487 6500732629 yigw (gtcfc:14.2)
(keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3840 b3840
Escherichia coli 562 -11536487

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871363	13376	35532	531	176

Description

6500732630 yigc:b3843 hypothetical 55.3 kd protein in rfah-rfe intergenic
region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli)
b3843 b3843 Escherichia coli 562 -11536488 7000691959 yigc yigc protein
(cl:conserved hypothetical protein s110936) (db:pir2.dat) D65189 D65189
Escherichia coli 562 -11536488 7500960518 yigc putative oxidoreductase
(fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli
k-12 mg1655 section 349 of 400 of the completegenome.) (nt:o497; ??? pct
identical to conceptual) (le:8728) (re:10221) (di:direct) AE000459 AE000459
g1790277 Escherichia coli 562 -11536488 5000693776 (de:(ecoli_3748)
(pn:hypothetical 55) (gn:yigc) (gtcfc:13.7:14.1) (ec:) (yigc_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3748
ECOLI_3748 Escherichia coli 562 10124114

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871383	13377	35533	1107	368

Description

6500732631 yijd:b3964 hypothetical 13.0 kd protein in udha-trma intergenic region:orfb (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b3964 b3964 Escherichia coli 562 -11536489 113379 yijd (de:hypothetical 13.0 kd protein in udha-trma intergenic region (orfb)) (db:swissprot) YIJD_ECOLI P27308 ESCHERICHIA COLI 562 -11536489 7000688054 yijd yijd protein (db:pir2.dat) G65203 G65203 Escherichia coli 562 -11536489 237182 yijd orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 360 of 400 of the completegenome.) (nt:ol19) (le:8657) (re:9016) (di:direct) AE000470 AE000470 g1790402 Escherichia coli 562 -11536489 7500937549 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:alternate name yijd) (le:27013) (re:27372) (di:direct) ECOUW89 U00006 g396311 Escherichia coli 562 -11536489 5000693833 (de:(ecoli_3862) (pn:hypothetical 13) (gn:yijd) (gtcfc:13.7:14.1) (ec:) (yijd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3862 ECOLI_3862 Escherichia coli 562 10055107

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871388	13378	35534	2157	718

Description

6500732632 yjba:b4030 hypothetical 15.6 kd protein in pgi-xyle intergenic region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b4030 b4030 Escherichia coli 562 -11536490 113613 yjba (de:hypothetical 15.6 kd protein in pgi-xyle intergenic region) (db:swissprot) YJBA_ECOLI P23896 ESCHERICHIA COLI 562 -11536490 7000688065 yjba yjba protein (cl:escherichia coli yjba protein) (db:pir2.dat) E65210 E65210 Escherichia coli 562 -11536490 237651 unknown protein (sr:escherichia coli (strain k-12) (clone: pej3.) dna) (db:genpept-bct1) (de:escherichia coli xylose-proton symport (xyle) gene, complete cdsand maltose transport (malg) gene, 3' end.) (nt:orf; putative) (le:1923) (re:2333) (di:complement) ECOXYLE J02812 g894087 Escherichia coli 562 -11536490 237236 yjba orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 366 of 400 of the completegenome.) (nt:ol36) (le:7036) (re:7446) (di:direct) AE000476 AE000476 g1790462 Escherichia coli 562 -11536490 7500937868 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:alternate name yjba) (le:105567) (re:105977) (di:direct) ECOUW89 U00006 g396365 Escherichia coli 562 -11536490 5000693852 (de:(ecoli_3916) (pn:hypothetical 15) (gn:yjba) (gtcfc:13.7:14.1) (ec:) (yjba_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3916 ECOLI_3916 Escherichia coli 562 10055341

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871400	13379	35535	2460	820

Description

6500732633 phnq:b4091 very hypothetical phnq protein (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b4091 b4091 Escherichia coli 562 -11536491 89610 phnq (de:very hypothetical phnq protein) (db:swissprot) PHNQ_ECOLI P16693 ESCHERICHIA COLI 562 -11536491 164291 phnq phnq protein (db:pir2.dat) C42732 C42732 Escherichia coli 562 -11536491 237299 phnq (sr:escherichia coli (strain:k-12, sub_strain:w3110) dna) (db:genpept-bct1) (de:escherichia coli phn operon genes.) (le:11046) (re:11453) (di:direct) ECOPHN D90227 g216606 Escherichia coli 562 -11536491 7500888038 phnq (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:annotated in genbank accession number j05260) (le:4739) (re:5146) (di:complement) ECOUW93 U14003 g536935 Escherichia coli 562 -11536491 235431 phnq orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 372 of 400 of the completegenome.) (nt:f135; annotated in genbank accession number) (le:9458) (re:9865) (di:complement) AE000482 AE000482 g1790529 Escherichia coli 562 -11536491 5000693882 (de:(ecoli_3977) (pn:function not assigned) (gn:phnq) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3977 ECOLI_3977 Escherichia coli 562 10031732

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871407	13380	35536	348	115

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871419	13381	35537	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871420	13382	35538	270	89

Description

5000693898 yjdc (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b4135 b4135 Escherichia coli 562 -11536492 162879
yjdc:cuta3 divalent cation tolerance protein cuta3:inner
membrane:hypothetical protein 191:yjdc protein (db:pir2.dat) S56363 S56363
Escherichia coli 562 -11536492 237343 cuta3 199 residue polypeptide
(db:genpept-bct1) (de:e.coli cuta1, cuta2, and cuta3 genes.) (le:2390)
(re:2989) (di:direct) ECCUTA123 Z36905 g581056 Escherichia coli 562
-11536492 7500959722 yjdc (db:genpept-bct1) (de:escherichia coli k-12
chromosomal region from 92.8 to 00.1 minutes.) (le:53561) (re:54160)
(di:complement) ECOUW93 U14003 g536979 Escherichia coli 562 -11536492
232601 yjdc orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 376 of 400 of the completegenome.)
(nt:fl99; this 199 aa orf is 100 pct identical to) (le:4106) (re:4705)
(di:complement) AE000486 AE000486 g1790577 Escherichia coli 562 -11536492
6500732634 yjdc (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0)
(db:gtc-escherichia coli) b4135 b4135 Escherichia coli 562 -11536492

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871421	13383	35539	1467	488

Description

GTC ORF with score 1365 to: (sr:schizosaccharomyces pombe (strain:pr745)
cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial
cds, clone: sy 1644.) (nt:similar to saccharomyces cerevisiae
dihydroxy-acid) (le:<1) (re:1544) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871426	13384	35540	444	147

Description

6500732635 ytfn:b4221 hypothetical 136.8 kd protein in msra-chpb intergenic
region (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli)
b4221 b4221 Escherichia coli 562 -11536493 116412 ytfn (de:hypothetical
136.8 kd protein in msra-chpb intergenic region) (db:swissprot) YTFN_ECOLI
P39321 ESCHERICHIA COLI 562 -11536493 7000688614 ytfn ytfn protein (cl:ytfn
protein) (db:pir2.dat) H65233 H65233 Escherichia coli 562 -11536493
7500952768 ytfn orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 383 of 400 of the
completegenome.) (nt:o1259; n-ter of this 492 aa orf is 100 pct) (le:6560)
(re:10339) (di:direct) AE000493 AE000493 g1790667 Escherichia coli 562
-11536493 5000693952 (de:(ecoli_4104) (pn:hypothetical 53) (gn:ytfn)
(gtcfc:13.7:14.1) (ec:) (ytfn_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_4104 ECOLI_4104 Escherichia coli 562
10124155

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871436	13385	35541	3519	1172

Description

6500732636 fimi:b4315 fimbrin-like protein fimi (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b4315 b4315 Escherichia coli 562 -11536494 71696 fimi (de:fimbrin-like protein fimi) (db:swissprot) FIMI_ECOLI P39264 ESCHERICHIA COLI 562 -11536494 163052 fimi fimi protein (cl:type 1 fimbrial protein) (db:pir2.dat) S56540 S56540 Escherichia coli 562 -11536494 7500881469 fimi (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:234452) (re:235099) (di:direct) ECOUW93 U14003 g537156 Escherichia coli 562 -11536494 237520 fimi fimbrial protein (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 392 of 400 of the completegenome.) (nt:o215) (le:3414) (re:4061) (di:direct) AE000502 AE000502 g1790770 Escherichia coli 562 -11536494 5000694015 (de:(ecoli_4198) (pn:fimbrin-like protein fimi) (gn:fimi) (gtcfc:13.7:14.1) (ec:) (fimi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4198 ECOLI_4198 Escherichia coli 562 10014254

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871481	13386	35542	432	144

Description

5000694055 yjjv (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b4378 b4378 Escherichia coli 562 -11536495 163765 yjjv yjjv protein:hypothetical protein o211 (db:pir2.dat) S56602 S56602 Escherichia coli 562 -11536495 7500960523 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o211) (le:304456) (re:305091) (di:direct) ECOUW93 U14003 g537218 Escherichia coli 562 -11536495 237583 yjjv orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:o211; this 211 aa orf is 99 pct identical to) (le:4273) (re:4908) (di:direct) AE000508 AE000508 g1790838 Escherichia coli 562 -11536495 6500732637 yjjv (gtcfc:14.2) (keggfc:14.2) (rileyfc:5.9.0) (db:gtc-escherichia coli) b4378 b4378 Escherichia coli 562 -11536495

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501871483	13387	35543	633	210

Description

5000691338 insa_1:insa_5:insa_6:insa:b0022 insertion element is1 protein insa (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0022 b0022 Escherichia coli 562 -11536496 236678 insa:b0022:b0265:b0275:b1894:b3444 (de:insertion element is1 protein insa) (db:swissprot) ISA1_ECOLI P03827 ESCHERICHIA COLI 562 -11536496 7502852286 insa:b0022:b0265:b0275:b1894:b3444 (de:insertion element is1 protein insa) (db:swissprot) ISA1_ECOLI P03827 SHIGELLA SONNEI 624 -11536496 157302 insa_6 insa protein (cl:insa protein) (db:pir2.dat) JN0134 JN0134 Escherichia coli 562 -11536496 7500884275 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #404(51.7-52.1 min.)) (nt:similar to (pir accession number jn0134)) (le:9768) (re:10043) (di:complement) D90860 D90860 g1799659 Escherichia coli 562 -11536496 233559 (db:genpept-bct1) (de:escherichia coli dna for insertion sequence is1a.) (nt:insa peptide (aa 1-91)) (le:498) (re:773) (di:complement) ECIS1A X52534 g581112 Escherichia coli 562 -11536496 7000685647 (db:genpept-bct1) (de:escherichia coli dna for insertion sequence is1e.) (nt:insa peptide (aa 1-91)) (le:151) (re:426) (di:direct) ECIS1E X52537 g581116 Escherichia coli 562 -11536496 243689 insa (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:19896) (re:20171) (di:complement) ECO110K D10483 g285761 Escherichia coli 562 -11536496 243706 insa insa peptide (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:364220) (re:364495) (di:direct) ECOUW67 U18997 g606379 Escherichia coli 562 -11536496 304041 insa insa protein (db:genpept-bct1) (de:escherichia coli insa, insb, and yiaj genes (plasmid pjb4).) (le:409) (re:684) (di:direct) ECPJB4 AJ223474 g2980622 Escherichia coli 562 -11536496 1500685300 insa (sr:insertion sequence is1 dna; escherichia coli dna; and escherichi) (db:genpept-bct1) (de:insertion element is1, from e. coli lacI gene.) (nt:putative) (le:111) (re:386) (di:direct) INS1ECLAC J01729 g149060 Insertion sequence IS1 2675 -11536496 6500732638 insa (sr:insertion sequence is1 dna) (db:genpept-bct1) (de:shigella sonnei insertion sequence is1 insa and insb genes,complete cds.) (nt:gtg start codon) (le:56) (re:331) (di:direct) INSIS1S M37615 g149095 Insertion sequence IS1 2675 -11536496 224813 insa_1 is1 protein insa (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 2 of 400 of the completegenome.) (nt:f91; 100 pct identical to isa1_ecoli sw: p03827) (le:9695) (re:9970) (di:complement) AE000112 AE000112 g1786204 Escherichia coli 562 -11536496 233238 insa_5 is1 protein insa (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:f91; 100 pct identical to isa1_ecoli sw: p03827) (le:1768) (re:2043) (di:complement) AE000283 AE000283 g1788204 Escherichia coli 562 -11536496 233243 insa_6 is1 protein insa (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 310 of 400 of the completegenome.) (nt:o91; 100 pct identical amino acid sequence and) (le:9873) (re:10148) (di:direct) AE000420 AE000420 g1789852 Escherichia coli

(le:9873) (re:10148) (di:direct) AE000420 AE000420 g1789852 Escherichia coli
562 -11536496 7500884276 insa insa (db:genpept-bct2) (de:escherichia coli

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871484	13388	35544	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871489	13389	35545	255	84

Description

6500732639 lspA:b0027 lipoprotein signal peptidase:prolipoprotein signal
peptidase:signal peptidase ii:spase ii (gtcfc:11.2:12.2) (ec:3.4.23.36)
(keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0027 b0027
Escherichia coli 562 -11536497 233564 lspA (ec:3.4.23.36) (de:peptidase)
(signal peptidase ii) (spase ii)) (db:swissprot) LSPA_ECOLI P00804
ESCHERICHIA COLI 562 -11536497 7000685767 lspA lipoprotein signal
peptidase::preurein leader peptidase:prolipoprotein signal peptidase:signal
peptidase ii (cl:lipoprotein signal peptidase) (ec:3.4.23.36) (db:pir1.dat)
(mp:1 min) ZPECL C64723 Escherichia coli 562 -11536497 5000691341
(db:genpept-bct1) (de:e.coli lspA gene for lipoprotein signal peptidase.)
(nt:lipoprotein signal peptidase) (le:439) (re:933) (di:direct) ECLIPPEP
X00776 g41923 Escherichia coli 562 -11536497 235022 lspA lipoprotein signal
peptidase (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1)
(de:e.coli k12 genome, 0-2.4min. region.) (le:24861) (re:25355) (di:direct)
ECO110K D10483 g216454 Escherichia coli 562 -11536497 7500885170 (sr:e.coli
dna, clone pmt521) (db:genpept-bct1) (de:e.coli lsp gene coding for
prolipoprotein signal peptidase, and 3'end of ileS gene coding for
isoleucyl-trna synthetase.) (nt:prolipoprotein signal peptidase (lsp))
(le:436) (re:930) (di:direct) ECOLSP K01990 g146670 Escherichia coli 562
-11536497 233319 lspA prolipoprotein signal peptidase spase ii (fn:enzyme;
protein, peptide secretion) (db:genpept-bct2) (ec:3.4.23.36) (de:escherichia
coli k-12 mg1655 section 3 of 400 of the completegenome.) (nt:ol64; 100 pct
identical to lspA_ecoli sw: p00804) (le:4548) (re:5042) (di:direct) AE000113
AE000113 g1786210 Escherichia coli 562 -11536497 82512 lspA (ec:3.4.23.36)
(de:peptidase) (signal peptidase ii) (spase ii)) (db:swissprot) LSPA_ECOLI
P00804 ESCHERICHIA COLI 562 -11536497

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871496	13390	35546	1134	378

Description

6500732640 yaad:slpa:b0028 probable fkbb-type 16 kd peptidyl-prolyl cis-trans isomerase:fkbp-type 16 kd peptidyl-prolyl cis-trans isomerase:ppiase:rotamase (gtcfc:14.3) (ec:5.2.1.8) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0028 b0028 Escherichia coli 562 -11536498 163242 yaad probable peptidylprolyl isomerase:16k fkbp-type:orf149 protein (ec:5.2.1.8) (db:pir2.dat) JE0402 JE0402 Escherichia coli 562 -11536498 233565 orf::1 (db:genpept-bct1) (de:e. coli lsp-dapb interval.) (le:146) (re:595) (di:direct) ECLSPDAP X54945 g41932 Escherichia coli 562 -11536498 7500881498 orf (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (nt:hypothetical 16.4k protein(pir:je0402)) (le:25480) (re:25929) (di:direct) ECO110K D10483 g216455 Escherichia coli 562 -11536498 233329 slpa probable fkbx-type 16kd peptidyl-prolyl (fn:putative enzyme; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 3 of 400 of the completengenome.) (nt:o149; 100 pct identical to fkbx_ecoli sw: p22563) (le:5167) (re:5616) (di:direct) AE000113 AE000113 g1786211 Escherichia coli 562 -11536498 71786 slpa (ec:5.2.1.8) (de:(ppiase) (rotamase)) (db:swissprot) FKBX_ECOLI P22563 ESCHERICHIA COLI 562 -11536498 5000691342 (de:(ecoli_28) (pn:probable fkbx-type 16kd peptidyl-prolyl cis-trans isomerase:a rotamase) (gn:yaad) (gtcfc:13.7:14.1) (ec:5.2.1.8) (fkbx_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_28 ECOLI_28 Escherichia coli 562 10014342

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871501	13391	35547	363	120

Description

6500732641 caie:b0035 carnitine operon protein caie (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0035 b0035 Escherichia coli 562 -11536499 62524 caie (de:carnitine operon protein caie) (db:swissprot) CAIE_ECOLI P39206 ESCHERICHIA COLI 562 -11536499 7000684746 caie protein caie (cl:ferripyochelin binding protein) (db:pir2.dat) C64724 C64724 Escherichia coli 562 -11536499 7500878117 caie possible synthesis of cofactor for carnitine (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 4 of 400 of the completengenome.) (nt:f203; 100 pct identical to caie_ecoli sw: p39206) (le:695) (re:1306) (di:complement) AE000114 AE000114 g1786219 Escherichia coli 562 -11536499 5000691345 (de:(ecoli_35) (pn:carnitine operon protein caie) (gn:caie) (gtcfc:13.7:14.1) (ec:) (caie_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_35 ECOLI_35 Escherichia coli 562 10005222

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871502	13392	35548	600	199

Description

6500732642 caid:b0036 carnitine racemase (gtcfc:9.13) (ec:5.-.-.-)
 (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0036 b0036
 Escherichia coli 562 -11536500 62523 caid (ec:5.-.-.-) (de:carnitine
 racemase,) (db:swissprot) CAID_ECOLI P31551 ESCHERICHIA COLI 562 -11536500
 7000684745 caid carnitine racemase (cl:enoyl-coa hydratase homology)
 (ec:5.-.-.-) (db:pir2.dat) D64724 D64724 Escherichia coli 562 -11536500
 7500878116 caid carnitine racemase (fn:enzyme; degradation of small
 molecules: amines) (db:genpept-bct2) (ec:5.-.-.-) (de:escherichia coli k-12
 mg1655 section 4 of 400 of the completegenome.) (nt:f297; 99 pct identical
 to caid_ecoli sw: p31551) (le:1291) (re:2184) (di:complement) AE000114
 AE000114 g1786220 Escherichia coli 562 -11536500 5000691346 (de:(ecoli_36)
 (pn:carnitine racemase) (gn:caid) (gtcfc:13.7:14.1) (ec:5.-.-.-)
 (caid_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli))
 ECOLI_36 ECOLI_36 Escherichia coli 562 10122625

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871523	13393	35549	510	169

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871529	13394	35550	426	141

Description

6500732643 caib:b0038 l-carnitine dehydratase:l-cdht (gtcfc:9.13)
 (ec:4.2.1.89) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0038
 b0038 Escherichia coli 562 -11536501 62521 caib (ec:4.2.1.89)
 (de:l-carnitine dehydratase, (l-cdht)) (db:swissprot) CAIB_ECOLI P31572
 ESCHERICHIA COLI 562 -11536501 163978 caib carnitine dehydratase
 (ec:4.2.1.89) (db:pir2.dat) S40559 S40559 Escherichia coli 562 -11536501
 7500878114 orf (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1)
 (de:e.coli k12 genome, 0-2.4min. region.) (nt:baif homolog(pir:f37844))
 (le:37555) (re:38772) (di:complement) ECO110K D10483 g216463 Escherichia
 coli 562 -11536501 233573 caib l-carnitine dehydratase (fn:enzyme; central
 intermediary metabolism: pool,) (db:genpept-bct2) (ec:4.2.1.89)
 (de:escherichia coli k-12 mg1655 section 4 of 400 of the completegenome.)
 (nt:f405; 100 pct identical to caib_ecoli sw: p31572) (le:3812) (re:5029)
 (di:complement) AE000114 AE000114 g1786222 Escherichia coli 562 -11536501
 5000691347 (de:(ecoli_38) (pn:l-carnitine dehydratase) (gn:caib)
 (gtcfc:13.7:14.1) (ec:4.2.1.89) (caib_ecoli) (keggfc:11.1) (rileyfc:5.7.0)
 (db:gtc-escherichia coli)) ECOLI_38 ECOLI_38 Escherichia coli 562 10005219

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871530	13395	35551	708	236

Description

6500732644 cait:b0040 probable carnitine transporter (gtcfc:12.2:9.13) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0040 b0040 Escherichia coli 562 -11536502 62525 cait (de:probable carnitine transporter) (db:swissprot) CAIT_ECOLI P31553 ESCHERICHIA COLI 562 -11536502 7000684747 cait probable carnitine transport protein (cl:escherichia coli probable carnitine transport protein) (db:pir2.dat) H64724 H64724 Escherichia coli 562 -11536502 7500878119 cait probable carnitine transporter (fn:putative transport; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 4 of 400 of the completegenome.) (nt:f504; 99 pct identical to cait_ecoli sw: p31553) (le:6331) (re:7845) (di:complement) AE000114 AE000114 g1786224 Escherichia coli 562 -11536502 5000691348 (de:(ecoli_40) (pn:probable carnitine transporter) (gn:cait) (gtcfc:13.7:14.1) (ec:) (cait_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_40 ECOLI_40 Escherichia coli 562 10122626

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871553	13396	35552	609	202

Description

6500732645 fixa:b0041 fixa protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0041 b0041 Escherichia coli 562 -11536503 7000689015 fixa electron transfer flavoprotein beta chain:fixa protein (cl:electron transfer flavoprotein beta chain) (db:pir2.dat) A64725 A64725 Escherichia coli 562 -11536503 7500953771 fixa probable flavoprotein subunit:carnitine (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 4 of 400 of the completegenome.) (nt:o268; 99 pct identical to fixa_ecoli sw: p31573) (le:8281) (re:9087) (di:direct) AE000114 AE000114 g1786225 Escherichia coli 562 -11536503 5000691349 (de:(ecoli_41) (pn:fixa protein) (gn:fixa) (gtcfc:13.7:14.1) (ec:) (fixa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_41 ECOLI_41 Escherichia coli 562 10122627

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871570	13397	35553	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871582	13398	35554	978	325

Description

6500732646 fixb:b0042 fixb protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0042 b0042 Escherichia coli 562 -11536504 71729 fixb (de:fixb protein) (db:swissprot) FIXB_ECOLI P31574 ESCHERICHIA COLI 562 -11536504 7000685251 fixb electron transfer flavoprotein alpha chain:fixb protein (cl:electron transfer flavoprotein alpha chain fixb) (db:pir2.dat) B64725 B64725 Escherichia coli 562 -11536504 7500881477 fixb (db:genpept-bct1) (de:e.coli fixa, fixb and fixc genes.) (le:1293) (re:2234) (di:direct) ECFIX X71977 g1130673 Escherichia coli 562 -11536504 232890 fixb probable flavoprotein subunit:carnitine (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 4 of 400 of the completegenome.) (nt:o313; 100 pct identical to fixb_ecoli sw: p31574) (le:9102) (re:10043) (di:direct) AE000114 AE000114 g1786226 Escherichia coli 562 -11536504 5000691350 (de:(ecoli_42) (pn:fixb protein) (gn:fixb) (gtcfc:13.7:14.1) (ec:) (fixb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_42 ECOLI_42 Escherichia coli 562 10014286

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871595	13399	35555	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871596	13400	35556	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871601	13401	35557	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871609	13402	35558	549	182

Description

6500732647 fixc:b0043 fixc protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0043 b0043 Escherichia coli 562 -11536505 71734 fixc (de:fixc protein) (db:swissprot) FIXC_ECOLI P31575 ESCHERICHIA COLI 562 -11536505 7000685252 fixc fixc protein (cl:fixc protein) (db:pir2.dat) C64725 C64725 Escherichia coli 562 -11536505 7500881478 fixc flavoprotein:electron transport (fn:putative carrier; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 4 of 400 of the completegenome.) (nt:o428; 99 pct identical to fixc_ecoli sw: p31575) (le:10094) (re:11380) (di:direct) AE000114 AE000114 g1786227 Escherichia coli 562 -11536505 5000691351 (de:(ecoli_43) (pn:fixc protein) (gn:fixc) (gtcfc:13.7:14.1) (ec:) (fixc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_43 ECOLI_43 Escherichia coli 562 10122628

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871616	13403	35559	765	254

Description

6500732648 apag:b0050 apag protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0050 b0050 Escherichia coli 562 -11536506 233585 apag (de:apag protein) (db:swissprot) APAG_ECOLI P05636 ESCHERICHIA COLI 562 -11536506 131323 apag apag protein (cl:apag protein) (db:pir1.dat) (mp:1 min) BVECAG A30273 Escherichia coli 562 -11536506 5000691355 (db:genpept-bct1) (de:e. coli apah gene for diadenosine tetraphosphatase.) (nt:urf (apag) (aa 1-375)) (le:1027) (re:1404) (di:direct) ECAPAH X04711 g40918 Escherichia coli 562 -11536506 7500876978 apag apag protein (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:50888) (re:51265) (di:complement) ECO110K D10483 g216475 Escherichia coli 562 -11536506 232360 apag orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 5 of 400 of the completegenome.) (nt:f125; 100 pct identical to apag_ecoli sw: p05636) (le:4067) (re:4444) (di:complement) AE000115 AE000115 g1786235 Escherichia coli 562 -11536506 7502852291 (db:genpept) (de:e. coli apah gene for diadenosine tetraphosphatase.) (nt:urf (apag) (aa 1-375)) (le:1027) (re:1404) (di:direct) ECAPAH X04711 g40918 Escherichia coli 562 -11536506 59780 apag (de:apag protein) (db:swissprot) APAG_ECOLI P05636 ESCHERICHIA COLI 562 -11536506

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871622	13404	35560	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871636	13405	35561	381	126

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871637	13406	35562	339	112

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871644	13407	35563	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871654	13408	35564	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871666	13409	35565	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871670	13410	35566	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871671	13411	35567	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871688	13412	35568	3999	1333

Description

6500732649 sura:b0053 survival protein sura precursor:peptidyl-prolyl
cis-trans isomerase sura:ppiase:rotamase c (gtcfc:14.3) (ec:5.2.1.8)
(keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0053 b0053
Escherichia coli 562 -11536507 99886 sura (ec:5.2.1.8) (de:sura), (ppiase)
(rotamase c)) (db:swissprot) SURA_ECOLI P21202 ESCHERICHIA COLI 562
-11536507 7000686700 sura probable peptidylprolyl isomerase:sura
precursor:survival protein sura (ec:5.2.1.8) (db:pir2.dat) (mp:1 min) E64726
E64726 Escherichia coli 562 -11536507 7500892274 sura survival protein
(fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 5 of 400 of the completgenome.) (nt:f428; 99 pct identical
(1 gap) to sura_ecoli) (le:6254) (re:7540) (di:complement) AE000115 AE000115
g1786238 Escherichia coli 562 -11536507 5000691356 (de:(ecoli_53)
(pn:survival protein sura precursor) (gn:sura) (gtcfc:13.7:14.1)
(ec:5.2.1.8) (sura_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia
coli)) ECOLI_53 ECOLI_53 Escherichia coli 562 10122633

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871689	13413	35569	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871690	13414	35570	1473	490

Description

6500732650 imp:osta:b0054 organic solvent tolerance protein precursor
(gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0054
b0054 Escherichia coli 562 -11536508 87921 imp:osta (de:organic solvent
tolerance protein precursor) (db:swissprot) OSTA_ECOLI P31554 ESCHERICHIA
COLI 562 -11536508 7000686062 imp organic solvent tolerance protein
precursor (cl:organic solvent tolerance protein) (db:pir2.dat) F64726 F64726
Escherichia coli 562 -11536508 5000691357 osta/imp (sr:escherichia coli
(strain:k-12, sub_strain:ost4251) dna) (db:genpept-bct2) (de:escherichia
coli yabh (pseudo), is5, is2, osta/imp and sura genes, comlete and partial
cds.) (le:3716) (re:6070) (di:direct) AB013134 AB013134 g3834368 Escherichia
coli 562 -11536508 7500887377 imp organic solvent tolerance (fn:phenotype;
adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli
k-12 mg1655 section 5 of 400 of the completgenome.) (nt:f784; 99 pct
identical to osta_ecoli sw: p31554) (le:7593) (re:9947) (di:complement)
AE000115 AE000115 g1786239 Escherichia coli 562 -11536508

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871691	13415	35571	1032	343

Description

6500732651 ftsi:pbpb:b0084 penicillin-binding protein 3 precursor:pbp-3 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0084 b0084 Escherichia coli 562 -11536509 227991 ftsi:pbpb (de:penicillin-binding protein 3 precursor (pbp-3)) (db:swissprot) PBP3_ECOLI P04286 ESCHERICHIA COLI 562 -11536509 130780 ftsi:pbpb penicillin-binding protein 3 precursor (cl:penicillin-binding protein 3) (db:pir1.dat) (mp:2 min) ZPECP3 A93123 Escherichia coli 562 -11536509 5000691370 pbp3 pbp3 protein (db:genpept-bct1) (de:e. coli 2 minute region.) (le:7943) (re:9709) (di:direct) EC2MIN X55034 g40852 Escherichia coli 562 -11536509 235361 ftsi penicillin-binding protein 3 precursor (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e.coli k12 genome, 0-2.4min. region.) (le:91067) (re:92833) (di:direct) ECO110K D10483 g216498 Escherichia coli 562 -11536509 304528 pbpb (sr:escherichia coli dna) (db:genpept-bct1) (de:e.coli pbpb gene (ftsi) coding for penicillin-binding protein 3.) (nt:penicillin-binding protein 3) (le:628) (re:2394) (di:direct) ECOPBPB K00137 g147111 Escherichia coli 562 -11536509 233608 ftsi septum formation:penicillin-binding protein 3 (fn:enzyme; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 8 of 400 of the completegenome.) (nt:o588; 100 pct identical to pbp3_ecoli sw: p04286) (le:7868) (re:9634) (di:direct) AE000118 AE000118 g1786272 Escherichia coli 562 -11536509 88731 ftsi:pbpb (de:penicillin-binding protein 3 precursor (pbp-3)) (db:swissprot) PBP3_ECOLI P04286 ESCHERICHIA COLI 562 -11536509

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871693	13416	35572	324	107

Description

6500732652 hofc:hopc:b0106 protein transport protein hofc (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0106 b0106 Escherichia coli 562 -11536510 77453 hofc:hopc (de:protein transport protein hofc) (db:swissprot) HOF_CECOLI P36646 ESCHERICHIA COLI 562 -11536510 7000685548 hofc:hopc protein transport protein hofc (cl:secretion protein xcps) (db:pir2.dat) B64733 B64733 Escherichia coli 562 -11536510 7500883452 hofc putative integral membrane protein involved in (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.) (nt:f400; 100 pct identical to 361 residues) (le:9278) (re:10480) (di:complement) AE000119 AE000119 g1786295 Escherichia coli 562 -11536510 5000691377 (de:(ecoli_106) (pn:protein transport protein hofc) (gn:hofc) (gtcfc:13.7:14.1) (ec: (hofc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_106 ECOLI_106 Escherichia coli 562 10122661

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871713	13417	35573	558	185

Description

6500732653 hofb:hopb:b0107 protein transport protein hofb (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0107 b0107 Escherichia coli 562 -11536511 77451 hofb:hopb (de:protein transport protein hofb) (db:swissprot) HOFB_ECOLI P36645 ESCHERICHIA COLI 562 -11536511 7000685547 hofb:hopb protein transport protein hofb (cl:secretion protein xcpr) (db:pir2.dat) C64733 C64733 Escherichia coli 562 -11536511 7500883450 hofb putative integral membrane protein involved in (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.) (nt:f461; 99 pct identical to hofb_ecoli sw: p36645) (le:10470) (re:11855) (di:complement) AE000119 AE000119 g1786296 Escherichia coli 562 -11536511 5000691378 (de:(ecoli_107) (pn:protein transport protein hofb) (gn:hofb) (gtcfc:13.7:14.1) (ec:) (hofb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_107 ECOLI_107 Escherichia coli 562 10122662

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871726	13418	35574	606	201

Description

6500732654 ppdd:b0108 prepilin peptidase dependent protein d precursor (gtcfc:10.11:12.8) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0108 b0108 Escherichia coli 562 -11536512 90763 ppdd (de:prepilin peptidase dependent protein d precursor) (db:swissprot) PPDD_ECOLI P36647 ESCHERICHIA COLI 562 -11536512 7000686164 ppdd prepilin peptidase dependent protein d precursor (cl:gonococcal fimbrial protein) (db:pir2.dat) D64733 D64733 Escherichia coli 562 -11536512 233786 ppdd prelipin peptidase dependent protein (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 9 of 400 of the completegenome.) (nt:f146; 100 pct identical to ppdd_ecoli sw: p36647) (le:11865) (re:12305) (di:complement) AE000119 AE000119 g1786297 Escherichia coli 562 -11536512 7500888357 ppdd prepilin-like peptidase dependent protein (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:escherichia coli ampd gene; quinolinate phosphoribosyltransferase(nadc) gene; prepilin-like peptidase dependent protein (ppdd) gene;hopb, hopc genes; gmp reductase (guac) gene.) (le:1472) (r... ECOAMPHSM L28105 g456042 Escherichia coli 562 -11536512 5000691379 (de:(ecoli_108) (pn:prepilin peptidase dependent protein d precursor function unknown) (gn:ppdd) (gtcfc:13.7:14.1) (ec:) (ppdd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_108 ECOLI_108 Escherichia coli 562 10032878

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871732	13419	35575	270	89

Description

6500732655 hrpb:b0148 atp-dependent helicase hrpb (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0148 b0148 Escherichia coli 562 -11536513 7000690858 hrpb atp-dependent helicase hrpb (cl:atp-dependent rna helicase hrpb:dead/h box helicase homology) (db:pir2.dat) D64738 D64738 Escherichia coli 562 -11536513 7500954375 hrpb helicase:atp-dependent (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 14 of 400 of the completegenome.) (nt:o824; 99 pct identical to 746 residues of) (le:1397) (re:3871) (di:direct) AE000124 AE000124 g1786342 Escherichia coli 562 -11536513 5000691398 (de:(ecoli_148) (pn:helicase, atp-dependent) (gn:hrpb) (gtcfc:13.7:14.1) (ec:) (hrpb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_148 ECOLI_148 Escherichia coli 562 10122681

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871751	13420	35576	438	145

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871754	13421	35577	1833	610

Description

6500732656 pfs:b0159 pfs protein:protein:p46 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0159 b0159 Escherichia coli 562 -11536514 89207 pfs (ec:3.2.2.16:3.2.2.9) (de:nucleosidase, (mta/sah nucleosidase) (p46)) (db:swissprot) PFS_ECOLI P24247 ESCHERICHIA COLI 562 -11536514 164441 pfs pfs protein:purine nucleoside phosphorylase homolog (cl:escherichia coli pfs protein) (db:pir2.dat) S45227 S45227 Escherichia coli 562 -11536514 239788 orf (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genome, 2.4-4.1 min region (110,917-193,643 bpfrom 0 min).) (nt:'purine nucleoside phosphorylase (deod) homology') (le:67051) (re:67749) (di:... ECO82K D26562 g473817 Escherichia coli 562 -11536514 301628 (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:similar to purine nucleoside phosphorylase (deod)) (le:9530) (re:10228) (di:complement) ECU70214 U70214 g1552737 Escherichia coli 562 -11536514 233690 pfs orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 15 of 400 of the completgenome.) (nt:f232; 100 pct identical to pfs_ecoli sw:) (le:4962) (re:5660) (di:complement) AE000125 AE000125 g1786354 Escherichia coli 562 -11536514 7000686124 mta/sah nucleosidase (db:genpept-bct2) (de:escherichia coli mta/sah nucleosidase gene, complete cds.) (le:1) (re:699) (di:direct) ECU24438 U24438 g2981267 Escherichia coli 562 -11536514 5000691403 (de:(ecoli_159) (pn:protein:p46) (gn:pfs) (gtcfc:13.7:14.1) (ec:) (pfs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_159 ECOLI_159 Escherichia coli 562 10031330

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871759	13422	35578	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871760	13423	35579	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871768	13424	35580	1563	520

Description

6500732657 mesj:b0188 cell cycle protein mesj (gtcfc:12.8) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0188 b0188 Escherichia coli 562 -11536515 83522 mesj (de:cell cycle protein mesj) (db:swissprot) MESJ_ECOLI P52097 ESCHERICHIA COLI 562 -11536515 7000685833 mesj cell cycle protein mesj (cl:hypothetical protein hi0404) (db:pir2.dat) D64743 D64743 Escherichia coli 562 -11536515 222546 yaen:a hypotheticala....:function yaen (sr:escherichia coli (strain:k-12, isolate:w3110) dna) (db:genpept-bct1) (de:escherichia coli genes for dnae, acca, ldcc, yaer, yaen, yaeo,yaep, yaeq, yaej, nlpe, yaef complete cds and partial cds.) (nt:similarity to yrd0_bacsu, ac p37563 in swiss-prot... D49445 D49445 g1122208 Escherichia coli 562 -11536515 239816 mesj (db:genpept-bct1) (de:e.coli orfs and mesj gene.) (nt:similar to acc.no. d26185) (le:991) (re:2289) (di:direct) ECMESJORF Z50870 g971394 Escherichia coli 562 -11536515 7500885508 yaen (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (nt:hypothetical) (le:43406) (re:44704) (di:direct) ECU70214 U70214 g1552765 Escherichia coli 562 -11536515 233375 mesj cell cycle protein (fn:orf; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 18 of 400 of the completegenome.) (nt:o432; 100 pct identical to mesj_ecoli sw: p52097) (le:2732) (re:4030) (di:direct) AE000128 AE000128 g1786386 Escherichia coli 562 -11536515 5000691413 (de:(ecoli_188) (pn:cell cycle protein mesj) (gn:mesj) (gtcfc:13.7:14.1) (ec:) (mesj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_188 ECOLI_188 Escherichia coli 562 10025736

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501871772	13425	35581	777	258

Description

6500732658 cutf:nlpe:b0192 copper homeostasis protein precursor:copper homeostasis protein cutf precursor:lipoprotein nlpe (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0192 b0192 Escherichia coli 562 -11536516 66851 cutf:nlpe (de:copper homeostasis protein cutf precursor (lipoprotein nlpe)) (db:swissprot) CUTF_ECOLI P40710 ESCHERICHIA COLI 562 -11536516 7000684943 cutf:nlpe copper homeostasis protein cutf precursor:lipoprotein nlpe (db:pir2.dat) H64743 H64743 Escherichia coli 562 -11536516 222551 nlpe nlpe:a lipoprotein (sr:escherichia coli (strain:k-12, isolate:w3110) dna) (db:genpept-bct1) (de:escherichia coli genes for dnae, acca, ldcc, yaer, yaen, yaeo,yaep, yaeq, yaej, nlpe, yaef complete cds and partial cds.) (le:6736) (re:7446) (di:direct) D49445 D49445 g1122213 Escherichia coli 562 -11536516 236177 cutf lipoprotein (fn:copper homeostasis) (sr:escherichia coli (strain mc4100) (clone: 1) dna) (db:genpept-bct1) (de:escherichia coli orf 140, lipoprotein (cutf), and lipoprotein(orf292) genes, complete cds.) (nt:amino acid features: lipobox (lmgc), aa 18-21,) (le:726) ... ECOCUTF L38619 g845337 Escherichia coli 562 -11536516 238737 nlpe lipoprotein nlpe (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:24825) (re:25535) (di:direct) ECOTSF D83536 g1208959 Escherichia coli 562 -11536516 239819 nlpe nlpe precursor (db:genpept-bct1) (de:escherichia coli outer membrane lipoprotein nlpe precursor (nlpe)gene, complete cds, and yaef gene, partial cds.) (nt:outer membrane lipoprotein; multi-copy suppressor) (le:390) (re:1100) (di:direct) ECU18345 U18345 g619673 Escherichia coli 562 -11536516 303254 nlpe lipoprotein nlpe (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:46344) (re:47054) (di:direct) ECU70214 U70214 g1552768 Escherichia coli 562 -11536516 234074 cutf copper homeostasis protein lipoprotein (fn:putative transport; detoxification) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 18 of 400 of the completegenome.) (nt:o236; 100 pct identical to cutf_ecoli sw: p40710;) (le:5670) (re:6380) (di:direct) AE000128 AE000128 g1786390 Escherichia coli 562 -11536516 5000691417 (de:(ecoli_192) (pn:copper homeostasis protein cutf precursor:lipoprotein nlpe) (gn:cutf) (gtcfc:13.7:14.1) (ec:) (cutf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_192 ECOLI_192 Escherichia coli 562 10009469

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871783	13426	35582	414	137

Description

6500732659 gmha:lpca:trfa:b0222 phosphoheptose isomerase (gtcfc:14.3) (ec:5.-.-.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0222 b0222 Escherichia coli 562 -11536517 74225 lpca:gmha:tfra (ec:5.-.-.-) (de:phosphoheptose isomerase,) (db:swissprot) LPCA_ECOLI P51001 ESCHERICHIA COLI 562 -11536517 7000685761 gmha phosphoheptose isomerase:gmha (cl:phosphoheptose isomerase) (ec:5.-.-.-) (db:pir2.dat) G64746 G64746 Escherichia coli 562 -11536517 239434 yafi (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohara') (db:genpept-bct1) (de:escherichia coli genes for 'yafh, yafi, yafj, yafk, yafq, dinj,yafl, yafm, fhia, mbha, dinp, yafn, yafo and yafp.) (nt:a weak similarity to yngb_clope (swiss... ECODINJ D38582 g984578 Escherichia coli 562 -11536517 234156 gmha phosphoheptose isomerase (fn:enzyme; surface polysaccharides and antigens) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 21 of 400 of the completegenome.) (nt:ol92; 100 pct identical to gmha_ecoli sw: p51001;) (le:132) (re:710) (di:direct) AE000131 AE000131 g1786416 Escherichia coli 562 -11536517 7500885109 gmha phosphoheptose isomerase (fn:synthesis of glyceromannoheptose 7-phosphate) (db:genpept-bct2) (de:escherichia coli phosphoheptose isomerase (gmha) gene, completecds.) (le:417) (re:995) (di:direct) ECU32590 U32590 g1079568 Escherichia coli 562 -11536517 5000691434 (de:(ecoli_215) (pn:lipopolysaccharide core biosynthesis; resistance to phages t4, t7, and p1; deficiency in conjugation) (gn:gmha) (gtcfc:13.7:14.1) (ec:5.-.-.-) (gmha_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia co) ECOLI_215 ECOLI_215 Escherichia coli 562 10016747

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871796	13427	35583	954	317

Description

6500732660 tra8_1:b0256 transposase for insertion sequence element is30 (gtcfc:13.5) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0256 b0256 Escherichia coli 562 -11536518 7500974856 is30 transposase (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:100902) (re:102053) (di:direct) ECU70214 U70214 g1552823 Escherichia coli 562 -11536518 239874 tra8_1 is30 transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 23 of 400 of the completegenome.) (nt:99 pct identical to tra8_ecoli sw: p37246) (le:6397) (re:7548) (di:direct) AE000133 AE000133 g1786450 Escherichia coli 562 -11536518 5000691459 (de:(ecoli_247) (pn:transposase for insertion sequence element is30) (gn:tra8_1) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_247 ECOLI_247 Escherichia coli 562 10122728

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871813	13428	35584	951	316

Description

6500732661 insb_2:insb_3:b0264 insertion element is1 protein insb
(gtcf:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0264
b0264 Escherichia coli 562 -11536519 157305 insb_4 insb protein (cl:insb
protein) (db:pir1.dat) IEECA1 JN0137 Escherichia coli 562 -11536519
7500953706 insb (sr:escherichia coli dna; insertion sequence dna; insertion
sequenc) (db:genpept-bct1) (de:escherichia coli insa gene, complete cds;
insb gene, complete cds.) (le:1570) (re:2073) (di:direct) ECOINSAB L20943
g304902 Escherichia coli 562 -11536519 7500953707 insb insb
(db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:120947)
(re:121450) (di:complement) ECU70214 U70214 g1552843 Escherichia coli 562
-11536519 234872 insb_2 is1 protein insb (fn:is, phage, tn;
transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 24 of 400 of the completegenome.) (nt:f167; 96 pct identical
to isb_ecoli sw: p03830) (le:3983) (re:4486) (di:complement) AE000134
AE000134 g1786459 Escherichia coli 562 -11536519 239894 insb_3 is1 protein
insb (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 25 of 400 of the completegenome.)
(nt:f167; 96 pct identical to isb_ecoli sw: p03830) (le:5398) (re:5901)
(di:complement) AE000135 AE000135 g1786470 Escherichia coli 562 -11536519
5000691467 (de:(ecoli_255) (pn:insertion element is1 protein insb)
(gn:insb_1:insb_2) (gtcf:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_255 ECOLI_255 Escherichia coli 562 10083658

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501871817	13429	35585	378	125

Description

5000691468 insa_2:insa_3:b0265 insertion element is1 protein insa (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0265 b0265 Escherichia coli 562 -11536520 135230 insa_3 insa protein (cl:insa protein) (db:pir1.dat) IEECB9 B93826 Escherichia coli 562 -11536520 223313 insa hypothetical protein insa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.2 - 22.6 min).) (le:15756) (re:16031) (di:direct) D90735 D90735 g1651482 Escherichia coli 562 -11536520 223315 insa hypothetical protein insa (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.5 - 22.9 min).) (le:4328) (re:4603) (di:direct) D90736 D90736 g1651485 Escherichia coli 562 -11536520 233242 (db:genpept-bct1) (de:e. coli dna with is1b and is30b insertion sequences.) (nt:insa peptide (aa 1-91)) (le:480) (re:755) (di:complement) ECIS1B X17345 g581113 Escherichia coli 562 -11536520 234871 (db:genpept-bct1) (de:escherichia coli dna for insertion sequence is1c.) (nt:insa peptide (aa 1-91)) (le:496) (re:771) (di:complement) ECIS1C X52535 g581114 Escherichia coli 562 -11536520 236221 (db:genpept-bct1) (de:escherichia coli dna for insertion sequence is1d.) (nt:insa peptide (aa 1-91)) (le:156) (re:431) (di:direct) ECIS1D X52536 g581115 Escherichia coli 562 -11536520 239884 insa (sr:escherichia coli dna; insertion sequence dna; insertion sequenc) (db:genpept-bct1) (de:escherichia coli insa gene, complete cds; insb gene, complete cds.) (le:1376) (re:1651) (di:direct) ECOINSAB L20943 g304901 Escherichia coli 562 -11536520 256249 hypothetical protein insa (sr:escherichia coli (strain:k12) dna) (db:genpept-bct1) (de:escherichia coli genome, 4.0 - 6.0 min region.) (le:88423) (re:88698) (di:complement) ECOTSF D83536 g1209003 Escherichia coli 562 -11536520 303298 insa insa (db:genpept-bct1) (de:escherichia coli chromosome minutes 4-6.) (le:109899) (re:110174) (di:complement) ECU70214 U70214 g1552833 Escherichia coli 562 -11536520 408121 insa (sr:insertion sequence is1 dna; transposon tn21 dna; and plasmid r10) (db:genpept-bct1) (de:plasmid r100 (beginning at 88.6 min.) is1r insertion element,mercuric ion resistance operon and transposon tn21.) (nt:putative) (le:158) (re:433) (di:direct) R1004 J01730 g294459 Plasmid R100 28399 -11536520 233239 insa_2 is1 protein insa (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 24 of 400 of the completegenome.) (nt:f91; 98 pct identical to isa1_ecoli sw: p03827) (le:4405) (re:4680) (di:complement) AE000134 AE000134 g1786460 Escherichia coli 562 -11536520 233241 insa_3 is1 protein insa (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 25 of 400 of the completegenome.) (nt:f91; 98 pct identical to isa1_ecoli sw: p03827) (le:5820) (re:6095) (di:complement) AE000135 AE000135 g1786471 Escherichia coli 562 -11536520 7500953705 insa (fn:transposition of insertion sequence is/r) (sr:artificial gene dna) (db:genpept-syn) (de:synthetic insertion sequence is/r encoding insa and insb genes bothessential for transposition.) (le:65) (re:340) (di:direct) SYNISR M27083 g755078 artificial sequence 81077 -11536520 7502852292 insa insa protein

g755078 artificial sequence 81077 -11536520 7502852292 insa insa protein
~~(sr:escherichia coli (strain:k12) dna, clone:kobara clone #225) (db:genpept)~~

ORF Name	NT ID	AA ID	NT	AA
			LENGTH	LENGTH
7501871820	13430	35586	1098	365
Description				

6500732663 eaeh:b0297 attaching and effacing protein homolog:attaching and effacing protein homolog precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0297 b0297 Escherichia coli 562 -11536521 69622 eaeh (de:attaching and effacing protein homolog precursor) (db:swissprot) EAEH_ECOLI P36943 ESCHERICHIA COLI 562 -11536521 7000685130 eaeh attaching and effacing protein homolog eaeh precursor (db:pir2.dat) A64756 A64756 Escherichia coli 562 -11536521 7500880782 eaeh (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:similar to attaching and effacing protein) (le:22155) (re:23042) (di:direct) ECU73857 U73857 g1657497 Escherichia coli 562 -11536521 239918 eaeh attaching and effacing protein:pathogenesis (fn:factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:o295; 100 pct identical to fragment eaeh_ecoli) (le:1973) (re:2860) (di:direct) AE000137 AE000137 g1786488 Escherichia coli 562 -11536521 5000691490 (de:(ecoli_281) (pn:attaching and effacing protein homolog:fragment) (gn:eaeh) (gtcfc:13.7:14.1) (ec:) (eaeh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_281 ECOLI_281 Escherichia coli 562 10122756

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501871822	13431	35587	549	182

Description

5000691491 tra5_1:tra5_2:tra5_3:tra5_4:b0299 hypothetical protein:putative transposase for insertion sequence is3 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.7.0) (db:gtc-escherichia coli) b0299 b0299 Escherichia coli 562 -11536522 7000689429 tra5_4 probable transposase (cl:transposase is3) (db:pir1.dat) TQECI3 C64756 Escherichia coli 562 -11536522 224624 is3 putative transposase for insertion sequence (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #357(46.5-46.8 min..)) (nt:orf_id:o357#13; similar to (swissprot accession) (le:13284) (re:14150) (di:direct) D90846 D90846 g1736794 Escherichia coli 562 -11536522 224635 is3 putative transposase for insertion sequence (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #358(46.6-46.9 min..)) (nt:orf_id:o357#13; similar to (swissprot accession) (le:7929) (re:8795) (di:direct) D90847 D90847 g1736806 Escherichia coli 562 -11536522 7500953648 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:putative transposase for insertion sequence is3) (le:23385) (re:24251) (di:direct) ECU73857 U73857 g1657499 Escherichia coli 562 -11536522 7500953649 (db:genpept-bct1) (de:escherichia coli chromosome minutes 6-8.) (nt:putative transposase for insertion sequence is3) (le:99329) (re:100195) (di:complement) ECU73857 U73857 g1657567 Escherichia coli 562 -11536522 7500953650 putative transposase (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:product of insertion sequence is3) (le:7769) (re:8635) (di:direct) ECU82598 U82598 g1778455 Escherichia coli 562 -11536522 239920 tra5_5 is3 putative transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 27 of 400 of the completegenome.) (nt:o288) (le:3203) (re:4069) (di:direct) AE000137 AE000137 g1786490 Escherichia coli 562 -11536522 239988 tra5_1 is3 putative transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 34 of 400 of the completegenome.) (nt:f288; 99 pct identical to tra5_ecoli sw: p05822) (le:1561) (re:2427) (di:complement) AE000144 AE000144 g1786570 Escherichia coli 562 -11536522 240051 tra5_2 is3 putative transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 50 of 400 of the completegenome.) (nt:o288; 99 pct identical to tra5_ecoli sw: p05822) (le:486) (re:1352) (di:direct) AE000160 AE000160 g1786753 Escherichia coli 562 -11536522 301264 tra5_3 is3 putative transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 94 of 400 of the completegenome.) (nt:f288; 99 pct identical to tra5_ecoli sw: p05822) (le:9486) (re:10352) (di:complement) AE000204 AE000204 g1787263 Escherichia coli 562 -11536522 301275 tra5_4 is3 putative transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 188 of 400 of the completegenome.) (nt:o288; 99 pct identical to tra5_ecoli sw: p05822) (le:5488) (re:6354) (di:direct) AE000298 AE000298 g1788405 Escherichia coli

(le:5488) (re:6354) (di:direct) AE000298 AE000298 g1788405 Escherichia coli
562 -11536522 6500732664 tra5_1:tra5_2:tra5_3:tra5_4 hypothetical

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501871824	13432	35588	495	164

Description

6500732665 araj:b0396 araj protein precursor:protein araj precursor
(gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0396
b0396 Escherichia coli 562 -11536523 59971 araj (de:protein araj precursor)
(db:swissprot) ARAJ_ECOLI P23910 ESCHERICHIA COLI 562 -11536523 162748 araj
chloramphenicol resistance protein homolog araj precursor (cl:streptomyces
lividans chloramphenicol resistance protein) (db:pir2.dat) (mp:9 min) B43750
B43750 Escherichia coli 562 -11536523 7500877067 araj (sr:e.coli dna)
(db:genpept-bct1) (de:e.coli sbcc gene, 3' end, araj gene, complete cds, and
araj orf.) (le:2143) (re:3327) (di:direct) ECOARAJ M64787 g145328
Escherichia coli 562 -11536523 233833 araj involved in either transport or
processing of (fn:transport; degradation of small molecules:)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 35 of 400 of the
completegenome.) (nt:f394; 100 pct identical to araj_ecoli sw: p23910)
(le:10173) (re:11357) (di:complement) AE000145 AE000145 g1786595 Escherichia
coli 562 -11536523 5000691562 (de:(ecoli_380) (pn:involved in either
transport or processing arabinose polymers) (gn:araj) (gtcfc:13.7:14.1)
(ec:) (araj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_380 ECOLI_380 Escherichia coli 562 10002704

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871826	13433	35589	816	271

Description

6500732666 thij:b0424 thij protein:4-methyl-5-b-hydroxyethyl-thiazole monophosphate biosynthesis enzyme (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0424 b0424 Escherichia coli 562 -11536524 120487 thij (de:enzyme) (db:swissprot) THIJ_ECOLI Q46948 ESCHERICHIA COLI 562 -11536524 7000686791 thij hydroxymethylpyrimidine kinase (cl:signal transduction protein dj-1) (ec:2.7.1.49) (db:pir2.dat) H64771 H64771 Escherichia coli 562 -11536524 240201 thij thij (fn:4-methyl-5(b-hydroxyethyl)-thiazole) (db:genpept-bct1) (de:escherichia coli 4-methyl-5(b-hydroxyethyl)-thiazole monophosphatebiosynthetic (thij) gene, complete cds, and apba gene, partial cds.) (le:332) (re:928) (di:direct) ECU34923 U34923 gl100872 Escherichia coli 562 -11536524 7500893069 thij 4-methyl-5 b-hydroxyethyl -thiazole (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:22501) (re:23097) (di:complement) ECU82664 U82664 gl773108 Escherichia coli 562 -11536524 239444 thij 4-methyl-5 beta-hydroxyethyl -thiazole (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 38 of 400 of the completgenome.) (nt:f198; 100 pct identical to gb: ecu34923_2) (le:10125) (re:10721) (di:complement) AE000148 AE000148 gl786626 Escherichia coli 562 -11536524 5000691574 (de:(ecoli_408) (pn:function not assigned) (gn:thij) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_408 ECOLI_408 Escherichia coli 562 10063508

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871833	13434	35590	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871846	13435	35591	465	154

Description

6500732667 cof:b0446 cof protein:protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0446 b0446 Escherichia coli 562 -11536525 7000690863 cof cof protein (cl:hypothetical protein hi0597) (db:pir2.dat) F64774 F64774 Escherichia coli 562 -11536525 240223 cof cof (fn:complementing deletion mutant for growth on) (db:genpept-bct1) (de:e.coli cof and ybae genes.) (nt:gtg start codon; another possible start codon at) (le:1162) (re:1992) (di:direct) ECCOFYBAE Z54355 g1019764 Escherichia coli 562 -11536525 7500959710 cof (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:46850) (re:47680) (di:direct) ECU82664 U82664 g1773130 Escherichia coli 562 -11536525 232534 cof orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 41 of 400 of the completegenome.) (nt:o276; 100 pct identical to cof_ecoli sw: p46891) (le:1851) (re:2681) (di:direct) AE000151 AE000151 g1786651 Escherichia coli 562 -11536525 5000691584 (de:(ecoli_430) (pn:protein) (gn:cof) (gtcfc:13.7:14.1) (ec:) (cof_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_430 ECOLI_430 Escherichia coli 562 10122828

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871870	13436	35592	2715	904

Description

GTC ORF with score 701 to: (db:genpept-bct2) (de:myxococcus xanthus saframycin mx1 synthetase b (safb), saframycinmx1 synthetase a (safa), and safc genes, complete cds.) (nt:contains two putative amino acid activating) (le:5491) (re:13308) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871897	13437	35593	417	138

Description

6500732668 glnk:b0450 nitrogen regulatory protein p-ii:nitrogen regulatory protein p-ii 2 (gtcfc:2.6) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0450 b0450 Escherichia coli 562 -11536526 73990 glnk (de:nitrogen regulatory protein p-ii 2) (db:swissprot) GLNK_ECOLI P38504 ESCHERICHIA COLI 562 -11536526 7000685410 glnk nitrogen regulatory protein p-ii.2 (cl:regulatory protein p-ii) (db:pir2.dat) B64775 B64775 Escherichia coli 562 -11536526 239575 glnk nitrogen regulatory protein p-ii 2 (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 41 of 400 of the completegenome.) (nt:o112; 100 pct identical to glnk_ecoli sw: p38504) (le:7049) (re:7387) (di:direct) AE000151 AE000151 g1786655 Escherichia coli 562 -11536526 7500882474 glnk glnk (fn:glutamine synthetase activity regulation) (sr:escherichia coli strain=k12) (db:genpept-bct2) (de:escherichia coli pii-homolog (glnk) gene, complete cds, putativeammonium transporter (amtb) gene, complete cds, and thioesterase ii(tesb) gene, partial... ECU40429 U40429 g1103923 Escherichia coli 562 -11536526 5000691586 (de:(ecoli_434) (pn:nitrogen regulatory protein p-ii 2) (gn:glnk) (gtcfc:13.7:14.1) (ec:) (glnk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_434 ECOLI_434 Escherichia coli 562 10016520

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871905	13438	35594	1140	379

Description

6500732669 acrr:b0464 potential acrab operon repressor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0464 b0464 Escherichia coli 562 -11536527 58302 acrr (de:potential acrab operon repressor) (db:swissprot) ACRR_ECOLI P34000 ESCHERICHIA COLI 562 -11536527 7000684508 acrr transcription regulator acrr:acrab operon repressor protein (cl:probable transcription repressor mtrr) (db:pir2.dat) G64776 G64776 Escherichia coli 562 -11536527 240239 acrr 25 kda protein (fn:potential regulator protein for acrae genes) (db:genpept-bct1) (de:escherichia coli acra, acrb, and acrr genes, complete cds.) (le:307) (re:954) (di:complement) ECU00734 U00734 g532309 Escherichia coli 562 -11536527 7500876378 acrr potential acrab operon repressor (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:65209) (re:65856) (di:direct) ECU82664 U82664 g1773146 Escherichia coli 562 -11536527 238441 acrr acrab operon repressor (fn:regulator; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 42 of 400 of the completegenome.) (nt:o215; 100 pct identical to acrr_ecoli sw: p34000) (le:9175) (re:9822) (di:direct) AE000152 AE000152 g1786669 Escherichia coli 562 -11536527 5000691595 (de:(ecoli_447) (pn:potential acrab operon repressor) (gn:acrr) (gtcfc:13.7:14.1) (ec:) (acrr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_447 ECOLI_447 Escherichia coli 562 10001082

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871906	13439	35595	183	60
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501871910	13440	35596	486	161
<u>Description</u>				

6500732670 recr:b0472 recombination protein recr (gtcfc:10.8) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0472 b0472 Escherichia coli 562 -11536528 240247 recr (de:recombination protein recr) (db:swissprot) RECR_ECOLI P12727 ESCHERICHIA COLI 562 -11536528 131405 recr recombination protein recr (cl:recr protein) (db:pir1.dat) BVECRR JU0106 Escherichia coli 562 -11536528 5000691600 (db:genpept-bct1) (de:e. coli recr gene.) (nt:recr product (aa 1-201)) (le:309) (re:914) (di:direct) ECRECR X15761 g42697 Escherichia coli 562 -11536528 7500889590 recr (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:73853) (re:74458) (di:direct) ECU82664 U82664 g1773154 Escherichia coli 562 -11536528 238040 recr recombination and repair (fn:putative enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 43 of 400 of the completegenome.) (nt:o201; 99 pct identical to recr_ecoli sw: p12727) (le:4431) (re:5036) (di:direct) AE000153 AE000153 g1786678 Escherichia coli 562 -11536528 93831 recr (de:recombination protein recr) (db:swissprot) RECR_ECOLI P12727 ESCHERICHIA COLI 562 -11536528

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871914	13441	35597	651	216

Description

6500732671 fsr:b0479 fosmidomycin resistance protein (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0479 b0479 Escherichia coli 562 -11536529 72412 fsr (de:fosmidomycin resistance protein) (db:swissprot) FSR_ECOLI P52067 ESCHERICHIA COLI 562 -11536529 1500685226 fsr fosmidomycin resistance protein (cl:fosmidomycin resistance protein) (db:pir2.dat) JC5041 JC5041 Escherichia coli 562 -11536529 240254 fsr fosmidomycin resistance protein (fn:the protein confers the resistance against) (sr:escherichia coli (strain:dh5alpha) dna) (db:genpept-bct1) (de:escherichia coli fsr gene for fosmidomycin resistance protein,complete cds.) (le:342) (re:1562) (di:direct) ECOFSR D73370 g1019360 Escherichia coli 562 -11536529 301373 fsr fosmidomycin resistance protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:82924) (re:84144) (di:complement) ECU82664 U82664 g1773161 Escherichia coli 562 -11536529 234401 fsr fosmidomycin resistance protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 44 of 400 of the completegenome.) (nt:f406; 100 pct identical to fsr_ecoli sw: p52067) (le:3457) (re:4677) (di:complement) AE000154 AE000154 g1786686 Escherichia coli 562 -11536529 5000691603 (de:(ecoli_462) (pn:fosmidomycin resistance protein) (gn:fsr) (gtcfc:13.7:14.1) (ec:)) (fsr_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_462 ECOLI_462 Escherichia coli 562 10014963

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871922	13442	35598	804	267

Description

6500732672 rhsd:b0497 rhsd protein precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0497 b0497 Escherichia coli 562 -11536530 5000691619 rhsd (de:rhds protein precursor) (db:swissprot) RHSD_ECOLI P16919 ESCHERICHIA COLI 562 -11536530 7000691908 rhsd rhds protein precursor (cl:rhdsf protein) (db:pir2.dat) H64780 H64780 Escherichia coli 562 -11536530 7500960451 rhsd rhds precursor (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:102709) (re:106989) (di:direct) ECU82664 U82664 g1773179 Escherichia coli 562 -11536530 240272 rhsd rhds protein in rhs element (fn:orf; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 46 of 400 of the completegenome.) (nt:o1426; 99 pct identical to rhsd_ecoli sw: p16919) (le:246) (re:4526) (di:direct) AE000156 AE000156 g1786706 Escherichia coli 562 -11536530

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871933	13443	35599	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871940	13444	35600	2334	777

Description

6500732673 gip:b0508 glyoxylate-induced protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0508 b0508 Escherichia coli 562 -11536531 73628 gip (de:glyoxylate-induced protein) (db:swissprot) GIP_ECOLI P30147 ESCHERICHIA COLI 562 -11536531 163265 gip glyoxylate-induced protein gip (cl:conserved hypothetical protein hi1013) (db:pir2.dat) JT0746 JT0746 Escherichia coli 562 -11536531 240282 orf258 glyoxylate-induced protein (fn:unknown) (sr:escherichia coli (strain k-12) f- dna) (db:genpept-bct1) (de:escherichia coli glyoxylate carboligase (gcl) gene, andglyoxylate-induced protein gene of unknown function, complete cds.) (le:1923) (re:2699) (di:direct) ECOGCL L03845 g146120 Escherichia coli 562 -11536531 7500882369 gip glyoxylate-induced protein (db:genpept-bct1) (de:escherichia coli minutes 9 to 11 genomic sequence.) (le:115158) (re:115934) (di:direct) ECU82664 U82664 g1773189 Escherichia coli 562 -11536531 234467 gip glyoxylate-induced protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 47 of 400 of the completegenome.) (nt:o258; 100 pct identical to gip_ecoli sw: p30147) (le:1869) (re:2645) (di:direct) AE000157 AE000157 g1786718 Escherichia coli 562 -11536531 5000691629 (de:(ecoli_491) (pn:glyoxylate-induced protein) (gn:gip) (gtcfc:13.7:14.1) (ec:) (gip_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_491 ECOLI_491 Escherichia coli 562 10016162

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871945	13445	35601	501	166

Description

6500732674 intd:int:b0537 prophage dlp12 integrase:prophage qsr integrase (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0537 b0537 Escherichia coli 562 -11536532 234874 intd:int (de:prophage dlp12 integrase (prophage qsr' integrase)) (db:swissprot) INTD_ECOLI P24218 ESCHERICHIA COLI 562 -11536532 157212 intd prophage dlp12 integrase (cl:phage p22 integrase) (db:pir2.dat) A33497 A33497 Escherichia coli 562 -11536532 5000691650 int (db:genpept-bct1) (de:e.coli qsr' prophage region including int, dnay and bent-9.) (nt:highly homologous to p22 phage int) (le:1132) (re:2295) (di:complement) ECINTY X51662 g41811 Escherichia coli 562 -11536532 234875 (sr:e.coli (strain k12) dna, clones pdc1 and pdm1614) (db:genpept-bct1) (de:e.coli argu-trna gene overlap with prophage dlp12 integrase gene,complete cds.) (nt:dlp12 integrase) (le:165) (re:1328) (di:complement) ECOINTDLP M27155 g455171 Escherichia coli 562 -11536532 240047 (sr:escherichia coli (clone: pdc1) dna; and insertion sequence is) (db:genpept-bct1) (de:e.coli integrase gene, complete cds and argu-trna gene.) (nt:integrase) (le:942) (re:2105) (di:direct) ECOINTDLPT M31074 g146497 Insertion sequence IS3 2679 -11536532 7500884181 intd dlp12 integrase (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:prophage dlp12 integrase) (le:5446) (re:6609) (di:complement) ECU82598 U82598 g1778451 Escherichia coli 562 -11536532 233225 intd prophage dlp12 integrase (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 49 of 400 of the completegenome.) (nt:f387; 100 pct identical to intd_ecoli sw: p24218) (le:8238) (re:9401) (di:complement) AE000159 AE000159 g1786748 Escherichia coli 562 -11536532 79554 intd:int (de:prophage dlp12 integrase (prophage qsr' integrase)) (db:swissprot) INTD_ECOLI P24218 ESCHERICHIA COLI 562 -11536532

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871946	13446	35602	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871947	13447	35603	990	329

Description

6500732675 ybcs:b0555 bacteriophage lambda lysozyme homolog:probable endolysin:lysis protein:lysozyme (gtcfc:13.1) (ec:3.2.1.17) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0555 b0555 Escherichia coli 562 -11536533 4000707646 ybcs (ec:3.2.1.-) (de:probable endolysin, (lysis protein) (lysozyme)) (db:swissprot) LYCV_ECOLI P78285 ESCHERICHIA COLI 562 -11536533 7000685772 ybcs lysozyme::endolysin:lysis protein ybcs (cl:phage t4 lysozyme:phage t4 lysozyme homology) (ec:3.2.1.17) (db:pir2.dat) (mp:12 min) A64788 A64788 Escherichia coli 562 -11536533 7500885202 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:18244) (re:18741) (di:direct) ECU82598 U82598 g1778468 Escherichia coli 562 -11536533 240064 ybcs bacteriophage lambda lysozyme homolog (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (ec:3.2.1.17) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:ol65; 99 pct identical to lycv_bppa2 sw: p10439) (le:502) (re:999) (di:direct) AE000161 AE000161 g1786768 Escherichia coli 562 -11536533 5000691664 (de:(ecoli_537) (pn:bacteriophage lambda lysozyme homolog) (gtcfc:13.7:14.1) (ec:3.2.1.17) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_537 ECOLI_537 Escherichia coli 562 10122893

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871950	13448	35604	237	78

Description

6500732676 ybcu:b0557 bacteriophage lambda bor protein homolog:bor protein homolog precursor (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0557 b0557 Escherichia coli 562 -11536534 4000707645 ybcu (de:bor protein homolog precursor) (db:swissprot) VBOR_ECOLI P77330 ESCHERICHIA COLI 562 -11536534 7000686937 ybcu ybcu protein (db:pir2.dat) C64788 C64788 Escherichia coli 562 -11536534 7500894006 (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:19231) (re:19524) (di:complement) ECU82598 U82598 g1778470 Escherichia coli 562 -11536534 240066 ybcu bacteriophage lambda bor protein homolog (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:f97; 96 pct identical amino acid sequence and equal) (le:1489) (re:1782) (di:complement) AE000161 AE000161 g1786770 Escherichia coli 562 -11536534 5000691665 (de:(ecoli_539) (pn:bacteriophage lambda bor protein homolog) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_539 ECOLI_539 Escherichia coli 562 10122895

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871960	13449	35605	558	185

Description

6500732677 nohb:b0560 dna packaging protein:prophage qsr dna packaging protein nul homolog (gtcfc:13.1:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0560 b0560 Escherichia coli 562 -11536535 86315 nohb (de:prophage qsr' dna packaging protein nul homolog) (db:swissprot) NOHB_ECOLI P31062 ESCHERICHIA COLI 562 -11536535 7000685979 nohb dna packaging protein homolog nohb:phage protein-related (cl:phage lambda dna packaging protein nul) (db:pir2.dat) F64788 F64788 Escherichia coli 562 -11536535 7500886517 nohb bacteriophage dna packaging protein (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 51 of 400 of the completegenome.) (nt:o181; 100 pct identical to fragment nohb_ecoli) (le:3723) (re:4268) (di:direct) AE000161 AE000161 g1786773 Escherichia coli 562 -11536535 5000691668 (de:(ecoli_542) (pn:prophage qsr" dna packaging protein nul homolog:fragment) (gn:nohb) (gtcfc:13.7:14.1) (ec:) (nohb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_542 ECOLI_542 Escherichia coli 562 10122898

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871965	13450	35606	384	127

Description

6500732678 rnk:b0610 regulator of nucleoside diphosphate kinase (gtcfc:12.13) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0610 b0610 Escherichia coli 562 -11536536 95741 rnk (de:regulator of nucleoside diphosphate kinase) (db:swissprot) RNK_ECOLI P40679 ESCHERICHIA COLI 562 -11536536 164568 rnk nucleoside diphosphate kinase regulator:rnk protein (db:pir2.dat) I57917 I57917 Escherichia coli 562 -11536536 223110 rnk regulator of nucleoside diphosphate kinase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #166) (db:genpept-bct1) (de:escherichia coli genomic dna. (13.5 - 13.9 min).) (le:13313) (re:13723) (di:complement) D90701 D90701 g1651248 Escherichia coli 562 -11536536 223114 rnk regulator of nucleoside diphosphate kinase (sr:escherichia coli(strain:k12) dna, clone:kohara clone #167) (db:genpept-bct1) (de:escherichia coli genomic dna. (13.7 - 14.0 min).) (le:5498) (re:5908) (di:complement) D90702 D90702 g1651253 Escherichia coli 562 -11536536 240123 rnk regulator of nucleoside diphosphate kinase (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (le:84187) (re:84597) (di:complement) ECU82598 U82598 g1778527 Escherichia coli 562 -11536536 235851 rnk regulator of nucleoside diphosphate kinase (fn:regulator; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 56 of 400 of the completegenome.) (nt:f136; 100 pct identical to rnk_ecoli sw: p40679) (le:6945) (re:7355) (di:complement) AE000166 AE000166 g1786827 Escherichia coli 562 -11536536 7500890457 rnk (sr:escherichia coli dna) (db:genpept-bct2) (de:escherichia coli rnk gene, complete cds.) (le:150) (re:560) (di:direct) ECORNK L37900 g598118 Escherichia coli 562 -11536536 5000691694 rnk rnk protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #166) (db:genpept) (de:escherichia coli genomic dna. (13.6 - 14.0 min).) (nt:orf_id:o167#5; similar to pir accession number) (le:13314) (re:13724) (di:complement) D90701 D90701 g1651248 Escherichia coli 562 -11536536 7502852296 rnk rnk protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #167) (db:genpept) (de:escherichia coli genomic dna. (13.7 - 14.1 min).) (nt:orf_id:o167#5; similar to pir accession number) (le:5498) (re:5908) (di:complement) D90702 D90702 g1651253 Escherichia coli 562 -11536536

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871975	13451	35607	240	79

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501871985	13452	35608	756	252
Description				
<p>6500732679 citb:crir:b0620 transcriptional regulator crir:transcriptional regulatory protein citb (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0620 b0620 Escherichia coli 562 -11536537 1500687349 citb:mpda:crir (de:transcriptional regulatory protein citb) (db:swissprot) CITB_ECOLI Q54149 ESCHERICHIA COLI 562 -11536537 7502852297 citb:mpda:crir (de:transcriptional regulatory protein citb) (db:swissprot) CITB_ECOLI Q54149 SHIGELLA FLEXNERI 623 -11536537 7000684827 crir transcription regulator crir (cl:transcription regulator crir:response regulator homology) (db:pir2.dat) B64796 B64796 Escherichia coli 562 -11536537 260391 crir homolog (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:similar to s. flexneri crir) (le:94492) (re:95172) (di:direct) ECU82598 U82598 g1778537 Escherichia coli 562 -11536537 7000684828 crir crir (db:genpept-bct1) (de:shigella flexneri positive transcriptional regulator crir (crir)gene, complete cds.) (nt:crir is a positive transcriptional regulator for) (le:42) (re:722) (di:direct) SFU29654 U29654 g912578 Shigella flexneri 623 -11536537 240133 citb sequence similarity to shigella regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 57 of 400 of the completgenome.) (nt:o226; 100 pct identical to shigella flexneri) (le:1803) (re:2483) (di:direct) AE000167 AE000167 g1786838 Escherichia coli 562 -11536537 7500878775 dpia two component response regulator (db:genpept-bct2) (de:escherichia coli citrate lyase beta-subunit (cite) gene, partialcds; and citrate lyase gamma-subunit (citd), citrate lyase ligase(citc), histidine kinase (dpib), and two component responseregulator (dpia) genes, complete cds.) (nt... ECU46667 U46667 g2734637 Escherichia coli 562 -11536537 5000691703 citb response regulator citb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #167) (db:genpept) (de:escherichia coli genomic dna. (13.7 - 14.1 min).) (nt:orf_id:o168#4; similar to pir accession number) (le:15803) (re:16483) (di:direct) D90702 D90702 g4062237 Escherichia coli 562 -11536537 7502852298 citb response regulator citb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf_id:o168#4; similar to pir accession number) (le:3726) (re:4406) (di:direct) D90703 D90703 g4062243 Escherichia coli 562 -11536537</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501871988	13453	35609	930	309

Description

6500732680 cspe:msmc:gica:b0623 cold shock-like protein:cold shock-like protein cspe (gtcfc:12.7) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0623 b0623 Escherichia coli 562 -11536538 152150 cspe:msmc:gica cold shock protein homolog cspe (cl:major cold shock protein:cold shock domain homology) (db:pir2.dat) S49050 S49050 Escherichia coli 562 -11536538 223116 cspe cold shock-like protein cspe (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept-bct1) (de:escherichia coli genomic dna. (13.9 - 14.3 min).) (le:8355) (re:8564) (di:direct) D90703 D90703 g1651256 Escherichia coli 562 -11536538 234481 cspe::msmc cspe msmc (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:escherichia coli cspe (msmc) gene, complete cds.) (le:885) (re:1094) (di:direct) ECOCSPE D28497 g471099 Escherichia coli 562 -11536538 7500955129 gica (fn:negative regulation of growth in cold) (sr:escherichia coli (sub_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli (strain: k-12) gica gene, complete cds.) (le:1277) (re:1486) (di:direct) ECOGICA L29054 g833769 Escherichia coli 562 -11536538 7500955130 cspe (sr:escherichia coli k-12) (db:genpept-bct1) (de:crca...crca (escherichia coli, k-12, genomic, 3 genes, 3145 nt).) (le:2214) (re:2423) (di:direct) S83396 S83396 Escherichia coli 562 -11536538 234067 cspe cold shock protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 57 of 400 of the completengenome.) (nt:o69; 100 pct identical to cspe_ecoli sw: p36997) (le:5233) (re:5442) (di:direct) AE000167 AE000167 g1786841 Escherichia coli 562 -11536538 7502852299 unknown (db:genpept-bct2) (de:vibrio cholerae unknown gene.) (nt:similar to gica) (le:351) (re:560) (di:direct) AF098260 AF098260 g3851642 Vibrio cholerae 666 -11536538 5000691706 cspe cspe protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #168) (db:genpept) (de:escherichia coli genomic dna. (14.0 - 14.4 min).) (nt:orf_id:o168#8; similar to pir accession number) (le:8355) (re:8564) (di:direct) D90703 D90703 g1651256 Escherichia coli 562 -11536538

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872011	13454	35610	624	207

Description

6500732681 phpb:b0638 phosphohistidine protein:phpb protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0638 b0638 Escherichia coli 562 -11536539 89659 cobc:phpb (ec:3.1.3.-) (de:alpha-ribazole-5'-phosphate phosphatase,) (db:swissprot) COBC_ECOLI P52086 ESCHERICHIA COLI 562 -11536539 7000686139 phpb phosphoglycerate mutase homolog phpb (cl:phosphoglycerate mutase homology) (db:pir2.dat) D64798 D64798 Escherichia coli 562 -11536539 7500888062 phpb phpb (fn:cobalamin synthesis (putative)) (db:genpept-bct1) (de:escherichia coli orfuu (orfuu) gene and putative cobalaminsynthesis phpb (phpb) gene, complete cds.) (nt:phosphohistidine protein; similar to salmonella) (le:667) (re:1278) (di:direct) ECU23163 U23163 g727431 Escherichia coli 562 -11536539 238775 phpb homolog of salmonella cobc:a phosphohistidine (fn:putative regulator; biosynthesis of cofactors,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 58 of 400 of the completegenome.) (nt:f203 was f204; 100 pct identical to phpb_ecoli) (le:7031) (re:7642) (di:complement) AE000168 AE000168 g1786857 Escherichia coli 562 -11536539 5000691715 phpb phpb protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #169) (db:genpept) (de:escherichia coli genomic dna. (14.3 - 14.7 min).) (nt:orf_id:o169#6; similar to swissprot accession) (le:5544) (re:6155) (di:complement) D90704 D90704 g4062256 Escherichia coli 562 -11536539

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872026	13455	35611	840	279

Description

6500732682 ybej:b0655 hypothtcal protein in gltj 5region:amino-acid abc transporter binding protein in gltj-cute intergenic region precursor (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0655 b0655 Escherichia coli 562 -11536540 103745 ybej (de:region precursor) (db:swissprot) YBEJ_ECOLI P37902 ESCHERICHIA COLI 562 -11536540 7000687325 ybej probable glutamate/aspartate-binding protein ybej:periplasmic (db:pir2.dat) E64800 E64800 Escherichia coli 562 -11536540 7500896668 ybej (db:genpept-bct1) (de:escherichia coli genomic sequence of minutes 9 to 12.) (nt:hypothetical protein) (le:127469) (re:128377) (di:complement) ECU82598 U82598 g1778573 Escherichia coli 562 -11536540 240169 ybej putative periplasmic binding transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 60 of 400 of the completegenome.) (nt:f302; 100 pct identical to fragment ybej_ecoli) (le:115) (re:1023) (di:complement) AE000170 AE000170 g1786876 Escherichia coli 562 -11536540 5000691729 (de:(ecoli_636) (pn:hypothtcal protein in gltj 5"region:fragment) (gn:ybej) (gtcfc:13.7:14.1) (ec:) (ybej_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_636 ECOLI_636 Escherichia coli 562 10122944

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872050	13456	35612	1410	469

Description

6500732683 rhsc:b0700 rhsc protein precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0700 b0700 Escherichia coli 562 -11536541 94323 rhsc (de:rhsc protein precursor) (db:swissprot) RHSC_ECOLI P16918 ESCHERICHIA COLI 562 -11536541 7000686323 rhsc rhsc protein precursor (db:pir2.dat) C64805 C64805 Escherichia coli 562 -11536541 223163 rhsc rhsc protein precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #174) (db:genpept-bct1) (de:escherichia coli genomic dna. (15.6 - 15.9 min).) (le:2769) (re:6962) (di:direct) D90709 D90709 g1651309 Escherichia coli 562 -11536541 300032 rhsc rhsc protein in rhs element (fn:orf; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 63 of 400 of the completegenome.) (nt:o1397; 99 pct identical to rhsc_ecoli sw: p16918) (le:8855) (re:13048) (di:direct) AE000173 AE000173 g1786917 Escherichia coli 562 -11536541 7500889763 rhs core protein (db:genpept-bct2) (de:escherichia coli rhs core protein and rhsc accessoryelement-encoded genes, complete cds.) (nt:with unique extension) (le:722) (re:4915) (di:direct) ECORHSCA L02373 g1857030 Escherichia coli 562 -11536541 5000691747 rhsc rhsc protein precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #174) (db:genpept) (de:escherichia coli genomic dna. (15.7 - 16.0 min).) (nt:orf_id:o174#4; similar to swissprot accession) (le:2769) (re:6962) (di:direct) D90709 D90709 g1651309 Escherichia coli 562 -11536541

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872051	13457	35613	564	187

Description

6500732684 ybfd:b0706 h repeat-associated protein in rhsc 3region:h repeat-associated protein in rhsc-phrb intergenic region:orf-h3 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0706 b0706 Escherichia coli 562 -11536542 110269 ybfd (de:h repeat-associated protein in rhsc-phrb intergenic region (orf-h3)) (db:swissprot) YBFD_ECOLI P28916 ESCHERICHIA COLI 562 -11536542 7000687334 ybfd h repeat-associated protein-like protein b0706:ybfd protein (db:pir2.dat) A64806 A64806 Escherichia coli 562 -11536542 235819 ybfd putative dna ligase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 64 of 400 of the completegenome.) (nt:o253; 100 pct identical to ybfd_ecoli sw: p28916) (le:3961) (re:4722) (di:direct) AE000174 AE000174 g1786924 Escherichia coli 562 -11536542 300036 rhsc -h3::orf unknown (db:genpept-bct2) (de:escherichia coli rhs core protein and rhsc accessoryelement-encoded genes, complete cds.) (le:9231) (re:9992) (di:direct) ECORHSCA L02373 g147642 Escherichia coli 562 -11536542 5000691753 ybfd h repeat-associated protein in rhsc 3region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #174) (db:genpept) (de:escherichia coli genomic dna. (15.7 - 16.0 min).) (nt:orf_id:o175#1; similar to swissprot accession) (le:11278) (re:12039) (di:direct) D90709 D90709 g4062299 Escherichia coli 562 -11536542 7502852300 ybfd h repeat-associated protein in rhsc 3region (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).) (nt:orf_id:o175#1; similar to swissprot accession) (le:816) (re:1577) (di:direct) D90710 D90710 g4062303 Escherichia coli 562 -11536542

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872054	13458	35614	243	80

Description

GTC ORF with score 101 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana chromosome ii bac t28m21 genomic sequence,complete sequence.) (nt:unknown protein) (le:97328:98826:99416) (re:98518:98940:99530) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872055	13459	35615	519	172

Description

6500732685 nei:b0714 endonuclease viii:dna n-glycosylase with an ap lyase activity:endonuclease viii (gtcfc:10.10) (ec:3.2.-.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0714 b0714 Escherichia coli 562 -11536543 7000685160 nei endonuclease viii (ec:3.2.-.-) (db:pir2.dat) (mp:16 min) A64807 A64807 Escherichia coli 562 -11536543 7500959730 nei endonuclease viii (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli gene for endonuclease viii, complete cds.) (le:125) (re:916) (di:direct) D89754 D89754 g2190281 Escherichia coli 562 -11536543 239557 nei endonuclease viii and dna n-glycosylase with an (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 64 of 400 of the completegenome.) (nt:o263; 100 pct identical to end8_ecoli sw: p50465) (le:11804) (re:12595) (di:direct) AE000174 AE000174 g1786932 Escherichia coli 562 -11536543 4000707056 nei endonuclease viii (db:genpept-bct2) (de:escherichia coli endonuclease viii (nei) gene, complete cds.) (nt:dna n-glycosylase with an ap lyase activity; dna) (le:1) (re:792) (di:direct) ECU38616 U38616 g1054938 Escherichia coli 562 -11536543 5000691760 nei endonuclease viii. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #175) (db:genpept) (de:escherichia coli genomic dna. (15.9 - 16.3 min).) (nt:orf_id:o175#9; similar to swissprot accession) (le:8659) (re:9450) (di:direct) D90710 D90710 g4062310 Escherichia coli 562 -11536543 70164 end8_ecoli (de:endonuclease viii.) P50465 P50465 Escherichia coli 562 -11536543

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872069	13460	35616	1419	472

Description

6500732686 farr:g30:b0730 fatty acyl responsive regulator:p30 protein (gtcfc:12.13:3.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0730 b0730 Escherichia coli 562 -11536544 7500881344 farr:g30 (de:fatty acyl responsive regulator (p30 protein)) (db:swissprot) FARR_ECOLI P13669 ESCHERICHIA COLI 562 -11536544 163906 farr:gp30 transcription regulator farr:fatty acyl-responsive:gp30 protein (cl:transcription regulator gntr) (db:pir2.dat) (mp:16.8 min) S04645 S04645 Escherichia coli 562 -11536544 5000691767 (db:genpept-bct1) (de:e.coli g30 gene and sucD gene (partial), encoding a possible transcriptional regulator (p30) and succinyl-coa synthetase alpha subunit.) (nt:p30 protein (aa 1-240)) (le:105) (re:827) (di:direct) ECG30SUC X15790 g41519 Escherichia coli 562 -11536544 232947 farr transcriptional regulator of succinylcoa (fn:regulator; energy metabolism, carbon: tca) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 66 of 400 of the complete genome.) (nt:f240; 100 pct identical to farr_ecoli sw: p13669;) (le:2307) (re:3029) (di:complement) AE000176 AE000176 g1786950 Escherichia coli 562 -11536544 71112 farr:g30 (de:fatty acyl responsive regulator (p30 protein)) (db:swissprot) FARR_ECOLI P13669 ESCHERICHIA COLI 562 -11536544

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872070	13461	35617	813	270

Description

6500732687 modf:phra:b0760 putative molybdenum transport atp-binding protein
 modf:photorepair protein phra (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.8.0)
 (db:gtc-escherichia coli) b0760 b0760 Escherichia coli 562 -11536545 83994
 modf:phra (de:protein phra)) (db:swissprot) MODF_ECOLI P31060 ESCHERICHIA
 COLI 562 -11536545 164094 modf:phra probable molybdenum transport protein
 modf:photorepair protein phra (cl:atp-binding cassette homology)
 (db:pir2.dat) (mp:17 min) JC6038 JC6038 Escherichia coli 562 -11536545
 239051 (db:genpept-bct1) (de:escherichia coli k12, substrain mc1000
 molybdenum transport (modr), (moda), (modb), (modc), (modd), genes, complete
 cds.) (nt:orf6) (le:355) (re:1827) (di:complement) ECU07867 U07867 g1147815
 Escherichia coli 562 -11536545 7500885755 modf modf (db:genpept-bct1)
 (de:escherichia coli molybdate transport operon (moda, modb, modc, modd),
 mode (mode) and modf (modf) genes, complete cds.) (le:54) (re:1526)
 (di:complement) ECU27192 U27192 g973219 Escherichia coli 562 -11536545
 238535 modf atp-binding component of molybdate transport (fn:transport;
 transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12
 mg1655 section 68 of 400 of the completegenome.) (nt:f490; 100 pct identical
 to modf_ecoli sw: p31060;) (le:7466) (re:8938) (di:complement) AE000178
 AE000178 g1786975 Escherichia coli 562 -11536545 5000691774 modf putative
 molybdenum transport atp-binding (sr:escherichia coli(strain:k12) dna,
 clone:kohara clone #179) (db:genpept) (de:escherichia coli genomic dna.
 (16.8 - 17.1 min).) (nt:orf_id:ol79#11; similar to swissprot accession)
 (le:12380) (re:13852) (di:complement) D90714 D90714 g4062327 Escherichia
 coli 562 -11536545

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501872073	13462	35618	330	110

Description

6500732688 ompx:b0814 outer membrane protein x precursor (gtcfc:11.1:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0814 b0814
 Escherichia coli 562 -11536546 87697 ompx (de:outer membrane protein x precursor) (db:swissprot) OMPX_ECOLI P36546 ESCHERICHIA COLI 562 -11536546
 164214 ompx outer membrane protein x precursor (db:pir2.dat) I55173 I55173
 Escherichia coli 562 -11536546 223213 ompx outer membrane protein x precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept-bct1) (de:escherichia coli genomic dna.(18.0 - 18.3 min).) (le:11767) (re:12282) (di:direct) D90718 D90718 g1651367 Escherichia coli 562 -11536546 223218 ompx outer membrane protein x precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept-bct1) (de:escherichia coli genomic dna.(18.2 - 18.5 min).) (le:4982) (re:5497) (di:direct) D90719 D90719 g1651373 Escherichia coli 562 -11536546 7500887182 ompx outer membrane protein (sr:escherichia coli (sub_strain mg1655, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli outer membrane protein (ompx) gene, complete cds.) (le:336) (re:851) (di:direct) ECOOMPXAA L37088 g559694 Escherichia coli 562 -11536546 235279 ompx outer membrane protein x (fn:membrane; outer membrane constituents) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 73 of 400 of the completegenome.) (nt:o171; 100 pct identical to ompx_ecoli sw: p36546) (le:8817) (re:9332) (di:direct) AE000183 AE000183 g1787034 Escherichia coli 562 -11536546 5000691808 ompx outer membrane protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #205) (db:genpept) (de:escherichia coli genomic dna. (18.1 - 18.4 min).) (nt:orf_id:o206#6; similar to pir accession number) (le:11767) (re:12282) (di:direct) D90718 D90718 g1651367 Escherichia coli 562 -11536546 7502852301 ompx outer membrane protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #206) (db:genpept) (de:escherichia coli genomic dna. (18.2 - 18.6 min).) (nt:orf_id:o206#6; similar to pir accession number) (le:4982) (re:5497) (di:direct) D90719 D90719 g1651373 Escherichia coli 562 -11536546

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501872083	13463	35619	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872089	13464	35620	1425	474

Description

6500732689 mdaa:mda18:b0851 modulator of drug activity a (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0851 b0851 Escherichia coli 562 -11536547 83272 nfsa:mdaa:mda18 (ec:1.-.-.-) (de:drug activity a)) (db:swissprot) NFSA_ECOLI P17117 ESCHERICHIA COLI 562 -11536547 164048 mdaa:mda18 drug activity modulator a (cl:nadph-flavin oxidoreductase homolog) (db:pir2.dat) (mp:18.7-19.0 min) I80318 I80318 Escherichia coli 562 -11536547 222512 nfsa oxygen-insensitive nadph nitroreductase (fn:reduction of nitroaromatic compounds) (sr:escherichia coli (strain:ab1157) dna, clone:paj102) (db:genpept-bct1) (de:escherichia coli dna for oxygen-insensitive nadph nitroreductase,complete cds.) (le:774) (re:1496) (di:direct) D38308 D38308 g1536786 Escherichia coli 562 -11536547 223227 mdaa modulator of drug activity a (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.0 - 19.3 min).) (le:7868) (re:8590) (di:direct) D90723 D90723 g1651385 Escherichia coli 562 -11536547 238752 mdaa modulator of drug activity a (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 77 of 400 of the completegenome.) (nt:o240; 100 pct identical to mdaa_ecoli sw: p17117) (le:3168) (re:3890) (di:direct) AE000187 AE000187 g1787075 Escherichia coli 562 -11536547 7500886405 mda18 (db:genpept-bct2) (de:escherichia coli modulator of drug activity (mda18) andglutaredoxin genes, complete cds.) (nt:encodes a 24 kda protein) (le:691) (re:1413) (di:direct) ECU18655 U18655 g609324 Escherichia coli 562 -11536547 5000691840 mda18 modulator of drug activity a. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #210) (db:genpept) (de:escherichia coli genomic dna. (19.1 - 19.4 min).) (nt:orf_id:o210#9; similar to swissprot accession) (le:7868) (re:8590) (di:direct) D90723 D90723 g1651385 Escherichia coli 562 -11536547

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872118	13465	35621	747	248

Description

6500732690 aqpz:bnip:b0875 aquaporin z:bacterial nodulin-like intrinsic protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0875 b0875 Escherichia coli 562 -11536548 59942 aqpz:bnip (de:aquaporin z (bacterial nodulin-like intrinsic protein)) (db:swissprot) AQPZ_ECOLI P48838 ESCHERICHIA COLI 562 -11536548 7000684598 aqpz:bnip aquaporin z:bacterial nodulin-like intrinsic protein (cl:nodulin-26) (db:pir2.dat) C64826 C64826 Escherichia coli 562 -11536548 7500877033 aqpz transmembrane water channel:aquaporin z (fn:transport; transport of small molecules: other) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 79 of 400 of the completegenome.) (nt:f231; 99 pct identical to aqpz_ecoli sw: p48838) (le:4267) (re:4962) (di:complement) AE000189 AE000189 gl787101 Escherichia coli 562 -11536548 5000691853 aqpz aquaporin z. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #211) (db:genpept) (de:escherichia coli genomic dna. (19.4 - 19.8 min).) (nt:orf_id:o212#2; similar to swissprot accession) (le:17631) (re:18326) (di:complement) D90724 D90724 g4062454 Escherichia coli 562 -11536548 7502852302 aqpz aquaporin z. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #212) (db:genpept) (de:escherichia coli genomic dna. (19.7 - 20.0 min).) (nt:orf_id:o212#2; similar to swissprot accession) (le:2289) (re:2984) (di:complement) D90725 D90725 g4062458 Escherichia coli 562 -11536548

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872132	13466	35622	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872141	13467	35623	864	287

Description

6500732691 cspd:csph:b0880 cold shock-like protein cspd (gtcfc:12.7)
(keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0880 b0880
Escherichia coli 562 -11536549 66663 cspd:csph (de:cold shock-like protein
cspd) (db:swissprot) CSPD_ECOLI P24245 ESCHERICHIA COLI 562 -11536549
7000684925 cspd:csph cold shock protein homolog cspd (cl:major cold shock
protein:cold shock domain homology) (db:pir2.dat) H64826 H64826 Escherichia
coli 562 -11536549 223240 cspd cold shock-like protein cspd (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #212) (db:genpept-bct1)
(de:escherichia coli genomic dna.(19.6 - 19.9 min).) (le:9303) (re:9527)
(di:complement) D90725 D90725 g1651400 Escherichia coli 562 -11536549
7500879494 cspd cold shock protein (fn:phenotype; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 80 of 400 of the
completegenome.) (nt:f74; 100 pct identical to cspd_ecoli sw: p24245)
(le:67) (re:291) (di:complement) AE000190 AE000190 g1787107 Escherichia coli
562 -11536549 5000691858 cspd cold shock-like protein cspd. (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #212) (db:genpept) (de:escherichia
coli genomic dna. (19.7 - 20.0 min).) (nt:orf_id:o213#5; similar to
swissprot accession) (le:9303) (re:9527) (di:complement) D90725 D90725
g1651400 Escherichia coli 562 -11536549

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872153	13468	35624	681	226

Description

6500732692 ftsk:b0890 cell division protein ftsk (gtcfc:12.8) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0890 b0890 Escherichia coli 562 -11536550 72456 ftsk (de:cell division protein ftsk) (db:swissprot) FTSK_ECOLI P46889 ESCHERICHIA COLI 562 -11536550 7000685325 ftsk cell division protein ftsk (db:pir2.dat) A64828 A64828 Escherichia coli 562 -11536550 223251 ftsk cell division protein ftsk (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.9 - 20.2 min).) (le:9104) (re:13093) (di:direct) D90726 D90726 g1651412 Escherichia coli 562 -11536550 223256 ftsk cell division protein ftsk (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept-bct1) (de:escherichia coli genomic dna.(20.0 - 20.3 min).) (le:2407) (re:6396) (di:direct) D90727 D90727 g1651418 Escherichia coli 562 -11536550 7500881838 ftsk cell division protein (fn:phenotype; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 81 of 400 of the completegenome.) (nt:ol329; 99 pct identical to ftsk_ecoli sw: p46889) (le:932) (re:4921) (di:direct) AE000191 AE000191 g1787117 Escherichia coli 562 -11536550 5000691860 ftsk cell division protein ftsk. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept) (de:escherichia coli genomic dna. (19.9 - 20.3 min).) (nt:orf_id:o215#3; similar to swissprot accession) (le:9104) (re:13093) (di:direct) D90726 D90726 g1651412 Escherichia coli 562 -11536550 7502852303 ftsk cell division protein ftsk. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept) (de:escherichia coli genomic dna. (20.1 - 20.4 min).) (nt:orf_id:o215#3; similar to swissprot accession) (le:2407) (re:6396) (di:direct) D90727 D90727 g1651418 Escherichia coli 562 -11536550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872170	13469	35625	570	189

Description

6500732693 lola:lpla:b0891 outer membrane lipoprotein carrier protein precursor:outer membrane lipoproteins carrier protein precursor:p20 (gtcfc:11.2:12.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0891 b0891 Escherichia coli 562 -11536551 82306 lola:lpla (de:outer membrane lipoproteins carrier protein precursor (p20)) (db:swissprot) LOLA_ECOLI P39178 ESCHERICHIA COLI 562 -11536551 164002 lola:lpla outer membrane lipoprotein carrier protein precursor (db:pir2.dat) S57828 S57828 Escherichia coli 562 -11536551 223252 lola outer membrane lipoproteins carrier protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept-bct1) (de:escherichia coli genomic dna.(19.9 - 20.2 min).) (le:13249) (re:13863) (di:direct) D90726 D90726 g1651413 Escherichia coli 562 -11536551 223257 lola outer membrane lipoproteins carrier protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept-bct1) (de:escherichia coli genomic dna.(20.0 - 20.3 min).) (le:6552) (re:7166) (di:direct) D90727 D90727 g1651419 Escherichia coli 562 -11536551 7500885093 lpla lipoprotein carrier protein precursor (fn:translocation of lipoproteins from the inner to) (sr:escherichia coli (strain:k12, isolate:mc4100) dna) (db:genpept-bct1) (de:escherichia coli lpla gene for lipoprotein carrier protein,complete cds.) (le:352) (re:966) (di:direct) ECOLPLAA D49398 g974728 Escherichia coli 562 -11536551 235005 lola periplasmic protein effects translocation of (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 81 of 400 of the completegenome.) (nt:o204; 100 pct identical to lola_ecoli sw: p39178;) (le:5077) (re:5691) (di:direct) AE000191 AE000191 g1787118 Escherichia coli 562 -11536551 5000691861 lola outer membrane lipoproteins carrier protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #214) (db:genpept) (de:escherichia coli genomic dna.(19.9 - 20.3 min).) (nt:orf_id:o215#4; similar to swissprot accession) (le:13249) (re:13863) (di:direct) D90726 D90726 g1651413 Escherichia coli 562 -11536551 7502852304 lola outer membrane lipoproteins carrier protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept) (de:escherichia coli genomic dna.(20.1 - 20.4 min).) (nt:orf_id:o215#4; similar to swissprot accession) (le:6552) (re:7166) (di:direct) D90727 D90727 g1651419 Escherichia coli 562 -11536551

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872177	13470	35626	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872179	13471	35627	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872182	13472	35628	411	136

Description

6500732694 dmsb:b0895 anaerobic dimethyl sulfoxide reductase chain b:dmsoreductase iron-sulfur subunit (gtcfc:2.7:12.12) (ec:1.8.99.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0895 b0895 Escherichia coli 562 -11536552 7000690855 dmsb anaerobic dimethylsulfoxide reductase:chain b (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (ec:1.-.-.-) (db:pir2.dat) (mp:20 min) F64828 F64828 Escherichia coli 562 -11536552 223260 dmsb dimethylsulfoxide reductase chain b (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept-bct1) (de:escherichia coli genomic dna.(20.0 - 20.3 min).) (le:12597) (re:13214) (di:direct) D90727 D90727 g1651422 Escherichia coli 562 -11536552 7500953896 dmsb anaerobic dimethyl sulfoxide reductase subunit (fn:enzyme; energy metabolism, carbon: anaerobic) (db:genpept-bct2) (ec:1.-.-.-) (de:escherichia coli k-12 mg1655 section 81 of 400 of the completegenome.) (nt:o205; 100 pct identical (2 gaps) to 204 residues) (le:11122) (re:11739) (di:direct) AE000191 AE000191 g1787122 Escherichia coli 562 -11536552 5000691863 dmsb dimethylsulfoxide reductase ec 1.8.-.- chain (sr:escherichia coli(strain:k12) dna, clone:kohara clone #215) (db:genpept) (de:escherichia coli genomic dna.(20.1 - 20.4 min).) (nt:orf_id:o215#8; similar to pir accession number) (le:12597) (re:13214) (di:direct) D90727 D90727 g1651422 Escherichia coli 562 -11536552

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872185	13473	35629	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872187	13474	35630	312	103

Description

6500732695 foca:b0904 probable formate transporter:formate channel:probable formate transporter 1:formate channel 1 (gtcfc:12.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0904 b0904 Escherichia coli 562 -11536553 72216 foca (de:probable formate transporter 1 (formate channel 1)) (db:swissprot) FOCA_ECOLI P21501 ESCHERICHIA COLI 562 -11536553 164376 foca probable formate transport protein:probable formate channel protein (cl:formate dehydrogenase focb) (db:pir2.dat) A32305 A32305 Escherichia coli 562 -11536553 223265 foca probable formate transporter (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.3 - 20.7 min).) (le:9302) (re:10159) (di:complement) D90728 D90728 g1651428 Escherichia coli 562 -11536553 223271 foca probable formate transporter (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (le:1769) (re:2626) (di:complement) D90729 D90729 g1651435 Escherichia coli 562 -11536553 7500881694 foca probable formate transporter formate channel (fn:putative transport; degradation of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 82 of 400 of the completegenome.) (nt:f285; 100 pct identical to foca_ecoli sw: p21501) (le:7925) (re:8782) (di:complement) AE000192 AE000192 g1787132 Escherichia coli 562 -11536553 5000691869 foca probable formate transporter (sr:escherichia coli(strain:k12) dna, clone:kohara clone #216) (db:genpept) (de:escherichia coli genomic dna. (20.4 - 20.8 min).) (nt:orf_id:o217#1; similar to pir accession number) (le:9302) (re:10159) (di:complement) D90728 D90728 g1651428 Escherichia coli 562 -11536553 7502852305 foca probable formate transporter (sr:escherichia coli(strain:k12) dna, clone:kohara clone #217) (db:genpept) (de:escherichia coli genomic dna. (20.5 - 20.9 min).) (nt:orf_id:o217#1; similar to pir accession number) (le:1769) (re:2626) (di:complement) D90729 D90729 g1651435 Escherichia coli 562 -11536553

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501872202	13475	35631	963	320

Description

6500732696 mukf:kicb:b0922 mukf protein:killing factor kicb (gtcfc:12.14) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0922 b0922 Escherichia coli 562 -11536554 84674 mukf:kicb (de:mukf protein (killing factor kicb)) (db:swissprot) MUKF_ECOLI P36567 ESCHERICHIA COLI 562 -11536554 163960 mukf:kicb mukf protein:killing factor kicb (db:pir2.dat) S43911 S43911 Escherichia coli 562 -11536554 223281 mukf killing factor kicb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept-bct1) (de:escherichia coli genomic dna. (20.8 - 21.2 min).) (le:6673) (re:7995) (di:direct) D90730 D90730 g1651446 Escherichia coli 562 -11536554 7500886086 mukf (sr:escherichia coli (sub_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli genes for smta, mukf, muke (complete cds) and genefor mukb (partial cds).) (le:1428) (re:2750) (di:direct) ECOMUKEF D26440 g450465 Escherichia coli 562 -11536554 235197 mukf mukf protein killing factor kicb (fn:factor; cell killing) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 84 of 400 of the completegenome.) (nt:o440; 100 pct identical to kicb_ecoli sw: p36567) (le:2674) (re:3996) (di:direct) AE000194 AE000194 g1787152 Escherichia coli 562 -11536554 5000691880 kicb mukf protein killing factor kicb . (sr:escherichia coli(strain:k12) dna, clone:kohara clone #218) (db:genpept) (de:escherichia coli genomic dna. (20.9 - 21.3 min).) (nt:orf_id:o218#8; similar to swissprot accession) (le:6673) (re:7995) (di:direct) D90730 D90730 g1651446 Escherichia coli 562 -11536554

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501872216	13476	35632	345	114

Description

6500732697 muke:kica:b0923 muke protein:kica protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0923 b0923 Escherichia coli 562 -11536555 84672 muke:kica (de:muke protein (kica protein)) (db:swissprot) MUKE_ECOLI P22524 ESCHERICHIA COLI 562 -11536555 7000685882 muke:kica muke protein:kica protein (db:pir2.dat) B64832 B64832 Escherichia coli 562 -11536555 7500886084 muke (sr:escherichia coli (sub_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:escherichia coli genes for smta, mukf, muke (complete cds) and genefor mukb (partial cds).) (le:2758) (re:3435) (di:direct) ECOMUKEF D26440 g450466 Escherichia coli 562 -11536555 235198 muke orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 84 of 400 of the completegenome.) (nt:o225; 100 pct identical to kica_ecoli sw: p22524) (le:4004) (re:4681) (di:direct) AE000194 AE000194 g1787153 Escherichia coli 562 -11536555 5000691881 (de:(ecoli_889) (pn:muke protein:kica protein) (gn:muke) (gtcfc:13.7:14.1) (ec:.) (muke_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_889 ECOLI_889 Escherichia coli 562 10026863

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872219	13477	35633	240	79

Description

6500732698 insb_4:b0988 insertion element is1 protein insb (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0988 b0988
Escherichia coli 562 -11536556 7500974825 insb hypothetical protein insb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.2 - 22.6 min).) (le:15950) (re:16453) (di:direct) D90735 D90735 g1651483 Escherichia coli 562 -11536556 223314 insb hypothetical protein insb (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept-bct1) (de:escherichia coli genomic dna. (22.5 - 22.9 min).) (le:4522) (re:5025) (di:direct) D90736 D90736 g1651486 Escherichia coli 562 -11536556 223316 insb_4 is1 protein insb (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 90 of 400 of the completegenome.) (nt:o167; 97 pct identical to isb_ecoli sw: p03830) (le:9533) (re:10036) (di:direct) AE000200 AE000200 g1787223 Escherichia coli 562 -11536556 5000691924 insb hypothetical protein insb insertion sequence (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf_id:o226#6; similar to pir accession number) (le:15946) (re:16449) (di:direct) D90735 D90735 g1651483 Escherichia coli 562 -11536556 7502852306 insb hypothetical protein insb insertion sequence (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf_id:o226#6; similar to pir accession number) (le:4522) (re:5025) (di:direct) D90736 D90736 g1651486 Escherichia coli 562 -11536556 157306 (de:hypothetical protein insb (insertion sequence is1d) -escherichia coli) JN0139 JN0139 Escherichia coli 562 -11536556

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872220	13478	35634	249	82

Description

6500732699 cspi:cspg:b0990 cold shock potein cspg:cold shock-like protein cspi (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0990 b0990 Escherichia coli 562 -11536557 4000707752 cspg:cspi (de:cold shock-like protein cspg) (db:swissprot) CSPG_ECOLI Q47130 ESCHERICHIA COLI 562 -11536557 7000684927 cspg:cspi cold shock protein cspg (cl:major cold shock protein:cold shock domain homology) (db:pir2.dat) D64840 D64840 Escherichia coli 562 -11536557 222701 cspg cspg (db:genpept-bct1) (de:escherichia coli major cold-shock proteins cspg (cspg) and csph(csph) genes, complete cds.) (nt:major cold-shock protein) (le:154) (re:366) (di:complement) AF003591 AF003591 g2226344 Escherichia coli 562 -11536557 4000707753 cspg cold shock potein cspg (sr:escherichia coli (strain:k12) cdna to mrna, clone_lib:kohar) (db:genpept-bct1) (de:escherichia coli mrna for cold shock protein cspg, complete cds.) (le:560) (re:772) (di:direct) D63344 D63344 g1468921 Escherichia coli 562 -11536557 7500879496 cspg homolog of salmonella cold shock protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 91 of 400 of the completengenome.) (nt:o70; 100 pct identical to gb: d63344) (le:234) (re:446) (di:direct) AE000201 AE000201 g2367114 Escherichia coli 562 -11536557 7502852307 csph csph protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3 - 22.7 min).) (nt:orf_id:o226#8; similar to pir accession number) (le:17380) (re:17592) (di:direct) D90735 D90735 g4062549 Escherichia coli 562 -11536557 7502852308 csph csph protein (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf_id:o226#8; similar to pir accession number) (le:5956) (re:6168) (di:direct) D90736 D90736 g4062706 Escherichia coli 562 -11536557

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872222	13479	35635	498	165

Description

GTC ORF with score 283 to: (or:Caenorhabditis elegans) (db:genpept-inv) (de:caenorhabditis elegans cosmid f19b6, complete sequence.) (nt:similarity to yeast uridine kinase (sw:urk1_yeast);) (le:13209:13386:14285) (re:13343:13734:14667) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872224	13480	35636	465	155

Description

6500732700 sfa:b0991 sfa protein:protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b0991 b0991 Escherichia coli 562 -11536558 98445 sfa (de:sfa protein) (db:swissprot) SFA_ECOLI P52634 ESCHERICHIA COLI 562 -11536558 7000686589 sfa sfa protein (db:pir2.dat) E64840 E64840 Escherichia coli 562 -11536558 239553 sfa suppresses faba and ts growth mutation (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 91 of 400 of the completegenome.) (nt:o76; 100 pct identical to sfa_ecoli sw: p52634) (le:620) (re:850) (di:direct) AE000201 AE000201 g1787225 Escherichia coli 562 -11536558 7500891565 sfa sfa (fn:suppresses the temperature-sensitive growth) (sr:escherichia coli strain=k-12) (db:genpept-bct2) (de:escherichia coli sfa (sfa) gene, complete cds.) (nt:suppressor of faba) (le:268) (re:498) (di:direct) ECU38541 U38541 g1055275 Escherichia coli 562 -11536558 5000691925 sfa sfa protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #225) (db:genpept) (de:escherichia coli genomic dna. (22.3- 22.7 min).) (nt:orf_id:o226#9; similar to swissprot accession) (le:17766) (re:17996) (di:direct) D90735 D90735 g4062550 Escherichia coli 562 -11536558 7502852309 sfa sfa protein. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #226) (db:genpept) (de:escherichia coli genomic dna. (22.6 - 23.0 min).) (nt:orf_id:o226#9; similar to swissprot accession) (le:6342) (re:6572) (di:direct) D90736 D90736 g4062707 Escherichia coli 562 -11536558

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872229	13481	35637	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872239	13482	35638	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872252	13483	35639	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872266	13484	35640	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872289	13485	35641	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872298	13486	35642	966	321

Description

6500732701 csgg:b1037 assembly /transport component in curli production:curli production assembly/transport component csgg precursor (gtcfc:12.6:11.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1037 b1037 Escherichia coli 562 -11536559 66634 csgg (de:curli production assembly/transport component csgg precursor) (db:swissprot) CSGG_ECOLI P52103 ESCHERICHIA COLI 562 -11536559 7000684920 csgg curli assembly factor csgc precursor:csgg protein (db:pir2.dat) (mp:23.15) S70783 S70783 Escherichia coli 562 -11536559 7500879458 csgg assembly /transport component in curli (db:genpept-bct1) (de:e.coli csgg, csgf, csge, csge, csge, csge, csge, csge, and orfc genes.) (le:133) (re:966) (di:complement) ECCSGABDG X90754 g1147559 Escherichia coli 562 -11536559 232584 csgg curli production assembly/transport component (fn:structural component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of 400 of the completegenome.) (nt:f277; 100 pct identical to csgg_ecoli sw: p52103) (le:5397) (re:6230) (di:complement) AE000205 AE000205 g1787274 Escherichia coli 562 -11536559 5000691959 csgg curli production assembly/transport component (sr:escherichia coli(strain:k12) dna, clone:kohara clone #230) (db:genpept) (de:escherichia coli genomic dna. (23.5 - 23.8 min).) (nt:orf_id:o231#5; similar to swissprot accession) (le:10916) (re:11749) (di:complement) D90740 D90740 g4062601 Escherichia coli 562 -11536559 7502852310 csgg curli production assembly/transport component (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231) (db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).) (nt:orf_id:o231#5; similar to swissprot accession) (le:4117) (re:4950) (di:complement) D90741 D90741 g4062610 Escherichia coli 562 -11536559

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872308	13487	35643	1374	457

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872328	13488	35644	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872329	13489	35645	345	114

Description

6500732702 csgf:b1038 assembly /transport component in curli
production:curli production assembly/transport component csgf precursor
(gtcfc:12.6:11.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli)
b1038 b1038 Escherichia coli 562 -11536560 66633 csgf (de:curli production
assembly/transport component csgf precursor) (db:swissprot) CSGF_ECOLI
P52104 ESCHERICHIA COLI 562 -11536560 7000684919 csgf curli
assembly/transport component csgf precursor:csgf protein (db:pir2.dat)
(mp:23.15) S70784 S70784 Escherichia coli 562 -11536560 7500879457 csgf
assembly /transport component in curli (db:genpept-bct1) (de:e.coli csgg,
csgf, csge, csge, csge, csge, csge, csge, csge, csge, csge, csge, csge,
(di:complement) ECCSGABDG X90754 g1147560 Escherichia coli 562 -11536560
232585 csgf curli production assembly/transport component (fn:structural
component; surface structures) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 95 of 400 of the completegenome.) (nt:f138; 100 pct identical
to csgf_ecoli sw: p52104) (le:6257) (re:6673) (di:complement) AE000205
AE000205 g1787275 Escherichia coli 562 -11536560 5000691960 csgf curli
production assembly/transport component (sr:escherichia coli(strain:k12)
dna, clone:kohara clone #230) (db:genpept) (de:escherichia coli genomic dna.
(23.5 - 23.8 min).) (nt:orf_id:o231#6; similar to swissprot accession)
(le:11776) (re:12192) (di:complement) D90740 D90740 g4062602 Escherichia
coli 562 -11536560 7502852311 csgf curli production assembly/transport
component (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231)
(db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).)
(nt:orf_id:o231#6; similar to swissprot accession) (le:4977) (re:5393)
(di:complement) D90741 D90741 g4062611 Escherichia coli 562 -11536560

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872330	13490	35646	756	251

Description

6500732703 csge:b1039 assembly /transport component in curli
production:curli production assembly/transport component csge precursor
(gtcfc:12.6:11.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli)
b1039 b1039 Escherichia coli 562 -11536561 66632 csge (de:curli production
assembly/transport component csge precursor) (db:swissprot) CSGE_ECOLI
P52105 ESCHERICHIA COLI 562 -11536561 7000684918 csge curli
assembly/transport component csge:csge protein (db:pir2.dat) (mp:23.15)
S70785 S70785 Escherichia coli 562 -11536561 7500879456 csge assembly
/transport component in curli (db:genpept-bct1) (de:e.coli csge, csge,
csge, csge, csge, and orf genes.) (le:1434) (re:1823) (di:complement)
ECCSGABDG X90754 g1147561 Escherichia coli 562 -11536561 232586 csge curli
production assembly/transport component (fn:structural component; surface
structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of
400 of the completegenome.) (nt:f129; 100 pct identical to csge_ecoli sw:
p52105) (le:6698) (re:7087) (di:complement) AE000205 AE000205 g1787276
Escherichia coli 562 -11536561 5000691961 csge curli production
assembly/transport component (sr:escherichia coli(strain:k12) dna,
clone:kohara clone #230) (db:genpept) (de:escherichia coli genomic dna.
(23.5 - 23.8 min).) (nt:orf_id:o231#7; similar to swissprot accession)
(le:12217) (re:12606) (di:complement) D90740 D90740 g4062603 Escherichia
coli 562 -11536561 7502852312 csge curli production assembly/transport
component (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231)
(db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).)
(nt:orf_id:o231#7; similar to swissprot accession) (le:5418) (re:5807)
(di:complement) D90741 D90741 g4062612 Escherichia coli 562 -11536561

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872336	13491	35647	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872346	13492	35648	300	99

Description

6500732704 csgd:b1040 putative regulatory protein:probable csgab operon transcriptional regulatory protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1040 b1040 Escherichia coli 562 -11536562 66631 csgd (de:probable csgab operon transcriptional regulatory protein) (db:swissprot) CSGD_ECOLI P52106 ESCHERICHIA COLI 562 -11536562 7000684917 csgd probable transcription regulator csgd (db:pir2.dat) (mp:23.15) S70786 S70786 Escherichia coli 562 -11536562 7500879455 csgd putative regulatory protein (db:genpept-bct1) (de:e.coli csgg, csgf, csge, csgd, csgb, csga, and orf genes.) (nt:necessary for transcription of the csgba operon) (le:1828) (re:2478) (di:complement) ECCSGABDG X90754 g1147562 Escherichia coli 562 -11536562 232587 csgd putative 2-component transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 95 of 400 of the completegenome.) (nt:f216; 100 pct identical to csgd_ecoli sw:) (le:7092) (re:7742) (di:complement) AE000205 AE000205 g1787277 Escherichia coli 562 -11536562 5000691962 csgd probable csgab operon transcriptional regulatory (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231) (db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).) (nt:orf_id:o231#8; similar to swissprot accession) (le:5812) (re:6462) (di:complement) D90741 D90741 g4062613 Escherichia coli 562 -11536562

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872360	13493	35649	1179	392

6500732705 cs.gb:bl041 nucleation component of curlin monomers:minor curlin subunit precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0)
(db:gtr-escherichia coli) bl041 bl041 Escherichia coli 562 -11536563 66630
cs.gb (de:minor curlin subunit precursor) (db:swissprot) CSGB_ECOLI P39828
ESCHERICHIA COLI 562 -11536563 7000684915 cs.gb curlin nucleator protein
cs.gb precursor:cs.gb protein:curlin nucleation component:minor curlin protein
(db:pir2.dat) (mp:23.15) S70787 S70787 Escherichia coli 562 -11536563
223335 cs.gb minor curlin subunit precursor (sr:escherichia coli(strain:k12)
dna, clone:kohara clone #231) (db:genpept-bct1) (de:escherichia coli genomic
dna. (23.6 - 23.9 min).) (le:7217) (re:7672) (di:direct) D90741 D90741
g1651510 Escherichia coli 562 -11536563 7500879453 cs.gb nucleation
component of curlin monomers (db:genpept-bct1) (de:e.coli cs.gb, cs.gf, cs.ge,
cs.gd, cs.gb, cs.ga, and orf genes.) (le:3233) (re:3688) (di:direct) ECCSGABDG
X90754 g1147563 Escherichia coli 562 -11536563 232588 cs.gb minor curlin
subunit precursor:similar to cs.ga (fn:structural component; surface
structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 95 of
400 of the complete genome.) (nt:o151 was 0160; 100 pct identical to
cs.gb_ecoli) (le:8497) (re:8952) (di:direct) AE000205 AE000205 g1787278
Escherichia coli 562 -11536563 5000691963 cs.gb minor curlin subunit
precursor. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #231)
(db:genpept) (de:escherichia coli genomic dna. (23.7 - 24.0 min).)
(nt:orf_id:o231#9; similar to swissprot accession) (le:7217) (re:7672)
(di:direct) D90741 D90741 g1651510 Escherichia coli 562 -11536563

Description

Hypothetical protein

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872418	13496	35652	420	139

Description

6500732706 flgn:b1070 flagella synthesis protein flgn (gtcfc:11.3)
 (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1070 b1070
 Escherichia coli 562 -11536564 71936 flgn (de:flagella synthesis protein
 flgn) (db:swissprot) FLGN_ECOLI P43533 ESCHERICHIA COLI 562 -11536564
 7000685274 flgn flagellar biosynthesis protein flgn (cl:flgn protein)
 (db:pir2.dat) C64850 C64850 Escherichia coli 562 -11536564 223348 flgn
 flagella synthesis protein flgn (sr:escherichia coli(strain:k12) dna,
 clone:kohara clone #233) (db:genpept-bct1) (de:escherichia coli genomic dna.
 (24.0 - 24.4 min).) (le:15780) (re:16196) (di:complement) D90743 D90743
 g1651525 Escherichia coli 562 -11536564 7500881564 flgn protein of
 flagellar biosynthesis (fn:phenotype; surface structures) (db:genpept-bct2)
 (de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.)
 (nt:fl138; 100 pct identical to fragment flgn_ecoli) (le:1660) (re:2076)
 (di:complement) AE000208 AE000208 g1787310 Escherichia coli 562 -11536564
 5000691985 flgn flagella synthesis protein flgn . (sr:escherichia
 coli(strain:k12) dna, clone:kohara clone #233) (db:genpept) (de:escherichia
 coli genomic dna. (24.1 - 24.5 min).) (nt:orf_id:o233#18; similar to
 swissprot accession) (le:15780) (re:16196) (di:complement) D90743 D90743
 g1651525 Escherichia coli 562 -11536564

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872422	13497	35653	873	290

Description

GTC ORF with score 226 to: (or:Homo sapiens) (sr:information)
 (db:genpept-pri2) (de:human pac clone dj318c15 from xq23, complete
 sequence.) (nt:very similar and perhaps identical to hs-cul-4b.;)
 (le:100599:103940) (re:100694:104092) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872423	13498	35654	471	156

Description

6500732707 flgi:flam:fla_fix:b1080 flagellar p-ring protein precursor (gtcfc:11.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1080 b1080 Escherichia coli 562 -11536565 118230 flgi:flam:fla::fix (de:flagellar p-ring protein precursor) (db:swissprot) FLGI_ECOLI P75941 ESCHERICHIA COLI 562 -11536565 7000685268 flgi:flam:fla_fix flagellar basal body p-ring protein precursor (cl:flagellar basal body p-ring protein flgi) (db:pir2.dat) E64851 E64851 Escherichia coli 562 -11536565 7500881560 flgi homolog of salmonella p-ring of flagella basal (fn:putative structure; surface structures) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 98 of 400 of the completegenome.) (nt:o365; 92 pct identical to flgi_salty sw: p15930) (le:8520) (re:9617) (di:direct) AE000208 AE000208 g1787320 Escherichia coli 562 -11536565 5000691986 flgi flagellar basal body p-ring protein precursor (sr:escherichia coli(strain:k12) dna, clone:kohara clone #234) (db:genpept) (de:escherichia coli genomic dna. (24.5 - 24.8 min).) (nt:orf_id:o234#4; similar to pir accession number) (le:3228) (re:4325) (di:direct) D90744 D90744 g4062658 Escherichia coli 562 -11536565

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872453	13499	35655	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872455	13500	35656	576	191

Description

6500732708 hemk:b1212 possibly protoporphyrinogen oxidase:possible
protoporphyrinogen oxidase (gtcfc:9.10) (ec:1.3.3.-) (keggfc:14.1)
(rileyfc:5.8.0) (db:gtc-escherichia coli) b1212 b1212 Escherichia coli 562
-11536566 76735 hemk (de:hemk protein) (db:swissprot) HEMK_ECOLI P37186
ESCHERICHIA COLI 562 -11536566 164431 hemk hemk protein::protoporphyrinogen
oxidase (ec:1.3.3.-) (db:pir2.dat) I83570 I83570 Escherichia coli 562
-11536566 223414 hemk possible protoporphyrinogen oxidase (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #247) (db:genpept-bct1)
(de:escherichia coli genomic dna. (27.0 -27.4 min).) (le:10356) (re:11189)
(di:direct) D90756 D90756 g1651602 Escherichia coli 562 -11536566 223421
hemk possible protoporphyrinogen oxidase (sr:escherichia coli(strain:k12)
dna, clone:kohara clone #248) (db:genpept-bct1) (de:escherichia coli genomic
dna (27.2-27.6 min).) (le:1218) (re:2051) (di:direct) D90757 D90757 g1651610
Escherichia coli 562 -11536566 238747 hemk possible protoporphyrinogen
oxidase (fn:putative enzyme; biosynthesis of cofactors,) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 109 of 400 of the completegenome.)
(nt:o277; 99 pct identical to pir: i83570; 99 pct) (le:9788) (re:10621)
(di:direct) AE000219 AE000219 g1787463 Escherichia coli 562 -11536566
7500883185 hemk (db:genpept-bct2) (de:escherichia coli kdsa operon genes,
complete cds.) (nt:possible protoporphyrinogen oxidase) (le:4236) (re:5069)
(di:direct) ECU18555 U18555 g968931 Escherichia coli 562 -11536566
5000692072 hemk protoporphyrinogen oxidase ec 1.3.3.4 hemk (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia
coli genomic dna. (27.1 - 27.5 min).) (nt:orf_id:o248#2; similar to pir
accession number) (le:10356) (re:11189) (di:direct) D90756 D90756 g1651602
Escherichia coli 562 -11536566 7502852313 hemk protoporphyrinogen oxidase
ec 1.3.3.4 hemk (sr:escherichia coli(strain:k12) dna, clone:kohara clone
#248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).)
(nt:orf_id:o248#2; similar to pir accession number) (le:1218) (re:2051)
(di:direct) D90757 D90757 g1651610 Escherichia coli 562 -11536566

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872458	13501	35657	699	232

Description

6500732709 chab:b1217 cation transport regulator chab (gtcfc:12.5) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) (gtcfc:cell processes-transport of cations (na_k_ca_nh4_etc_)) b1217 b1217 Escherichia coli 562 -11536567 64202 chab (de:cation transport regulator chab) (db:swissprot) CHAB_ECOLI P39162 ESCHERICHIA COLI 562 -11536567 7000684803 chab cation transport regulator chab (db:pir2.dat) F64868 F64868 Escherichia coli 562 -11536567 223417 chab cation transport regulator chab (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept-bct1) (de:escherichia coli genomic dna.(27.0 -27.4 min).) (le:16381) (re:16611) (di:direct) D90756 D90756 g1651605 Escherichia coli 562 -11536567 223424 chab cation transport regulator chab (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept-bct1) (de:escherichia coli genomic dna (27.2-27.6 min).) (le:7243) (re:7473) (di:direct) D90757 D90757 g1651613 Escherichia coli 562 -11536567 7500878627 chab cation transport regulator (sr:escherichia coli (strain nm8191) (library: delta-b) dna) (db:genpept-bct1) (de:escherichia coli (nm8191) calcium/proton antiporter protein (chaa,chac and chab) genes, complete cds.) (nt:putative) (le:1688) (re:1918) (di:complement) ECOCHAABC L28709 g495779 Escherichia coli 562 -11536567 233971 chab cation transport regulator (fn:regulator; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 110 of 400 of the completegenome.) (nt:o76; 100 pct identical to chab_ecoli sw: p39162) (le:2265) (re:2495) (di:direct) AE000220 AE000220 g1787469 Escherichia coli 562 -11536567 5000692075 chab cation transport regulator chab. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247) (db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).) (nt:orf_id:o248#7; similar to swissprot accession) (le:16381) (re:16611) (di:direct) D90756 D90756 g1651605 Escherichia coli 562 -11536567 7502852314 chab cation transport regulator chab. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia coli genomic dna. (27.3 - 27.7 min).) (nt:orf_id:o248#7; similar to swissprot accession) (le:7243) (re:7473) (di:direct) D90757 D90757 g1651613 Escherichia coli 562 -11536567

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872465	13502	35658	246	81

Description

6500732710 chac:b1218 cation transport protein chac (gtcfc:12.5)
(keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) (gtcfc:cell
processes-transport of cations (na_k_ca_nh4_etc_)) b1218 b1218 Escherichia
coli 562 -11536568 64203 chac (de:cation transport protein chac)
(db:swissprot) CHAC_ECOLI P39163 ESCHERICHIA COLI 562 -11536568 7000684804
chac cation transport protein chac (db:pir2.dat) G64868 G64868 Escherichia
coli 562 -11536568 223418 chac cation transport protein chac
(sr:escherichia coli(strain:k12) dna, clone:kohara clone #247)
(db:genpept-bct1) (de:escherichia coli genomic dna.(27.0 -27.4 min).)
(le:16748) (re:17464) (di:direct) D90756 D90756 g1651606 Escherichia coli
562 -11536568 223425 chac cation transport protein chac (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #248) (db:genpept-bct1)
(de:escherichia coli genomic dna (27.2-27.6 min).) (le:7610) (re:8326)
(di:direct) D90757 D90757 g1651614 Escherichia coli 562 -11536568
7500878628 chac cation transport regulator (fn:transport; transport of
small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
110 of 400 of the completgenome.) (nt:o238; 99 pct identical to chac_ecoli
sw: p39163) (le:2632) (re:3348) (di:direct) AE000220 AE000220 g1787470
Escherichia coli 562 -11536568 5000692076 chac cation transport protein
chac. (sr:escherichia coli(strain:k12) dna, clone:kohara clone #247)
(db:genpept) (de:escherichia coli genomic dna. (27.1 - 27.5 min).)
(nt:orf_id:o248#8; similar to swissprot accession) (le:16748) (re:17464)
(di:direct) D90756 D90756 g1651606 Escherichia coli 562 -11536568
7502852315 chac cation transport protein chac. (sr:escherichia
coli(strain:k12) dna, clone:kohara clone #248) (db:genpept) (de:escherichia
coli genomic dna. (27.3 - 27.7 min).) (nt:orf_id:o248#8; similar to
swissprot accession) (le:7610) (re:8326) (di:direct) D90757 D90757 g1651614
Escherichia coli 562 -11536568

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872466	13503	35659	1230	409

Description

6500732711 ordl:b1301 putative oxidoreductase:probable oxidoreductase ordl
(gtcfc:14.3) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia
coli) b1301 b1301 Escherichia coli 562 -11536569 87866 ordl (ec:1.-.-.-)
(de:probable oxidoreductase ordl,) (db:swissprot) ORDL_ECOLI P37906
ESCHERICHIA COLI 562 -11536569 7000686058 ordl probable oxidoreductase:ordl
(cl:hypothetical protein hi0499) (ec:1.-.-.-) (db:pir2.dat) H64878 H64878
Escherichia coli 562 -11536569 223543 ordl probable oxidoreductase ordl ec
1.-.-.-. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda
minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#257(29.1-29.6 min.)) (nt:orf_id:o257#10; similar to (swissprot accession)
(le:11602) (re:12882) (di:direct) D90768 D90768 g1742131 Escherichia coli
562 -11536569 239555 ordl probable oxidoreductase (fn:putative enzyme; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 118
of 400 of the completegenome.) (nt:o426; 100 pct identical to gb:
ecu38543_1) (le:4897) (re:6177) (di:direct) AE000228 AE000228 g1787559
Escherichia coli 562 -11536569 300333 ordl oxidoreductase (sr:escherichia
coli strain=k-12) (db:genpept-bct2) (de:escherichia coli oxidoreductase
(ordl) and gaba-aminotransferase(goag) genes, complete cds.)
(nt:hypothetical 47.1kda protein; ordl; orfy) (le:1) (re:1281) (di:direct)
ECU38543 U38543 g1054921 Escherichia coli 562 -11536569 5000692117
(de:(ecoli_1261) (pn:probable oxidoreductase ordl) (gn:ordl)
(gtcfc:13.7:14.1) (ec:1.-.-.-) (ordl_ecoli) (keggfc:11.1) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_1261 ECOLI_1261 Escherichia coli 562
10030007

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872476	13504	35660	216	71

Description

6500732712 psipa:b1304 phage shock protein a (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1304 b1304 Escherichia coli 562 -11536570 7000691881 psipa phage shock protein a (db:pir2.dat) C64879 C64879 Escherichia coli 562 -11536570 223546 psipa phage shock protein a (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf_id:o257#13; similar to (pir accession number) (le:15449) (re:16117) (di:direct) D90768 D90768 g1742134 Escherichia coli 562 -11536570 300344 psipa phage shock protein a (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o257#13; similar to (pir accession number) (le:1453) (re:2121) (di:direct) D90769 D90769 g1742143 Escherichia coli 562 -11536570 300336 psipa phage shock protein:inner membrane protein (fn:factor; phage-related functions and prophages) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 118 of 400 of the completegenome.) (nt:o222; 100 pct identical to psipa_ecoli sw: p23853;) (le:8744) (re:9412) (di:direct) AE000228 AE000228 g2367118 Escherichia coli 562 -11536570 223554 psipa phage shock protein a (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o257#13; similar to (pir accession number) (le:1453) (re:2121) (di:direct) D90769 D90769 g1742143 Escherichia coli 562 -11536570

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872492	13505	35661	1389	462

Description

6500732713 pspb:b1305 phage shock protein b (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1305 b1305 Escherichia coli 562 -11536571 300337 pspb (de:phage shock protein b) (db:swissprot) PSPB_ECOLI P23854 ESCHERICHIA COLI 562 -11536571 164272 pspb phage shock protein b (db:pir2.dat) S17122 S17122 Escherichia coli 562 -11536571 223547 pspb phage shock protein b (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf_id:o257#14; similar to (pir accession number) (le:16171) (re:16395) (di:direct) D90768 D90768 g1742135 Escherichia coli 562 -11536571 300345 pspb phage shock protein b (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o257#14; similar to (pir accession number) (le:2175) (re:2399) (di:direct) D90769 D90769 g1742144 Escherichia coli 562 -11536571 5000692120 pspb pspb protein (db:genpept-bct1) (de:e.coli stress-induced psp operon dna.) (le:1220) (re:1444) (di:direct) ECPSP X57560 g42540 Escherichia coli 562 -11536571 237930 pspb phage shock protein (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 118 of 400 of the completegenome.) (nt:o74; 100 pct identical to pspb_ecoli sw: p23854; cg) (le:9466) (re:9690) (di:direct) AE000228 AE000228 g1787563 Escherichia coli 562 -11536571 91999 pspb (de:phage shock protein b) (db:swissprot) PSPB_ECOLI P23854 ESCHERICHIA COLI 562 -11536571 223555 pspb phage shock protein b (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o257#14; similar to (pir accession number) (le:2175) (re:2399) (di:direct) D90769 D90769 g1742144 Escherichia coli 562 -11536571

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501872499	13506	35662	258	85

Description

6500732714 pspc:b1306 phage shock protein c (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1306 b1306 Escherichia coli 562 -11536572 300338 pspc (de:phage shock protein c) (db:swissprot) PSPC_ECOLI P23855 ESCHERICHIA COLI 562 -11536572 164273 pspc phage shock protein c (db:pir2.dat) S17123 S17123 Escherichia coli 562 -11536572 223548 pspc phage shock protein c (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf_id:o257#15; similar to (pir accession number) (le:16395) (re:16754) (di:direct) D90768 D90768 g1742136 Escherichia coli 562 -11536572 300346 pspc phage shock protein c (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o257#15; similar to (pir accession number) (le:2399) (re:2758) (di:direct) D90769 D90769 g1742145 Escherichia coli 562 -11536572 5000692121 pspc pspc protein (db:genpept-bct1) (de:e.coli stress-induced psp operon dna.) (le:1444) (re:1803) (di:direct) ECPSP X57560 g42541 Escherichia coli 562 -11536572 237931 pspc phage shock protein:activates phage (fn:factor; phage-related functions and prophages) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 118 of 400 of the completegenome.) (nt:o119; 100 pct identical to pspc_ecoli sw: p23855;) (le:9690) (re:10049) (di:direct) AE000228 AE000228 g1787564 Escherichia coli 562 -11536572 92007 pspc (de:phage shock protein c) (db:swissprot) PSPC_ECOLI P23855 ESCHERICHIA COLI 562 -11536572 223556 pspc phage shock protein c (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o257#15; similar to (pir accession number) (le:2399) (re:2758) (di:direct) D90769 D90769 g1742145 Escherichia coli 562 -11536572

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872502	13507	35663	693	230

Description

6500732715 pspd:b1307 phage shock protein d (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1307 b1307 Escherichia coli 562 -11536573 300339 pspd (de:phage shock protein d) (db:swissprot) PSPD_ECOLI P23856 ESCHERICHIA COLI 562 -11536573 164274 pspd phage shock protein d (db:pir2.dat) S17124 S17124 Escherichia coli 562 -11536573 223549 pspd phage shock protein d (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf_id:o257#16; similar to (pir accession number) (le:16763) (re:16984) (di:direct) D90768 D90768 g1742137 Escherichia coli 562 -11536573 300347 pspd phage shock protein d (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o257#16; similar to (pir accession number) (le:2767) (re:2988) (di:direct) D90769 D90769 g1742146 Escherichia coli 562 -11536573 5000692122 pspd pspd protein (db:genpept-bct1) (de:e.coli stress-induced psp operon dna.) (le:1812) (re:2033) (di:direct) ECPSP X57560 g42542 Escherichia coli 562 -11536573 237932 pspd phage shock protein (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 118 of 400 of the completegenome.) (nt:o73; 100 pct identical to pspd_ecoli sw: p23856) (le:10058) (re:10279) (di:direct) AE000228 AE000228 g1787565 Escherichia coli 562 -11536573 92016 pspd (de:phage shock protein d) (db:swissprot) PSPD_ECOLI P23856 ESCHERICHIA COLI 562 -11536573 223557 pspd phage shock protein d (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o257#16; similar to (pir accession number) (le:2767) (re:2988) (di:direct) D90769 D90769 g1742146 Escherichia coli 562 -11536573

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872511	13508	35664	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872526	13509	35665	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872540	13510	35666	774	257

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872543	13511	35667	390	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872544	13512	35668	543	180

Description

6500732716 pspe:b1308 phage shock protein e precursor (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1308 b1308 Escherichia coli 562 -11536574 300340 pspe (de:phage shock protein e precursor) (db:swissprot) PSPE_ECOLI P23857 ESCHERICHIA COLI 562 -11536574 164275 pspe phage shock protein e precursor (cl:glpe protein) (db:pir2.dat) S17125 S17125 Escherichia coli 562 -11536574 223550 pspe phage shock protein e (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #257(29.1-29.6 min.)) (nt:orf_id:o257#17; similar to (pir accession number) (le:17059) (re:17373) (di:direct) D90768 D90768 g1742138 Escherichia coli 562 -11536574 300348 pspe phage shock protein e (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o257#17; similar to (pir accession number) (le:3063) (re:3377) (di:direct) D90769 D90769 g1742147 Escherichia coli 562 -11536574 5000692123 pspe pspe protein (db:genpept-bct1) (de:e.coli stress-induced psp operon dna.) (le:2108) (re:2422) (di:direct) ECPSP X57560 g42543 Escherichia coli 562 -11536574 237933 pspe phage shock protein (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 119 of 400 of the completegenome.) (nt:o104; 100 pct identical to pspe_ecoli sw: p23857;) (le:68) (re:382) (di:direct) AE000229 AE000229 g1787567 Escherichia coli 562 -11536574 92020 pspe (de:phage shock protein e precursor) (db:swissprot) PSPE_ECOLI P23857 ESCHERICHIA COLI 562 -11536574 223558 pspe phage shock protein e (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #258(29.5-29.8 min.)) (nt:orf_id:o257#17; similar to (pir accession number) (le:3063) (re:3377) (di:direct) D90769 D90769 g1742147 Escherichia coli 562 -11536574

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872562	13513	35669	252	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872563	13514	35670	291	96

Description

GTC ORF with score 144 to: (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 223 of 400 of the completegenome.) (nt:o316; residues 11-309 are 66 pct identical to) (le:2709) (re:3659) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872565	13515	35671	393	130

Description

6500732717 tpx:b1324 thiol peroxidase:scavengase p20 (gtcfc:12.12) (ec:1.11.1.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1324 b1324 Escherichia coli 562 -11536575 7000691868 tpx thiol peroxidase:tpx:scavengase p20 (cl:thiol peroxidase) (ec:1.11.1.-) (db:pir2.dat) JC5504 JC5504 Escherichia coli 562 -11536575 1500689807 tpx thiol peroxidase (fn:enzyme; detoxification) (db:genpept-bct2) (ec:1.11.1.-) (de:escherichia coli k-12 mg1655 section 120 of 400 of the completegenome.) (nt:f168; 99 pct identical to gb: ecu33213_1) (le:6467) (re:6973) (di:complement) AE000230 AE000230 g1787584 Escherichia coli 562 -11536575 7500960390 scavengase p20 (db:genpept-bct2) (de:escherichia coli scavengase p20 gene, complete cds.) (nt:thiol peroxidase) (le:1) (re:507) (di:direct) ECU93212 U93212 g1931625 Escherichia coli 562 -11536575 5000692138 (de:(ecoli_1284) (pn:thiol peroxidase:p20) (gn:tpx) (gtcfc:13.7:14.1) (ec:1.11.1.-) (tpx_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1284 ECOLI_1284 Escherichia coli 562 10123265

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872568	13516	35672	363	120

Description

6500732718 lar:b1348 restriction alleviation and modification enhancement protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1348 b1348 Escherichia coli 562 -11536576 81518 lar (de:restriction alleviation and modification enhancement protein) (db:swissprot) LAR_ECOLI P33229 ESCHERICHIA COLI 562 -11536576 7000685707 lar restriction alleviation and modification enhancement protein:lar protein (db:pir2.dat) G64884 G64884 Escherichia coli 562 -11536576 223621 lar restriction alleviation and modification (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #262(30.3-30.5 min.)) (nt:orf_id:o262#7; similar to (swissprot accession) (le:9532) (re:9726) (di:complement) D90773 D90773 g1742214 Escherichia coli 562 -11536576 300394 lar restriction alleviation and modification (fn:enzyme; phage-related functions and prophages) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 122 of 400 of the completegenome.) (nt:f64; 100 pct identical lar_ecoli sw: p33229) (le:9103) (re:9297) (di:complement) AE000232 AE000232 g1787610 Escherichia coli 562 -11536576 5000692158 (de:(ecoli_1308) (pn:restriction alleviation and modification enhancement) (gn:lar) (gtcfc:13.7:14.1) (ec:) (lar_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1308 ECOLI_1308 Escherichia coli 562 10023754

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872584	13517	35673	429	142

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872592	13518	35674	2676	892

Description

6500732719 hslj:b1379 beta-lactamase precursor:heat shock protein hslj
 (gtcfc:12.7:13.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli)
 b1379 b1379 Escherichia coli 562 -11536577 77892 hslj (de:heat shock
 protein hslj) (db:swissprot) HSLJ_ECOLI P52644 ESCHERICHIA COLI 562
 -11536577 7000685563 hslj heat shock protein precursor hslj (db:pir2.dat)
 F64888 F64888 Escherichia coli 562 -11536577 223657 hslj heat shock protein
 hslj. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #264(30.7-31.1
 min.)) (nt:orf_id:o264#7; similar to (swissprot accession) (le:15680)
 (re:16102) (di:complement) D90775 D90775 g1742252 Escherichia coli 562
 -11536577 300435 hslj heat shock protein hslj. (sr:escherichia coli
 (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
 (de:e.coli genomic dna, kohara clone #265(30.9-31.2 min.))
 (nt:orf_id:o264#7; similar to (swissprot accession) (le:5398) (re:5820)
 (di:complement) D90776 D90776 g1742258 Escherichia coli 562 -11536577
 300430 hslj heat shock protein hslj (fn:factor; adaptations, atypical
 conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 125
 of 400 of the completegenome.) (nt:f140; 100 pct identical to hslj_ecoli sw:
 p52644) (le:299) (re:721) (di:complement) AE000235 AE000235 g1787644
 Escherichia coli 562 -11536577 223662 hslj heat shock protein hslj.
 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #265(30.9-31.2
 min.)) (nt:orf_id:o264#7; similar to (swissprot accession) (le:5398)
 (re:5820) (di:complement) D90776 D90776 g1742258 Escherichia coli 562
 -11536577 5000692185 (de:(ecoli_1339) (pn:heat shock protein hslj)
 (gn:hslj) (gtcfc:13.7:14.1) (ec:) (hslj_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli)) ECOLI_1339 ECOLI_1339 Escherichia coli 562
 10020251

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872610	13519	35675	1014	337
<u>Description</u>				
5000692206 tra8_2:tra8_3:b1404 transposase for insertion sequence element is30:is30 transposase (gtcfc:13.5) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1404 b1404 Escherichia coli 562 -11536578 300460 b0256:b1404:b4284 (de:transposase for insertion sequence element is30) (db:swissprot) TRA8_ECOLI P37246 ESCHERICHIA COLI 562 -11536578 163937 tra8_2 transposase (cl:insertion sequence element is30 transposase) (db:pir2.dat) F65241 F65241 Escherichia coli 562 -11536578 223687 is30 transposase for insertion sequence element (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #267(31.4-31.7 min.)) (nt:orf_id:o267#11; similar to (swissprot accession) (le:13357) (re:14508) (di:direct) D90778 D90778 g1742285 Escherichia coli 562 -11536578 223694 is30 transposase for insertion sequence element (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #268(31.6-32.0 min.)) (nt:orf_id:o267#11; similar to (swissprot accession) (le:2068) (re:3219) (di:direct) D90779 D90779 g1651648 Escherichia coli 562 -11536578 300467 (db:genpept-bct1) (de:e. coli k12 mobile genetic element is30.) (nt:put. is30 transposase) (le:63) (re:1214) (di:direct) ECIS30 X00792 g404301 Escherichia coli 562 -11536578 6500732720 is30 transposase (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:198300) (re:199451) (di:complement) ECOUW93 U14003 g537125 Escherichia coli 562 -11536578 233249 tra8_2 is30 transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 127 of 400 of the completegenome.) (nt:o383; 99 pct identical to tra8_ecoli sw: p37246) (le:5900) (re:7051) (di:direct) AE000237 AE000237 g1787671 Escherichia coli 562 -11536578 237489 tra8_3 is30 transposase (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 389 of 400 of the completegenome.) (nt:f383; 99 pct identical amino acid sequence and) (le:962) (re:2113) (di:complement) AE000499 AE000499 g1790736 Escherichia coli 562 -11536578 7500893360 b0256:b1404:b4284 (de:transposase for insertion sequence element is30) (db:swissprot) TRA8_ECOLI P37246 ESCHERICHIA COLI 562 -11536578 7000689487 tra8_2 transposase insertion sequence is30 (cl:insertion sequence element is30 transposase) (db:pir) F65241 F65241 Escherichia coli 562 -11536578				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872612	13520	35676	210	69

Description

6500732721 acpd:b1412 acyl carrier protein phosphodiesterase:acp
phosphodiesterase (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0)
(db:gtc-escherichia coli) b1412 b1412 Escherichia coli 562 -11536579
7000690848 acpd acyl-carrier-protein phosphodiesterase, acpd) (cl:acyl
carrier protein phosphodiesterase) (ec:3.1.4.14) (db:pir2.dat) G64892 G64892
Escherichia coli 562 -11536579 223699 acyl carrier protein
phosphodiesterase acp (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #268(31.6-32.0 min.)) (nt:orf_id:o268#8; similar to (swissprot
accession) (le:14964) (re:15569) (di:complement) D90779 D90779 g1742298
Escherichia coli 562 -11536579 223703 acyl carrier protein
phosphodiesterase acp (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #269(31.8-32.1 min.)) (nt:orf_id:o268#8; similar to (swissprot
accession) (le:5107) (re:5712) (di:complement) D90780 D90780 g1742303
Escherichia coli 562 -11536579 300472 acpd acyl carrier protein
phosphodiesterase (fn:enzyme; fatty acid and phosphatidic acid)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 128 of 400 of the
completegenome.) (nt:f201; 90 pct identical to acpd_ecoli sw: p41407 but)
(le:8168) (re:8773) (di:complement) AE000238 AE000238 g1787680 Escherichia
coli 562 -11536579 5000692214 (de:(ecoli_1372) (pn:acyl carrier protein
phosphodiesterase:fragment) (gn:acpd) (gtcfc:13.7:14.1) (ec:) (acpd_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1372
ECOLI_1372 Escherichia coli 562 10119587

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872615	13521	35677	786	261

Description

GTC ORF with score 293 to: (de:(yhr020w) (pn:putative prolyl-trna synthetase
yhr020w:proline--trna ligase:prors:strong similarity to human
glutamyl-prolyl-trna synthetase and fruit fly multifunctional aminoacyl-trna
synthetase) (gtcfc:5.10:10.6) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872626	13522	35678	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872631	13523	35679	450	150
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872635	13524	35680	417	138
<u>Description</u>				

6500732722 hrpa:b1413 atp-dependent helicase hrpa (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1413 b1413 Escherichia coli 562 -11536580 77622 hrpa (de:atp-dependent helicase hrpa) (db:swissprot) HRPA_ECOLI P43329 ESCHERICHIA COLI 562 -11536580 7000685559 hrpa atp-dependent helicase hrpa (cl:unassigned dead/h box helicases:dead/h box helicase homology) (db:pir2.dat) H64892 H64892 Escherichia coli 562 -11536580 223704 atp-dependent helicase hrpa homolog. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #269(31.8-32.1 min.)) (nt:orf_id:o269#1; similar to (swissprot accession) (le:5970) (re:9815) (di:direct) D90780 D90780 g1742304 Escherichia coli 562 -11536580 7500883524 hrpa helicase:atp-dependent (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 128 of 400 of the completegenome.) (nt:o1281; 98 pct identical (4 gaps) to hrpa_ecoli) (le:9031) (re:12876) (di:direct) AE000238 AE000238 g1787681 Escherichia coli 562 -11536580 5000692215 (de:(ecoli_1373) (pn:helicase, atp-dependent) (gn:hrpa) (gtcfc:13.7:14.1) (ec:) (hrpa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1373 ECOLI_1373 Escherichia coli 562 10119590

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872642	13525	35681	1416	471

Description

6500732723 rhse:b1456 rhse protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1456 b1456 Escherichia coli 562 -11536581 94325 rhse (de:rhse protein) (db:swissprot) RHSE_ECOLI P24211 ESCHERICHIA COLI 562 -11536581 7000686324 rhse rhse protein (db:pir2.dat) (mp:32 min) C64898 C64898 Escherichia coli 562 -11536581 223763 rhse rhse protein fragment . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #274(32.7-33.0 min.)) (nt:orf_id:o274#4; similar to (swissprot accession) (le:10126) (re:12174) (di:direct) D90785 D90785 g1742368 Escherichia coli 562 -11536581 223770 rhse rhse protein fragment . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #275(32.8-33.2 min.)) (nt:orf_id:o274#4; similar to (swissprot accession) (le:4194) (re:6242) (di:direct) D90786 D90786 g1742376 Escherichia coli 562 -11536581 300528 rhse rhse protein in rhs element (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 132 of 400 of the completegenome.) (nt:o682; 99 pct identical to rhse_ecoli sw: p24211 but) (le:9030) (re:11078) (di:direct) AE000242 AE000242 g1787728 Escherichia coli 562 -11536581 5000692250 (de:(ecoli_1416) (pn:rhse protein:fragment) (gn:rhse) (gtcfc:13.7:14.1) (ec:) (rhse_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1416 ECOLI_1416 Escherichia coli 562 10119618

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501872652	13526	35682	498	165

Description

6500732724 ydcc:b1460 h repeat-associated protein in rhse-narv intergenic region:orf-h (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1460 b1460 Escherichia coli 562 -11536582 111250 ydcc (de:h repeat-associated protein in rhse-narv intergenic region (orf-h)) (db:swissprot) YDCC_ECOLI P28917 ESCHERICHIA COLI 562 -11536582 7000687516 ydcc h repeat-associated protein-like protein b1460:ydcc protein (db:pir2.dat) G64898 G64898 Escherichia coli 562 -11536582 300532 ydcc h repeat-associated protein in rhse-narv (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #274(32.7-33.0 min.)) (nt:orf_id:o274#9; similar to (swissprot accession) (le:14052) (re:15188) (di:direct) D90785 D90785 g1742372 Escherichia coli 562 -11536582 223774 ydcc h repeat-associated protein in rhse-narv (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #275(32.8-33.2 min.)) (nt:orf_id:o274#9; similar to (swissprot accession) (le:8120) (re:9256) (di:direct) D90786 D90786 g1742380 Escherichia coli 562 -11536582 300538 ydcc h repeat-associated protein in rhse-narv (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #276(33.0-33.3 min.)) (nt:orf_id:o274#9; similar to (swissprot accession) (le:2046) (re:3182) (di:direct) D90787 D90787 g1742393 Escherichia coli 562 -11536582 235830 orf-h (fn:unknown) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli h repeat-associated orf, complete cds.) (le:165) (re:1301) (di:direct) ECORHSEA L02372 g147651 Escherichia coli 562 -11536582 299931 (db:genpept-bct1) (de:escherichia coli rhse genetic element; defective rhse core protein,complete cds; complete orf-e2; h-rpt subelement; complete orf-h.) (nt:orfh; putative) (le:3926) (re:5062) (di:direct) ECORHSEX L19083 g304947 Escherichia coli 562 -11536582 235827 ydcc putative receptor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 133 of 400 of the completegenome.) (nt:o378; 100 pct identical to ydcc_ecoli sw:) (le:1351) (re:2487) (di:direct) AE000243 AE000243 g1787733 Escherichia coli 562 -11536582 223767 ydcc h repeat-associated protein in rhse-narv (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #274(32.7-33.0 min.)) (nt:orf_id:o274#9; similar to (swissprot accession) (le:14052) (re:15188) (di:direct) D90785 D90785 g1742372 Escherichia coli 562 -11536582 223786 ydcc h repeat-associated protein in rhse-narv (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #276(33.0-33.3 min.)) (nt:orf_id:o274#9; similar to (swissprot accession) (le:2046) (re:3182) (di:direct) D90787 D90787 g1742393 Escherichia coli 562 -11536582 5000692254 (de:(ecoli_1420) (pn:h repeat-associated protein in rhse-narv intergenic region:orf-h) (gn:ydcc) (gtcfc:13.7:14.1) (ec:) (ydcc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1420 ECOLI_1420 Escherichia coli 562 10052980

ECOLI_1420 Escherichia coli 562 10052980

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501872661	13527	35683	342	113
Description				
<p>6500732725 naru:b1469 nitrite extrusion protein:nitrite extrusion protein 2:nitrite facilitator 2 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1469 b1469 Escherichia coli 562 -11536583 85254 naru (de:nitrite extrusion protein 2 (nitrite facilitator 2)) (db:swissprot) NARU_ECOLI P37758 ESCHERICHIA COLI 562 -11536583 7000685930 naru nitrite extrusion protein naru (cl:nitrate transport protein nark) (db:pir2.dat) S11431 H64899 Escherichia coli 562 -11536583 223794 naru nitrite extrusion protein 2 nitrite facilitator (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #276(33.0-33.3 min.)) (nt:orf_id:o276#8; similar to (swissprot accession) (le:12902) (re:14290) (di:complement) D90787 D90787 g1742401 Escherichia coli 562 -11536583 300548 naru nitrite extrusion protein 2 nitrite facilitator (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #277(33.2-33.6 min.)) (nt:orf_id:o276#8; similar to (swissprot accession) (le:476) (re:1864) (di:complement) D90788 D90788 g1742404 Escherichia coli 562 -11536583 300546 naru nitrite extrusion protein 2 (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:f462; 99 pct identical to gb: ecnarg_1) (le:71) (re:1459) (di:complement) AE000244 AE000244 g1787743 Escherichia coli 562 -11536583 5000692259 naru nitrite extrusion protein 2 (fn:transport; transport of small molecules:) (db:genpept) (de:escherichia coli k-12 mg1655 section 134 of 400 of the completegenome.) (nt:f462; 99 pct identical to gb: ecnarg_1) (le:71) (re:1459) (di:complement) AE000244 AE000244 g1787743 Escherichia coli 562 -11536583 223796 naru nitrite extrusion protein 2 nitrite facilitator (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #277(33.2-33.6 min.)) (nt:orf_id:o276#8; similar to (swissprot accession) (le:476) (re:1864) (di:complement) D90788 D90788 g1742404 Escherichia coli 562 -11536583</p>				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872662	13528	35684	264	87

Description

6500732726 noha:b1548 prophage qin dna packaging protein nul homolog (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1548 b1548 Escherichia coli 562 -11536584 86314 noha (de:prophage qin dna packaging protein nul homolog) (db:swissprot) NOHA_ECOLI P31061 ESCHERICHIA COLI 562 -11536584 7000685978 noha dna packaging protein homolog noha:phage protein-related (cl:phage lambda dna packaging protein nul) (db:pir2.dat) G64909 G64909 Escherichia coli 562 -11536584 223930 noha prophage qin dna packaging protein nul homolog (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o308#6; similar to (swissprot accession) (le:7792) (re:8361) (di:complement) D90798 D90798 g1742548 Escherichia coli 562 -11536584 300649 noha homolog of qin prophage packaging protein nul (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 142 of 400 of the completegenome.) (nt:f189; residues 1-147 are 100 pct identical to) (le:3413) (re:3982) (di:complement) AE000252 AE000252 g1787830 Escherichia coli 562 -11536584 5000692324 (de:(ecoli_1508) (pn:prophage qin dna packaging protein nul homolog:fragment) (gn:noha) (gtcfc:13.7:14.1) (ec:) (noha_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1508 ECOLI_1508 Escherichia coli 562 10119698

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872663	13529	35685	588	196

Description

GTC ORF with score 224 to: (sr:thale cress) (db:genpept-pln1) (de:arabidopsis thaliana dna chromosome 4, bac clone t10i14 (essaiiproject).) (nt:similarity to probable membrane protein,) (le:39821:40029:40279) (re:39917:40236:40450) (di:complementjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501872679	13530	35686	801	266

Description

6500732727 cspf:b1558 cold shock-like protein cspf (gtcfc:14.3)
(keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1558 b1558
Escherichia coli 562 -11536585 66666 cspf (de:cold shock-like protein cspf)
(db:swissprot) CSPF_ECOLI P39819 ESCHERICHIA COLI 562 -11536585 7000684926
cspf cold shock protein homolog cspf (cl:major cold shock protein:cold shock
domain homology) (db:pir2.dat) A64911 A64911 Escherichia coli 562 -11536585
4000707009 cspf cspf (db:genpept-bct1) (de:escherichia coli major
cold-shock proteins cspb (cspb) and cspf(cspf) genes, complete cds.)
(nt:major cold-shock protein) (le:645) (re:857) (di:direct) AF003590
AF003590 g2226342 Escherichia coli 562 -11536585 223945 cspf cold
shock-like protein cspf. (sr:escherichia coli (strain:k12) dna,
clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
kohara clone #307(35.1-35.5 min.)) (nt:orf_id:o308#14; similar to
(swissprot accession) (le:13849) (re:14061) (di:direct) D90798 D90798
g1742553 Escherichia coli 562 -11536585 223967 cspf cold shock-like protein
cspf. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7
min.)) (nt:orf_id:o308#14; similar to (swissprot accession) (le:3822)
(re:4034) (di:direct) D90799 D90799 g1742564 Escherichia coli 562 -11536585
300686 cspf cold shock-like protein cspf. (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o308#14; similar to
(swissprot accession) (le:598) (re:810) (di:direct) D90800 D90800 g1742587
Escherichia coli 562 -11536585 300664 cspf cold shock protein
(fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 142 of 400 of the completegenome.) (nt:o70; 100 pct identical
to cspf_ecoli sw: p39819) (le:9470) (re:9682) (di:direct) AE000252 AE000252
g1787840 Escherichia coli 562 -11536585 223935 cspf cspf (db:genpept-bct1)
(de:escherichia coli major cold-shock proteins cspb (cspb) and cspf(cspf)
genes, complete cds.) (nt:major cold-shock protein) (le:645) (re:857)
(di:direct) AF003590 AF003590 g2226342 Escherichia coli 562 -11536585
300654 cspf cold shock-like protein cspf. (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o308#14; similar to
(swissprot accession) (le:598) (re:810) (di:direct) D90800 D90800 g1742587
Escherichia coli 562 -11536585 5000692333 (de:(ecoli_1518) (pn:cold
shock-like protein cspf) (gn:cspf) (gtcfc:13.7:14.1) (ec:) (cspf_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1518
ECOLI_1518 Escherichia coli 562 10009284

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872682	13531	35687	1341	447

Description

6500732728 rspa:b1581 starvation sensing protein rspa (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1581 b1581 Escherichia coli 562 -11536586 97490 rspa (de:starvation sensing protein rspa) (db:swissprot) RSPA_ECOLI P38104 ESCHERICHIA COLI 562 -11536586 164584 rspa starvation sensing protein rspa (db:pir2.dat) I59589 I59589 Escherichia coli 562 -11536586 223963 rspa starvation sensing protein rspa. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #308(35.3-35.7 min.)) (nt:orf_id:o309#13; similar to (swissprot accession) (le:15894) (re:17108) (di:complement) D90799 D90799 g1742582 Escherichia coli 562 -11536586 300704 rspa starvation sensing protein rspa. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o309#13; similar to (swissprot accession) (le:12670) (re:13884) (di:complement) D90800 D90800 g1742605 Escherichia coli 562 -11536586 300682 rspa (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli rspa and rspb genes, complete cds.) (nt:putative) (le:304) (re:1518) (di:direct) ECORSPAB L31628 g495782 Escherichia coli 562 -11536586 235940 rspa starvation sensing protein (fn:phenotype; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 144 of 400 of the completegenome.) (nt:f404; 100 pct identical to rspa_ecoli sw: p38104;) (le:1155) (re:2369) (di:complement) AE000254 AE000254 g1787864 Escherichia coli 562 -11536586 223985 rspa starvation sensing protein rspa. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #309(35.4-35.7 min.)) (nt:orf_id:o309#13; similar to (swissprot accession) (le:12670) (re:13884) (di:complement) D90800 D90800 g1742605 Escherichia coli 562 -11536586 5000692349 (de:(ecoli_1540) (pn:starvation sensing protein rspa) (gn:rspa) (gtcfc:13.7:14.1) (ec:) (rspa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1540 ECOLI_1540 Escherichia coli 562 10039380

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872685	13532	35688	360	119

Description

6500732729 mlc:b1594 protein:making large colonies protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1594 b1594 Escherichia coli 562 -11536587 83818 mlc (de:mlc protein (making large colonies protein)) (db:swissprot) MLC_ECOLI P50456 ESCHERICHIA COLI 562 -11536587 7000685851 mlc making large colonies protein (cl:n-acetylglucosamine repressor:glucose kinase homology) (db:pir2.dat) D64915 D64915 Escherichia coli 562 -11536587 223996 mlc mlc protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #310(35.7-36.0 min.)) (nt:orf_id:o311#8; similar to (swissprot accession) (le:11971) (re:13191) (di:complement) D90801 D90801 g1742617 Escherichia coli 562 -11536587 224006 mlc mlc protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #311(35.7-36.1 min.)) (nt:orf_id:o311#8; similar to (swissprot accession) (le:9998) (re:11218) (di:complement) D90802 D90802 g1742628 Escherichia coli 562 -11536587 300714 mlc putative nagc-like transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 145 of 400 of the completegenome.) (nt:f406; 99 pct identical to pir: jc2515) (le:2187) (re:3407) (di:complement) AE000255 AE000255 g1787878 Escherichia coli 562 -11536587 5000692361 (de:(ecoli_1553) (pn:protein) (gn:mlc) (gtcfc:13.7:14.1) (ec:) (mlc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1553 ECOLI_1553 Escherichia coli 562 10119717

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872687	13533	35689	414	137

Description

6500732730 uidc:gusc:b1615 membrane associated protein:membrane-associated protein uidc precursor (gtcfc:11.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1615 b1615 Escherichia coli 562 -11536588 7000691862 uidc:gusc membrane-associated protein uidc precursor (db:pir2.dat) A64918 A64918 Escherichia coli 562 -11536588 7500960382 uidc membrane-associated protein (fn:membrane; inner membrane) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 147 of 400 of the completegenome.) (nt:f417; this 417 aa orf is 24 pct identical (37 gaps)) (le:3163) (re:4416) (di:complement) AE000257 AE000257 g1787901 Escherichia coli 562 -11536588 5000692376 (de:(ecoli_1574) (pn:membrane associated protein) (gn:gusc) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1574 ECOLI_1574 Escherichia coli 562 10123399

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872693	13534	35690	756	252

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872694	13535	35691	807	268

Description

6500732731 uidb:gusb:uidp:b1616 glucuronide carrier protein:glucuronide permease (gtcfc:12.2:1.4) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1616 b1616 Escherichia coli 562 -11536589 103371 uidb:gusb:uidp (de:glucuronide carrier protein (glucuronide permease)) (db:swissprot) UIDB_ECOLI P30868 ESCHERICHIA COLI 562 -11536589 7000686868 uidb:gusb glucuronide permease uidb (cl:melibiose carrier protein) (db:pir2.dat) B64918 B64918 Escherichia coli 562 -11536589 224045 uidb:gusb:uidp glucuronide carrier protein glucuronide (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min.)) (nt:orf_id:o314#2; similar to (swissprot accession) (le:7574) (re:8947) (di:complement) D90805 D90805 g1742670 Escherichia coli 562 -11536589 300740 uidb glucuronide permease (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 147 of 400 of the completegenome.) (nt:f457; 99 pct identical to uidb_ecoli sw: p30868;) (le:4467) (re:5840) (di:complement) AE000257 AE000257 g1787902 Escherichia coli 562 -11536589 5000692377 (de:(ecoli_1575) (pn:glucuronide permease) (gn:uidb) (gtcfc:13.7:14.1) (ec:) (uidb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1575 ECOLI_1575 Escherichia coli 562 10119734

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872699	13536	35692	204	67

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501872720	13537	35693	1050	349

Description

6500732732 uidr:gusr:b1618 glucuronide repressor:uid operon repressor:gus operon repressor (gtcfc:12.13:1.4) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1618 b1618 Escherichia coli 562 -11536590 118654 uidr:gusr (de:uid operon repressor (gus operon repressor)) (db:swissprot) UIDR_ECOLI_Q59431 ESCHERICHIA COLI 562 -11536590 7000686869 gusr:uidr glucuronide repressor gusr (db:pir2.dat) D64918 D64918 Escherichia coli 562 -11536590 224047 potential acrab operon repressor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #314(36.3-36.7 min..)) (nt:orf_id:o314#4; similar to (swissprot accession) (le:11146) (re:11736) (di:complement) D90805 D90805 g1742672 Escherichia coli 562 -11536590 300742 gusr glucuronide repressor (db:genpept-bct1) (de:escherichia coli k-12 gusrabc operon.) (nt:start codon is uncertain, could be 488 or 497) (le:485) (re:1075) (di:direct) ECOGUSRABC M14641 g868019 Escherichia coli 562 -11536590 234590 uidr repressor for uid operon (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 147 of 400 of the completegenome.) (nt:f196; 100 pct identical to gb: ecogusrabc_2) (le:8039) (re:8629) (di:complement) AE000257 AE000257 g1787904 Escherichia coli 562 -11536590 5000692378 (de:(ecoli_1577) (pn:glucuronide repressor) (gn:gusr) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1577 ECOLI_1577 Escherichia coli 562 10060943

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872722	13538	35694	348	116

Description

6500732733 sodc:b1646 copper-zinc superoxide dismutase:superoxide dismutase precursor:cu-zn (gtcfc:12.12) (ec:1.15.1.1) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1646 b1646 Escherichia coli 562 -11536591 98805 sodc (ec:1.15.1.1) (de:(bacteriocuprein)) (db:swissprot) SODC_ECOLI P53635 ESCHERICHIA COLI 562 -11536591 164666 sodc superoxide dismutase:cu-zn sodc precursor (cl:superoxide dismutase (cu-zn)) (ec:1.15.1.1) (db:pir2.dat) (mp:37 min) JC6004 JC6004 Escherichia coli 562 -11536591 7500891817 sodc copper-zinc superoxide dismutase (sr:escherichia coli strain=w3110) (db:genpept-bct1) (ec:1.15.1.1) (de:escherichia coli copper-zinc superoxide dismutase (sodc) gene,complete cds.) (le:224) (re:745) (di:direct) ECU51242 U51242 g1256446 Escherichia coli 562 -11536591 239707 sodc superoxide dismutase precursor cu-zn (fn:enzyme; detoxification) (db:genpept-bct2) (ec:1.15.1.1) (de:escherichia coli k-12 mg1655 section 149 of 400 of the completegenome.) (nt:f173; 100 pct identical to gb: ecu51242_1) (le:11741) (re:12262) (di:complement) AE000259 AE000259 g1787934 Escherichia coli 562 -11536591 5000692397 (de:(ecoli_1605) (pn:superoxide dismutase precursor:cu-zn) (gn:sodc) (gtcfc:13.7:14.1) (ec:1.15.1.1) (sodc_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1605 ECOLI_1605 Escherichia coli 562 10040671

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872747	13539	35695	264	87

Description

6500732734 osme:anr:b1739 osmotically inducible protein e precursor:activator of ntr-like gene (gtcfc:12.11) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1739 b1739 Escherichia coli 562 -11536592 300850 osme:anr (de:gene)) (db:swissprot) OSME_ECOLI P23933 ESCHERICHIA COLI 562 -11536592 164212 osme:arn osmotically inducible protein e precursor (db:pir2.dat) I57918 I57918 Escherichia coli 562 -11536592 224208 osme:arn osme protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #326(39.1-39.4 min.)) (nt:orf_id:o326#8; similar to (pir accession number) (le:7278) (re:7616) (di:complement) D90817 D90817 g1742845 Escherichia coli 562 -11536592 300856 osme:arn osme protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #327(39.2-39.5 min.)) (nt:orf_id:o326#8; similar to (pir accession number) (le:1646) (re:1984) (di:complement) D90818 D90818 g1742852 Escherichia coli 562 -11536592 236003 anr activator of ntr-like gene (db:genpept-bct1) (de:e.coli anr gene for activator of ntr-like gene.) (le:85) (re:423) (di:direct) ECANRG X60186 g40914 Escherichia coli 562 -11536592 5000692458 osme (db:genpept-bct1) (de:e.coli osme gene.) (le:284) (re:622) (di:direct) ECOSMEG X75957 g908847 Escherichia coli 562 -11536592 232358 osme activator of ntr1 gene (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 159 of 400 of the completegenome.) (nt:f112; 100 pct identical to osme_ecoli sw: p23933;) (le:692) (re:1030) (di:complement) AE000269 AE000269 g1788035 Escherichia coli 562 -11536592 87912 osme:anr (de:gene)) (db:swissprot) OSME_ECOLI P23933 ESCHERICHIA COLI 562 -11536592 224214 osme:arn osme protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #327(39.2-39.5 min.)) (nt:orf_id:o326#8; similar to (pir accession number) (le:1646) (re:1984) (di:complement) D90818 D90818 g1742852 Escherichia coli 562 -11536592

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872750	13540	35696	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872755	13541	35697	435	145

Description

6500732735 cspc:msmb:b1823 cold shock-like protein cspc (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1823 b1823 Escherichia coli 562 -11536593 152148 cspc:msmb cold shock protein homolog cspc (cl:major cold shock protein:cold shock domain homology) (db:pir2.dat) (mp:41 min) S43618 S43618 Escherichia coli 562 -11536593 224317 cspc:msmb cold shock protein cspc (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o335#6; similar to (pir accession number) (le:8390) (re:8599) (di:complement) D90826 D90826 g1736467 Escherichia coli 562 -11536593 234065 cspc cold-shock protein (sr:escherichia coli (strain tap90) (library: kohara) dna) (db:genpept-bct1) (de:escherichia coli cold-shock protein (cspc) gene, complete cds.) (le:686) (re:895) (di:direct) ECOCSPC L28430 g479005 Escherichia coli 562 -11536593 300957 cspc::msmb cspc msmb (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:escherichia coli cspc (msmb) gene, complete cds.) (le:243) (re:452) (di:direct) ECOCSPCA D28496 g460698 Escherichia coli 562 -11536593 234064 cspc cold shock protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 166 of 400 of the completegenome.) (nt:f69; 100 pct identical to cspc_ecoli sw: p36996; cg) (le:8910) (re:9119) (di:complement) AE000276 AE000276 g1788126 Escherichia coli 562 -11536593 5000692527 (de:(ecoli_1780) (pn:cold shock-like protein cspc) (gn:cspc) (gtcfc:13.7:14.1) (ec:) (cspc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1780 ECOLI_1780 Escherichia coli 562 10080171

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872756	13542	35698	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872759	13543	35699	387	128

Description

6500732736 htpx:b1829 heat shock protein htpx (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1829 b1829 Escherichia coli 562 -11536594 78025 htpx (de:heat shock protein htpx) (db:swissprot) HTPX_ECOLI P23894 ESCHERICHIA COLI 562 -11536594 163166 htpx heat shock protein htpx (cl:heat-shock protein htpx) (db:pir2.dat) A43659 A43659 Escherichia coli 562 -11536594 224320 htpx heat shock protein htpx (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #335(40.9-41.3 min.)) (nt:orf_id:o335#10; similar to (pir accession number) (le:12859) (re:13740) (di:complement) D90826 D90826 g1736470 Escherichia coli 562 -11536594 300960 htpx (sr:e.coli (strain k-12) dna, clone pr6) (db:genpept-bct1) (de:e.coli htpx protein (htpx) gene, complete cds.) (le:285) (re:1166) (di:direct) ECOHTPX M58470 g146412 Escherichia coli 562 -11536594 234703 htpx heat shock protein:integral membrane protein (fn:orf; adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 167 of 400 of the completegenome.) (nt:f293; 100 pct identical to htpx_ecoli sw: p23894;) (le:3140) (re:4021) (di:complement) AE000277 AE000277 g1788133 Escherichia coli 562 -11536594 5000692533 (de:(ecoli_1786) (pn:heat shock protein htpx) (gn:htpx) (gtcfc:13.7:14.1) (ec:) (htpx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1786 ECOLI_1786 Escherichia coli 562 10020364

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872760	13544	35700	567	188

Description

GTC ORF with score 284 to: (de:(yal061w) (pn:hypothetical zinc-type alcohol dehydrogenase-like protein in gdh3-cne1 intergenic region:similarity to alcohol) (gn:fun50) (gtcfc:2.2) (ec:) (yag1_yeast) (keggfc:11.2) (sgdfc:1.5.1:2.6.0) (db:gtc-saccharomyces)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872761	13545	35701	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872764	13546	35702	282	93

Description

6500732737 yebl:b1857 31.1 kd protein in msbb-ruvb intergenic region:31.1 kd protein in msbb-ruvb intergenic region precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1857 b1857 Escherichia coli 562 -11536595 111494 znua (de:high-affinity zinc uptake system protein znua precursor) (db:swissprot) ZNUA_ECOLI P39172 ESCHERICHIA COLI 562 -11536595 7000687594 yebl adhesin homolog yebl precursor:31.1k protein msbb-ruvb intergenic region (cl:hypothetical protein hi0119) (db:pir2.dat) A64948 A64948 Escherichia coli 562 -11536595 224348 yebl 31.1 kd protein in msbb-ruvb intergenic region (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #336gap(41.6-41.9 min.)) (nt:orf_id:o336gap#10; similar to (swissprot accession) (le:11177) (re:12163) (di:complement) D90828 D90828 g1736500 Escherichia coli 562 -11536595 300988 yebl putative adhesin (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 170 of 400 of the completegenome.) (nt:f328; 98 pct identical to yebl_ecoli sw: p39172) (le:70) (re:1056) (di:complement) AE000280 AE000280 g1788164 Escherichia coli 562 -11536595 5000692553 (de:(ecoli_1814) (pn:31) (gn:yebl) (gtcfc:13.7:14.1) (ec:) (yebl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1814 ECOLI_1814 Escherichia coli 562 10119876

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872766	13547	35703	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872767	13548	35704	504	167

Description

6500732738 bisz:b1872 biotin sulfoxide reductase 2 (gtcfc:14.3) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1872 b1872 Escherichia coli 562 -11536596 7000690860 bisz biotin sulfoxide reductase:2 (cl:trimethylamine-n-oxide reductase) (ec:1.8.4.-) (db:pir2.dat) H64949 H64949 Escherichia coli 562 -11536596 7500959706 bisz biotin sulfoxide reductase 2 (fn:enzyme; central intermediary metabolism) (db:genpept-bct2) (ec:1.-.-.-) (de:escherichia coli k-12 mg1655 section 171 of 400 of the completegenome.) (nt:f815; this 815 aa orf is 98 pct identical (1 gap)) (le:113) (re:2560) (di:complement) AE000281 AE000281 g1788180 Escherichia coli 562 -11536596 5000692563 (de:(ecoli_1829) (pn:biotin sulfoxide reductase 2) (gn:bisz) (gtcfc:13.7:14.1) (ec:1.-.-.-) (bisz_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1829 ECOLI_1829 Escherichia coli 562 10123498

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872795	13549	35705	294	97

Description

GTC ORF with score 94 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid w01b11.) (nt:similar to s. cerevisiae sla2 (gb:z22811)) (le:7267:7620:8331) (re:7532:7688:8416) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872798	13550	35706	1044	348

Description

6500732739 cutc:b1874 copper homeostasis protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1874 b1874 Escherichia coli 562 -11536597 7000690864 cutc copper homeostasis protein (db:pir2.dat) B64950 B64950 Escherichia coli 562 -11536597 7500959714 cutc copper homeostasis protein (fn:putative transport; detoxification) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 171 of 400 of the completegenome.) (nt:f146; 100 pct identical to cutc_ecoli sw: p46719;) (le:4055) (re:4495) (di:complement) AE000281 AE000281 g1788182 Escherichia coli 562 -11536597 5000692565 (de:(ecoli_1831) (pn:copper homeostasis protein cutc) (gn:cutc) (gtcfc:13.7:14.1) (ec:) (cutc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1831 ECOLI_1831 Escherichia coli 562 10123499

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872805	13551	35707	729	242

Description

6500732740 yeci:b1902 ferritin-like protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1902 b1902 Escherichia coli 562 -11536598 7500922938 yeci (de:hypothetical 18.9 kd protein in araf-ftn intergenic region) (db:swissprot) YECI_ECOLI P52091 ESCHERICHIA COLI 562 -11536598 7000690877 yeci ferritin-like protein (cl:ferritin) (db:pir2.dat) F64953 F64953 Escherichia coli 562 -11536598 224409 yeci ferritin like protein 2. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf_id:o341#1; similar to (swissprot accession) (le:3455) (re:3958) (di:direct) D90832 D90832 g1736565 Escherichia coli 562 -11536598 7500922940 yeci ferritin-like protein (fn:putative carrier; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 173 of 400 of the completegenome.) (nt:o167; residues 6-132 are 98 pct identical to) (le:9752) (re:10255) (di:direct) AE000283 AE000283 g1788212 Escherichia coli 562 -11536598 301049 yeci ferritin like protein 2. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf_id:o341#1; similar to (swissprot accession) (le:3455) (re:3958) (di:direct) D90832 D90832 g1736565 Escherichia coli 562 -11536598 5000692572 (de:(ecoli_1859) (pn:hypothetical 19) (gn:yeci) (gtcfc:13.7:14.1) (ec:) (yeci_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1859 ECOLI_1859 Escherichia coli 562 10119903

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872806	13552	35708	669	222

Description

6500732741 uvry:b1914 23.9 kd protein in uvrc-sdia intergenic region:uvry protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1914 b1914 Escherichia coli 562 -11536599 301057 uvry (de:uvry protein) (db:swissprot) UVRV_ECOLI P07027 ESCHERICHIA COLI 562 -11536599 130888 uvry hypothetical 24k protein uvrc-sdia intergenic region (cl:regulatory protein coma:response regulator homology) (db:pir1.dat) (mp:42 min) QQEC24 A26750 Escherichia coli 562 -11536599 224417 uvry (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min..)) (nt:orf_id:o341#11; similar to (pir accession number) (le:11233) (re:11889) (di:complement) D90832 D90832 g1736573 Escherichia coli 562 -11536599 240371 (sr:e.coli (k12; ab1157) dna) (db:genpept-bct1) (de:e.coli excision repair gene (uvrc), 5' end, and 24 kd protein,complete cds.) (nt:24 kd protein (ttg start codon)) (le:103) (re:759) (di:direct) ECOUVRCA M24615 g551848 Escherichia coli 562 -11536599 5000692577 (db:genpept-bct1) (de:escherichia coli uvrc gene regulatory region.) (nt:24 kd protein (aa 1-218)) (le:103) (re:759) (di:direct) ECUVRCA X05398 g581252 Escherichia coli 562 -11536599 236307 uvry putative 2-component transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:f218; 100 pct identical to uvry_ecoli sw:) (le:6731) (re:7387) (di:complement) AE000284 AE000284 g1788222 Escherichia coli 562 -11536599 104057 uvry (de:uvry protein) (db:swissprot) UVRV_ECOLI P07027 ESCHERICHIA COLI 562 -11536599

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872814	13553	35709	429	142

Description

6500732742 fliy:b1920 fliy protein precursor:sulfate starvation-induced protein 7:ssi7 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1920 b1920 Escherichia coli 562 -11536600 72037 fliy (de:fliy protein precursor (sulfate starvation-induced protein 7) (ssi7)) (db:swissprot) FLIY_ECOLI P39174 ESCHERICHIA COLI 562 -11536600 7000685306 fliy fliy protein precursor:sulfate starvation-induced protein ssi7 (cl:lysine-arginine-ornithine-binding protein) (db:pir2.dat) E64955 E64955 Escherichia coli 562 -11536600 224423 fliy fliy protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #341(42.7-43.1 min.)) (nt:orf_id:o341#17; similar to (swissprot accession) (le:16115) (re:16915) (di:complement) D90832 D90832 g1736579 Escherichia coli 562 -11536600 301070 fliy fliy protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.)) (nt:orf_id:o341#17; similar to (swissprot accession) (le:1328) (re:2128) (di:complement) D90833 D90833 g1736587 Escherichia coli 562 -11536600 238741 fliy putative periplasmic binding transport protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 174 of 400 of the completegenome.) (nt:f266; 100 pct identical to fliy_ecoli sw: p39174) (le:11613) (re:12413) (di:complement) AE000284 AE000284 g1788228 Escherichia coli 562 -11536600 301063 fliy fliy (fn:member of the extracellular solute-binding) (db:genpept-bct2) (de:escherichia coli flia operon sigma f (flia), fliz (fliz), and fliy(fliy) genes, complete cds.) (nt:ambiguous start, 1605..1661 or 1656..1661 may also) (le:1662) (re:2462) (di:direct) ECU18539 U18539 g687652 Escherichia coli 562 -11536600 224430 fliy fliy protein precursor. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #342(43.0-43.4 min.)) (nt:orf_id:o341#17; similar to (swissprot accession) (le:1328) (re:2128) (di:complement) D90833 D90833 g1736587 Escherichia coli 562 -11536600 5000692582 (de:(ecoli_1874) (pn:fliy protein precursor) (gn:fliy) (gtcfc:13.7:14.1) (ec:) (fliy_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1874 ECOLI_1874 Escherichia coli 562 10014593

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872816	13554	35710	639	212

Description

6500732743 fliz:b1921 fliz protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1921 b1921 Escherichia coli 562 -11536601 7000690883 fliz fliz protein (db:pir2.dat) F64955 F64955 Escherichia coli 562 -11536601 238740 fliz orf:hypothetical protein (fn:structural component; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 175 of 400 of the completegenome.) (nt:f195; 100 pct identical to fliz_ecoli sw: p52627) (le:74) (re:661) (di:complement) AE000285 AE000285 g1788230 Escherichia coli 562 -11536601 7500959741 fliz fliz (db:genpept-bct2) (de:escherichia coli flia operon sigma f (flia), fliz (fliz), and fliy(fliy) genes, complete cds.) (le:987) (re:1574) (di:direct) ECU18539 U18539 g687651 Escherichia coli 562 -11536601 5000692583 (de:(ecoli_1875) (pn:fliz protein) (gn:fliz) (gtcfc:13.7:14.1) (ec:)) (fliz_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1875 ECOLI_1875 Escherichia coli 562 10123508

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872817	13555	35711	1449	482

Description

6500732744 nac:b1988 nitrogen assimilation regulatory protein:nitrogen assimilation control protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1988 b1988 Escherichia coli 562 -11536602 118642 nac (de:control protein) (db:swissprot) NAC_ECOLI Q47005 ESCHERICHIA COLI 562 -11536602 7000685902 nac nitrogen assimilation control protein (db:pir2.dat) D64963 D64963 Escherichia coli 562 -11536602 224489 nitrogen assimilation regulatory protein nac. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #347(44.2-44.5 min.)) (nt:orf_id:o347#7; similar to (swissprot accession) (le:9804) (re:10721) (di:complement) D90837 D90837 g1736650 Escherichia coli 562 -11536602 239729 nac nitrogen assimilation control protein (fn:regulator; central intermediary metabolism) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 180 of 400 of the completegenome.) (nt:f310; 100 pct identical to gb: ecu56736_1) (le:8901) (re:9818) (di:complement) AE000290 AE000290 g1788297 Escherichia coli 562 -11536602 301129 nac nac (fn:transcription regulator, positive) (db:genpept-bct2) (de:escherichia coli nitrogen assimilation control (nac) gene, completecds, trna-asn gene, partial sequence and cbl (cbl) gene, partialcds.) (nt:lysr family member; description: nitrogen) (le:427... ECU56736 U56736 g1373226 Escherichia coli 562 -11536602 5000692621 (de:(ecoli_1937) (pn:nitrogen assimilation control protein) (gn:nac) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1937 ECOLI_1937 Escherichia coli 562 10060915

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872845	13556	35712	1719	573

Description

6500732745 erfk:b1990 31.6 kd protein in cobt 3region precursor:protein
 erfk/srfk precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0)
 (db:gtc-escherichia coli) b1990 b1990 Escherichia coli 562 -11536603 70508
 erfk (de:protein erfk/srfk precursor) (db:swissprot) ERFK_ECOLI P39176
 ESCHERICHIA COLI 562 -11536603 7000685182 erfk erfk protein precursor
 (cl:conserved hypothetical protein b0819) (db:pir2.dat) E64963 E64963
 Escherichia coli 562 -11536603 224490 erfk protein erfk/srfk precursor.
 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #347(44.2-44.5
 min.)) (nt:orf_id:o347#8; similar to (swissprot accession) (le:11179)
 (re:12111) (di:complement) D90837 D90837 g1736651 Escherichia coli 562
 -11536603 301130 erfk unknown (db:genpept-bct1) (de:escherichia coli
 cobinamide kinase and guanylyltransferase (cobu),cobalamin synthase (cobs),
 namn::dmb phosphoribosyl transferase,and (erfk) genes, complete cds, asn
 trna (asn) gene, complete sequence, and insertion sequence is5, ... ECU33333
 U33333 g1008488 Escherichia coli 562 -11536603 239440 erfk orf:hypothetical
 protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
 section 181 of 400 of the complete genome.) (nt:f310; 100 pct identical to
 erfk_ecoli sw: p39176) (le:325) (re:1257) (di:complement) AE000291 AE000291
 g1788299 Escherichia coli 562 -11536603 5000692622 (de:(ecoli_1938)
 (pn:protein erfk) (gn:erfk) (gtcfc:13.7:14.1) (ec:) (erfk_ecoli)
 (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1938
 ECOLI_1938 Escherichia coli 562 10013087

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872846	13557	35713	1368	455

Description

6500732746 cobt:b1991 nicotinate-nucleotide--dimethylbenzimidazole
phosphoribosyl transferase:nicotinate-nucleotide--dimethylbenzimidazole
phosphoribosyltransferase:nn:dbi prt:n1-alpha-phosphoribosyltransferase
(gtcfc:14.3) (ec:2.4.2.21) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia
coli) b1991 b1991 Escherichia coli 562 -11536604 65288 cobt (ec:2.4.2.21)
(de:(ec 2.4.2.21) (nn:dbi prt) (n1-alpha-phosphoribosyltransferase))
(db:swissprot) COBT_ECOLI P36562 ESCHERICHIA COLI 562 -11536604 7000684859
cobt nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
(ec:2.4.2.21) (db:pir2.dat) F64963 F64963 Escherichia coli 562 -11536604
224491 cobt nicotinate-nucleotide--dimethylbenzimidazole (sr:escherichia
coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
(de:e.coli genomic dna, kohara clone #347(44.2-44.5 min..))
(nt:orf_id:o347#9; similar to (swissprot accession) (le:12176) (re:13255)
(di:complement) D90837 D90837 g1736652 Escherichia coli 562 -11536604
301131 cobt nicotinate-nucleotide dimethylbenzimidazole-p (fn:enzyme;
biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:2.4.2.21)
(de:escherichia coli k-12 mg1655 section 181 of 400 of the completegenome.)
(nt:f359; 99 pct identical to cobt_ecoli sw: p36562; cg) (le:1322) (re:2401)
(di:complement) AE000291 AE000291 g1788300 Escherichia coli 562 -11536604
5000692623 (de:(ecoli_1939) (pn:nicotinate-nucleotide
dimethylbenzimidazole-p phosphoribosyl transferase) (gn:cobt)
(gtcfc:13.7:14.1) (ec:2.4.2.21) (cobt_ecoli) (keggfc:11.1) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_1939 ECOLI_1939 Escherichia coli 562
10119941

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872875	13558	35714	543	180

Description

6500732747 cobs:b1992 cobalamin:5-phosphate synthase (gtcfc:14.3)
 (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1992 b1992
 Escherichia coli 562 -11536605 65284 cobs (de:cobalamin (5'-phosphate)
 synthase) (db:swissprot) COBS_ECOLI P36561 ESCHERICHIA COLI 562 -11536605
 7000684858 cobs cobalamin 5-phosphate synthase (db:pir2.dat) G64963 G64963
 Escherichia coli 562 -11536605 224492 cobs cobalamin 5-phosphate synthase.
 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #347(44.2-44.5
 min.)) (nt:orf_id:o347#10; similar to (swissprot accession) (le:13267)
 (re:14010) (di:complement) D90837 D90837 g1736653 Escherichia coli 562
 -11536605 301137 cobs cobalamin 5-phosphate synthase. (sr:escherichia coli
 (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
 (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.))
 (nt:orf_id:o347#10; similar to (swissprot accession) (le:45) (re:788)
 (di:complement) D90838 D90838 g1736659 Escherichia coli 562 -11536605
 301132 cobs cobalamin 5-phosphate synthase (fn:enzyme; biosynthesis of
 cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
 section 181 of 400 of the completegenome.) (nt:f259; 99 pct identical to
 cobs_ecoli sw: p36561; cg) (le:2413) (re:3156) (di:complement) AE000291
 AE000291 g1788301 Escherichia coli 562 -11536605 224497 cobs cobalamin
 5-phosphate synthase. (sr:escherichia coli (strain:k12) dna,
 clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna,
 kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o347#10; similar to
 (swissprot accession) (le:45) (re:788) (di:complement) D90838 D90838
 g1736659 Escherichia coli 562 -11536605 5000692624 (de:(ecoli_1940)
 (pn:cobalamin 5"-phosphate synthase) (gn:cobs) (gtcfc:13.7:14.1) (ec:)
 (cobs_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
 ECOLI_1940 ECOLI_1940 Escherichia coli 562 10119942

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872880	13559	35715	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872888	13560	35716	261	86

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501872919	13561	35717	2970	990

Description

6500732748 cobu:b1993 cobinamide kinase and guanylyltransferase:cobinamide kinase / cobinamide phosphate guanylyltransferase (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b1993 b1993 Escherichia coli 562 -11536606 65292 cobu (de:cobinamide kinase / cobinamide phosphate guanylyltransferase) (db:swissprot) COBU_ECOLI P46886 ESCHERICHIA COLI 562 -11536606 7000684860 cobu cobinamide kinase and guanylyltransferase (cl:cobinamide kinase) (db:pir2.dat) H64963 H64963 Escherichia coli 562 -11536606 224493 cobu cobinamide kinase / cobinamide phosphate (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #347(44.2-44.5 min.)) (nt:orf_id:o347#11; similar to (swissprot accession) (le:14007) (re:14552) (di:complement) D90837 D90837 g1736654 Escherichia coli 562 -11536606 301138 cobu cobinamide kinase / cobinamide phosphate (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o347#11; similar to (swissprot accession) (le:785) (re:1330) (di:complement) D90838 D90838 g1736660 Escherichia coli 562 -11536606 301133 cobu cobinamide kinase and guanylyltransferase (db:genpept-bct1) (de:escherichia coli cobinamide kinase and guanylyltransferase (cobu),cobalamin synthase (cobs), namn::dmb phosphoribosyl transferase,and (erfk) genes, complete cds, asn trna (asn) gene, completesequence, and insertion sequence is5, ... ECU33333 U33333 g1008485 Escherichia coli 562 -11536606 239437 cobu cobinamide kinase/cobinamide phosphate (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 181 of 400 of the completegenome.) (nt:f181; 100 pct identical to cobu_ecoli sw: p46886) (le:3153) (re:3698) (di:complement) AE000291 AE000291 g1788302 Escherichia coli 562 -11536606 224498 cobu cobinamide kinase / cobinamide phosphate (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #348(44.5-44.9 min.)) (nt:orf_id:o347#11; similar to (swissprot accession) (le:785) (re:1330) (di:complement) D90838 D90838 g1736660 Escherichia coli 562 -11536606 5000692625 (de:(ecoli_1941) (pn:cobinamide kinase) (gn:cobu) (gtcfc:13.7:14.1) (ec:) (cobu_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1941 ECOLI_1941 Escherichia coli 562 10007943

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872920	13562	35718	1689	562

Description

6500732749 rfc:b2035 o-antigen polymerase (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2035 b2035 Escherichia coli 562 -11536607 94194 rfc (de:o-antigen polymerase) (db:swissprot) RFC_ECOLI P37748 ESCHERICHIA COLI 562 -11536607 164395 rfc o-antigen polymerase (db:pir2.dat) I69644 I69644 Escherichia coli 562 -11536607 301200 rfc o-antigen polymerase. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf_id:o351#11; similar to (swissprot accession) (le:12360) (re:13526) (di:complement) D90841 D90841 g1736725 Escherichia coli 562 -11536607 301212 rfc o-antigen polymerase. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#11; similar to (swissprot accession) (le:3149) (re:4315) (di:complement) D90842 D90842 g1736738 Escherichia coli 562 -11536607 238584 wbbh (db:genpept-bct1) (de:escherichia coli k-12 dtdp-d-glucose 4,6-dehydratase (rmlb), dtdp-6-deoxy-l-mannose-dehydrogenase (rmlb), glucose-1-phosphatethymidyltransferase (rmla), dtdp-6-deoxy-d-glucose-3,5 epimerase(rmlc), putative o-antigen transporter (... ECU09876 U09876 g508243 Escherichia coli 562 -11536607 238054 wbbh o-antigen polymerase (fn:enzyme; macromolecule metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 184 of 400 of the completgenome.) (nt:f388; formerly designated rfc) (le:8817) (re:9983) (di:complement) AE000294 AE000294 g1788347 Escherichia coli 562 -11536607 297657 wbbh o-antigen polymerase (db:genpept-bct2) (de:escherichia coli k12 glucose-1-phosphate thymidyltransferase (rmla)gene, partial cds; dtdp-6-deoxy-l-xylo-4-hexulose 4-reductase(rmlc), membrane protein (wzx), dehydrogenase (glf), o-antigenpolymerase (wbbh), nucleotide sugar synt... ECRFBA U03041 g510254 Escherichia coli 562 -11536607 224560 rfc o-antigen polymerase. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #351(45.1-45.5 min.)) (nt:orf_id:o351#11; similar to (swissprot accession) (le:12360) (re:13526) (di:complement) D90841 D90841 g1736725 Escherichia coli 562 -11536607 224572 rfc o-antigen polymerase. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #352(45.3-45.7 min.)) (nt:orf_id:o351#11; similar to (swissprot accession) (le:3149) (re:4315) (di:complement) D90842 D90842 g1736738 Escherichia coli 562 -11536607 5000692653 (de:(ecoli_1983) (pn:o-antigen polymerase) (gn:rfc) (gtcfc:13.7:14.1) (ec:) (rfc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_1983 ECOLI_1983 Escherichia coli 562 10036177

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872927	13563	35719	381	126

Description

6500732750 pbpg:b2134 penicillin-binding protein 7
precursor:pbp-7:d-alanyl-d-alanine-endopeptidase:dd-endopeptidase
(gtcfc:14.3) (ec:3.4.99.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2134 b2134 Escherichia coli 562 -11536608 88738 pbpg (ec:3.4.99.-) (de:endopeptidase), (dd-endopeptidase)) (db:swissprot) PBP7_ECOLI P33364
ESCHERICHIA COLI 562 -11536608 7000686090 pbpg penicillin-binding protein 7 precursor (db:pir2.dat) (mp:47 min) E64981 E64981 Escherichia coli 562 -11536608 7500887698 yohb (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:47 to 48 centisome region of e.coli k12 bhb2600.) (nt:similar to carboxypeptidases and penicillin binding) (le:36708) (re:37649) (di:complement) ECOHU47 U00007 g405864 Escherichia coli 562 -11536608 234744 pbpg penicillin-binding protein 7 (fn:putative enzyme; murein sacculus,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 192 of 400 of the completegenome.) (nt:f313; 100 pct identical to pbp7_ecoli sw: p33364;) (le:9213) (re:10154) (di:complement) AE000302 AE000302 g1788455 Escherichia coli 562 -11536608 5000692722 (de:(ecoli_2083) (pn:penicillin-binding protein 7 precursor:pbp-7) (gn:pbpg) (gtcfc:13.7:14.1) (ec:3.4.99.-) (pbp7_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2083 ECOLI_2083 Escherichia coli 562 10030865

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872930	13564	35720	216	71

Description

6500732751 ccmh:b2194 cytochrome c-type biogenesis protein ccmh precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2194 b2194 Escherichia coli 562 -11536609 63475 ccmh (de:cytochrome c-type biogenesis protein ccmh precursor) (db:swissprot) CCMH_ECOLI P33925
ESCHERICHIA COLI 562 -11536609 7000684774 ccmh cytochrome c-type biogenesis protein ccmh precursor (db:pir2.dat) H64988 H64988 Escherichia coli 562 -11536609 7500878367 yejp (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:probably part of aeg-46.5 operon; homolog of) (le:18411) (re:19463) (di:complement) ECOHU49 U00008 g405919 Escherichia coli 562 -11536609 234796 ccmh possible subunit of heme lyase (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f350; 100 pct identical to ccmh_ecoli sw: p33925) (le:1082) (re:2134) (di:complement) AE000309 AE000309 g1788522 Escherichia coli 562 -11536609 5000692766 (de:(ecoli_2143) (pn:required for biogenesis of c-type cytochromes) (gn:ccmh) (gtcfc:13.7:14.1) (ec:) (ccmh_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2143 ECOLI_2143 Escherichia coli 562 10006144

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872936	13565	35721	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872940	13566	35722	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501872947	13567	35723	849	282

Description

6500732752 dsbe:ccmg:b2195 thiol:disulfide interchange protein dsbe precursor:cytochrome c biogenesis protein ccmg (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2195 b2195 Escherichia coli 562 -11536610 69314 dsbe:ccmg (de:biogenesis protein ccmg) (db:swissprot) DSBE_ECOLI P33926 ESCHERICHIA COLI 562 -11536610 7000685101 dsbe thiol:disulfide interchange protein dsbe precursor (cl:cytochrome c biogenesis protein cycx) (db:pir2.dat) A64989 A64989 Escherichia coli 562 -11536610 7500880673 yejq (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:probable thioredoxin; may be part of aeg-46.5) (le:19460) (re:20017) (di:complement) ECOHU49 U00008 g405920 Escherichia coli 562 -11536610 234797 dsbe disulfide oxidoreductase in biogenesis of (fn:enzyme; energy metabolism, carbon: electron) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f185; 100 pct identical to dsbe_ecoli sw: p33926;) (le:2131) (re:2688) (di:complement) AE000309 AE000309 g1788523 Escherichia coli 562 -11536610 5000692767 (de:(ecoli_2144) (pn:disulfide oxidoreductase:in biogenesis of cytochrome c) (gn:dsbe) (gtcfc:13.7:14.1) (ec:) (dsbe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2144 ECOLI_2144 Escherichia coli 562 10011897

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872986	13568	35724	261	86

Description

6500732753 ccmf:b2196 cytochrome c-type biogenesis protein ccmf (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2196 b2196 Escherichia coli 562 -11536611 63468 ccmf (de:cytochrome c-type biogenesis protein ccmf) (db:swissprot) CCMF_ECOLI P33927 ESCHERICHIA COLI 562 -11536611 7000684773 ccmf cytochrome c-type biogenesis protein ccmf (cl:nrfe protein) (db:pir2.dat) B64989 B64989 Escherichia coli 562 -11536611 7500878365 yejr (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:may be part of aeg-46.5 operon; strong match to) (le:20014) (re:21957) (di:complement) ECOHU49 U00008 g405921 Escherichia coli 562 -11536611 234798 ccmf cytochrome c-type biogenesis protein (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f647; 100 pct identical to ccmf_ecoli sw: p33927) (le:2685) (re:4628) (di:complement) AE000309 AE000309 g1788524 Escherichia coli 562 -11536611 5000692768 (de:(ecoli_2145) (pn:cytochrome c-type biogenesis protein ccmf) (gn:ccmf) (gtcfc:13.7:14.1) (ec:) (ccmf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2145 ECOLI_2145 Escherichia coli 562 10006137

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501872987	13569	35725	339	112

Description

6500732754 ccme:b2197 cytochrome c-type biogenesis protein ccme (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2197 b2197 Escherichia coli 562 -11536612 63464 ccme (de:cytochrome c-type biogenesis protein ccme) (db:swissprot) CCME_ECOLI P33928 ESCHERICHIA COLI 562 -11536612 7000684772 ccme cytochrome c-type biogenesis protein ccme (db:pir2.dat) C64989 C64989 Escherichia coli 562 -11536612 7500878363 yejs (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:may be part of aeg-46.5 operon.) (le:21954) (re:22433) (di:complement) ECOHU49 U00008 g405922 Escherichia coli 562 -11536612 234799 ccme cytochrome c biogenesis:possible subunit of a (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f159; 100 pct identical to ccme_ecoli sw: p33928) (le:4625) (re:5104) (di:complement) AE000309 AE000309 g1788525 Escherichia coli 562 -11536612 5000692769 (de:(ecoli_2146) (pn:cytochrome c-type biogenesis protein ccme) (gn:ccme) (gtcfc:13.7:14.1) (ec:) (ccme_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2146 ECOLI_2146 Escherichia coli 562 10006133

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873025	13570	35726	2520	840

Description

6500732755 ccmd:b2198 heme exporter protein d:cytochrome c-type biogenesis protein ccmd (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2198 b2198 Escherichia coli 562 -11536613 63458 ccmd (de:heme exporter protein d (cytochrome c-type biogenesis protein ccmd)) (db:swissprot) CCMD_ECOLI P36770 ESCHERICHIA COLI 562 -11536613 7000684771 ccmd heme exporter protein d (cl:heme export protein d) (db:pir2.dat) D64989 D64989 Escherichia coli 562 -11536613 7500878361 yojm (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (le:22430) (re:22639) (di:complement) ECOHU49 U00008 g453988 Escherichia coli 562 -11536613 234800 ccmd heme exporter protein c (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f69; 100 pct identical to ccmd_ecoli sw: p36770) (le:5101) (re:5310) (di:complement) AE000309 AE000309 g1788526 Escherichia coli 562 -11536613 5000692770 (de:(ecoli_2147) (pn:heme exporter protein d:cytochrome c-type biogenesis protein ccmd) (gn:ccmd) (gtcfc:13.7:14.1) (ec:) (ccmd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2147 ECOLI_2147 Escherichia coli 562 10006127

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873027	13571	35727	204	67

Description

6500732756 ccmc:b2199 heme exporter protein c:cytochrome c-type biogenesis protein ccmc (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2199 b2199 Escherichia coli 562 -11536614 63451 ccmc (de:heme exporter protein c (cytochrome c-type biogenesis protein ccmc)) (db:swissprot) CCMC_ECOLI P33929 ESCHERICHIA COLI 562 -11536614 7000684770 ccmc heme exporter protein c (cl:helc protein) (db:pir2.dat) E64989 E64989 Escherichia coli 562 -11536614 7500878359 ccmc heme exporter protein c (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f245; 100 pct identical to ccmc_ecoli sw: p33929) (le:5307) (re:6044) (di:complement) AE000309 AE000309 g1788527 Escherichia coli 562 -11536614 5000692771 (de:(ecoli_2148) (pn:heme exporter protein c:cytochrome c-type biogenesis protein ccmc) (gn:ccmc) (gtcfc:13.7:14.1) (ec:) (ccmc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2148 ECOLI_2148 Escherichia coli 562 10006120

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873076	13572	35728	726	241

Description

6500732757 ccmb:b2200 heme exporter protein b:cytochrome c-type biogenesis protein ccmb (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2200 b2200 Escherichia coli 562 -11536615 63446 ccmb (de:heme exporter protein b (cytochrome c-type biogenesis protein ccmb)) (db:swissprot) CCMB_ECOLI P33930 ESCHERICHIA COLI 562 -11536615 7000684769 ccmb heme exporter protein b (cl:cytochrome c biogenesis protein cycw) (db:pir2.dat) F64989 F64989 Escherichia coli 562 -11536615 7500878357 yejv (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:may be part of aeg-46.5 operon; homolog of) (le:23414) (re:24076) (di:complement) ECOHU49 U00008 g405925 Escherichia coli 562 -11536615 234802 ccmb heme exporter protein b:cytochrome c-type (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f220; 100 pct identical to ccmb_ecoli sw: p33930) (le:6086) (re:6748) (di:complement) AE000309 AE000309 g1788528 Escherichia coli 562 -11536615 5000692772 (de:(ecoli_2149) (pn:heme exporter protein b:cytochrome c-type biogenesis protein ccmb) (gn:ccmb) (gtcfc:13.7:14.1) (ec:) (ccmb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2149 ECOLI_2149 Escherichia coli 562 10006115

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873077	13573	35729	987	328

Description

6500732758 ccma:b2201 heme exporter protein a:cytochrome c-type biogenesis atp-binding protein ccma (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2201 b2201 Escherichia coli 562 -11536616 63441 ccma (de:protein ccma)) (db:swissprot) CCMA_ECOLI P33931 ESCHERICHIA COLI 562 -11536616 7000684768 ccma heme exporter protein a (cl:cytochrome c biogenesis protein cycv:atp-binding cassette homology) (db:pir2.dat) G64989 G64989 Escherichia coli 562 -11536616 7500878355 yejw (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:abc-type atp-dependent transporter; may be part of) (le:24073) (re:24690) (di:complement) ECOHU49 U00008 g405926 Escherichia coli 562 -11536616 234803 ccma atp binding protein of heme exporter a (fn:transport; protein, peptide secretion) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f205; 100 pct identical to ccma_ecoli sw: p33931) (le:6745) (re:7362) (di:complement) AE000309 AE000309 g1788529 Escherichia coli 562 -11536616 5000692773 (de:(ecoli_2150) (pn:atp binding protein,:cytochrome c-type biogenesis atp-binding protein ccma) (gn:ccma) (gtcfc:13.7:14.1) (ec:) (ccma_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2150 ECOLI_2150 Escherichia coli 562 10006110

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873086	13574	35730	615	204

Description

6500732759 napc:b2202 cytochrome c-type protein napc (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2202 b2202 Escherichia coli 562 -11536617 85223 napc (de:cytochrome c-type protein napc) (db:swissprot) NAPC_ECOLI P33932 ESCHERICHIA COLI 562 -11536617 7000685916 napc cytochrome c-type protein napc (cl:denitrification system component nirt:nirt homology) (db:pir2.dat) H64989 H64989 Escherichia coli 562 -11536617 7500886290 yejx (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:may be part of aeg-46.5 operon; strong similarity) (le:24709) (re:25311) (di:complement) ECOHU49 U00008 g405927 Escherichia coli 562 -11536617 234804 napc cytochrome c-type protein (fn:putative enzyme; energy metabolism, carbon:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f200; 100 pct identical to napc_ecoli sw: p33932) (le:7381) (re:7983) (di:complement) AE000309 AE000309 g1788530 Escherichia coli 562 -11536617 5000692774 (de:(ecoli_2151) (pn:cytochrome c-type protein) (gn:napc) (gtcfc:13.7:14.1) (ec:) (napc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2151 ECOLI_2151 Escherichia coli 562 10027404

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873091	13575	35731	2064	687

Description

GTC ORF with score 143 to: (or:Gallus gallus) (sr:chicken (lambda nm1149-gizzard and okayama-berg plasmid-oviduc) (db:genpept-vrt) (de:chicken smooth muscle caldesmon mrna, complete cds.) (nt:smooth muscle caldesmon) (le:235) (re:2505) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873092	13576	35732	786	261

Description

6500732760 napb:b2203 cytochrome c-type protein napb precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2203 b2203
 Escherichia coli 562 -11536618 7000685915 napb cytochrome c-type protein napb precursor (cl:cytochrome c-type protein napb) (db:pir2.dat) A64990
 A64990 Escherichia coli 562 -11536618 7500886288 napb cytochrome c-type protein (fn:carrier; energy metabolism, carbon: electron) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f156; 100 pct identical to 133 residues) (le:7993) (re:8463) (di:complement) AE000309 AE000309 g1788531 Escherichia coli 562 -11536618 85221 napb (de:cytochrome c-type protein napb precursor) (db:swissprot) NAPB_ECOLI P33933 ESCHERICHIA COLI 562 -11536618 5000692775 (de:(ecoli_2152) (pn:cytochrome c-type protein) (gn:napb) (gtcfc:13.7:14.1) (ec:) (napb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2152 ECOLI_2152 Escherichia coli 562 10123599

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873133	13577	35733	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873145	13578	35734	1464	487

Description

6500732761 naph:b2204 ferredoxin-type protein naph (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2204 b2204
 Escherichia coli 562 -11536619 85230 naph (de:ferredoxin-type protein naph) (db:swissprot) NAPH_ECOLI P33934 ESCHERICHIA COLI 562 -11536619 7000685920 naph ferredoxin-type protein naph (cl:hypothetical protein hi0346) (db:pir2.dat) B64990 B64990 Escherichia coli 562 -11536619 7500886296 yejz (sr:escherichia coli k12 bhb2600) (db:genpept-bct1) (de:centisome 49 region of e.coli k12 bhb2600.) (nt:may be part of aeg-46.5 operon; weak match to) (le:25766) (re:26629) (di:complement) ECOHU49 U00008 g405929 Escherichia coli 562 -11536619 234806 naph ferredoxin-type protein:electron transfer (fn:carrier; energy metabolism, carbon: electron) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the completegenome.) (nt:f287; 100 pct identical to naph_ecoli sw: p33934) (le:8439) (re:9302) (di:complement) AE000309 AE000309 g1788532 Escherichia coli 562 -11536619 5000692776 (de:(ecoli_2153) (pn:ferredoxin-type protein, electron transfer) (gn:naph) (gtcfc:13.7:14.1) (ec:) (naph_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2153 ECOLI_2153 Escherichia coli 562 10027411

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873149	13579	35735	1134	377

Description

6500732762 napg:b2205 ferredoxin-type protein napg (gtcfc:14.3)
 (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2205 b2205
 Escherichia coli 562 -11536620 85228 napg (de:ferredoxin-type protein napg)
 (db:swissprot) NAPG_ECOLI P33936 ESCHERICHIA COLI 562 -11536620 7000685919
 napg ferredoxin-type protein napg (cl:conserved hypothetical protein hi0345)
 (db:pir2.dat) C64990 C64990 Escherichia coli 562 -11536620 7500886294 napg
 ferredoxin-type protein:electron transfer (fn:carrier; energy metabolism,
 carbon: electron) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section
 199 of 400 of the completegenome.) (nt:f231; 100 pct identical to napg_ecoli
 sw: p33936) (le:9289) (re:9984) (di:complement) AE000309 AE000309 g1788533
 Escherichia coli 562 -11536620 5000692777 (de:(ecoli_2154)
 (pn:ferredoxin-type protein, electron transfer) (gn:napg) (gtcfc:13.7:14.1)
 (ec:) (napg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
 ECOLI_2154 ECOLI_2154 Escherichia coli 562 10027409

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873163	13580	35736	405	134

Description

6500732763 napf:b2208 ferredoxin-type protein napf (gtcfc:14.3)
 (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2208 b2208
 Escherichia coli 562 -11536621 85226 napf (de:ferredoxin-type protein napf)
 (db:swissprot) NAPF_ECOLI P33939 ESCHERICHIA COLI 562 -11536621 7000685918
 napf ferredoxin-type protein napf (db:pir2.dat) F64990 F64990 Escherichia
 coli 562 -11536621 224675 napf ferredoxin-type protein napf.
 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #373(49.5-49.9
 min.)) (nt:orf_id:o372#3; similar to (swissprot accession) (le:2522)
 (re:3016) (di:complement) D90850 D90850 g1736849 Escherichia coli 562
 -11536621 301315 yojg (sr:escherichia coli k12 bhb2600) (db:genpept-bct1)
 (de:centisome 49 region of e.coli k12 bhb2600.) (nt:probable ferredoxin or
 fe-s protein; probably part) (le:30054) (re:30548) (di:complement) ECOHU49
 U00008 g453990 Escherichia coli 562 -11536621 234811 napf ferredoxin-type
 protein:electron transfer (fn:carrier; energy metabolism, carbon: electron)
 (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 199 of 400 of the
 completegenome.) (nt:f164; 100 pct identical to napf_ecoli sw: p33939)
 (le:12727) (re:13221) (di:complement) AE000309 AE000309 g1788536 Escherichia
 coli 562 -11536621 5000692779 (de:(ecoli_2157) (pn:ferredoxin-type protein,
 electron transfer) (gn:napf) (gtcfc:13.7:14.1) (ec:) (napf_ecoli)
 (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2157
 ECOLI_2157 Escherichia coli 562 10027407

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873181	13581	35737	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873182	13582	35738	255	84

Description

6500732764 inaa:b2237 inaa protein (gtcfc:14.3) (keggfc:14.2)
(rileyfc:5.8.0) (db:gtc-escherichia coli) b2237 b2237 Escherichia coli 562
-11536622 79384 inaa (de:inaa protein) (db:swissprot) INAA_ECOLI P27294
ESCHERICHIA COLI 562 -11536622 7000685632 inaa inaa protein (db:pir2.dat)
C64994 C64994 Escherichia coli 562 -11536622 224743 inaa inaa protein.
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #377(50.5-50.9
min.)) (nt:similar to (swissprot accession number p27294)) (le:9106)
(re:9756) (di:complement) D90855 D90855 g1799584 Escherichia coli 562
-11536622 7500884144 inaa ph-inducible protein involved in stress
(fn:phenotype; adaptations, atypical conditions) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 203 of 400 of the completegenome.)
(nt:f216; 98 pct identical to inaa_ecoli sw: p27294) (le:9359) (re:10009)
(di:complement) AE000313 AE000313 g1788569 Escherichia coli 562 -11536622
5000692797 (de:(ecoli_2186) (pn:inaa protein) (gn:inaa) (gtcfc:13.7:14.1)
(ec:) (inaa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_2186 ECOLI_2186 Escherichia coli 562 10120044

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873185	13583	35739	522	173

Description

6500732765 ais:b2252 ais protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2252 b2252 Escherichia coli 562 -11536623 59014 ais (de:ais protein) (db:swissprot) AIS_ECOLI P45565 ESCHERICHIA COLI 562 -11536623 7000684546 ais aluminium-inducible protein (db:pir2.dat) B64996 B64996 Escherichia coli 562 -11536623 224762 ais ais protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #379(50.8-51.2 min.)) (nt:similar to (swissprot accession number p45565)) (le:8410) (re:9012) (di:complement) D90856 D90856 g1799604 Escherichia coli 562 -11536623 7500876711 ais protein induced by aluminum (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completegenome.) (nt:f200; 100 pct identical to ais_ecoli sw: p45565;) (le:2727) (re:3329) (di:complement) AE000315 AE000315 g1788586 Escherichia coli 562 -11536623 5000692807 (de:(ecoli_2201) (pn:protein) (gn:ais) (gtcfc:13.7:14.1) (ec:) (ais_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2201 ECOLI_2201 Escherichia coli 562 10120057

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873186	13584	35740	783	260

Description

6500732766 pmrd:b2259 polymyxin b resistance protein pmrd (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2259 b2259 Escherichia coli 562 -11536624 7000691887 pmrd polymyxin b resistance protein pmrd (db:pir2.dat) A64997 A64997 Escherichia coli 562 -11536624 7500960414 pmrd polymyxin resistance protein b (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 205 of 400 of the completegenome.) (nt:f98; this 98 aa orf is 100 pct identical to) (le:10981) (re:11277) (di:complement) AE000315 AE000315 g1788593 Escherichia coli 562 -11536624 5000692814 (de:(ecoli_2208) (pn:polymyxin b resistance protein pmrd) (gn:pmrd) (gtcfc:13.7:14.1) (ec:) (pmrd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2208 ECOLI_2208 Escherichia coli 562 10123617

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873202	13585	35741	303	100

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873221	13586	35742	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873222	13587	35743	342	113

Description

GTC ORF with score 219 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873223	13588	35744	1080	359

Description

6500732767 lrha:genr:b2289 nadh dehydrogenase operon transcriptional regulator:probable transcriptional regulator lrha (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2289 b2289 Escherichia coli 562 -11536625 82471 lrha:genr (de:probable transcriptional regulator lrha) (db:swissprot) LRHA_ECOLI P36771 ESCHERICHIA COLI 562 -11536625 7000685765 lrha transcription regulator of nadh dehydrogenase operon (cl:hypothetical protein b1875) (db:pir2.dat) G65000 G65000 Escherichia coli 562 -11536625 7500885155 lrha nadh dehydrogenase transcriptional regulator (fn:regulator; energy metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 208 of 400 of the completegenome.) (nt:f312; this 312 aa orf is 100 pct identical to) (le:1829) (re:2767) (di:complement) AE000318 AE000318 g1788626 Escherichia coli 562 -11536625 5000692826 (de:(ecoli_2238) (pn:nadh dehydrogenase operon transcriptional regulator) (gn:lrha) (gtcfc:13.7:14.1) (ec:) (lrha_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2238 ECOLI_2238 Escherichia coli 562 10123630

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873227	13589	35745	642	213

Description

GTC ORF with score 252 to: (fn:involved in production of the virulence factor) (db:genpept-pln1) (de:cochliobolus heterostrophus polyketide synthase (pks1) gene,complete cds.) (le:1324:1599:2141:2703) (re:1524:2083:2661:3353) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873238	13590	35746	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873241	13591	35747	1137	378

Description

6500732768 dedd:b2314 dedd protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2314 b2314 Escherichia coli 562 -11536626 68174 dedd (de:dedd protein) (db:swissprot) DEDD_ECOLI P09549 ESCHERICHIA COLI 562 -11536626 7000684999 dedd dedd protein (cl:dedd protein) (db:pir1.dat) (mp:50 min) XMECDD H65003 Escherichia coli 562 -11536626 224849 dedd dedd protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #406(52.2-52.5 min.)) (nt:similar to (pir accession number e29803)) (le:14599) (re:15234) (di:complement) D90862 D90862 g1799697 Escherichia coli 562 -11536626 224857 dedd dedd protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to (pir accession number e29803)) (le:1664) (re:2299) (di:complement) D90863 D90863 g1799706 Escherichia coli 562 -11536626 7500880128 (sr:e.coli (strain k12) dna, clone psi210) (db:genpept-bct1) (de:e.coli histidine (hist, 3' end), deda, dedb (acetyl-coa carboxylasebeta subunit) complete cds, dedc, dedd, dede (complete cds.), andamidophosphoribosyltransferase (purf), segment 1.) (nt:... ECOHISPUR1 M68934 g146366 Escherichia coli 562 -11536626 234661 dedd putative lipoprotein (fn:putative membrane; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 210 of 400 of the completegenome.) (nt:f211; 100 pct identical to dedd_ecoli sw:) (le:5091) (re:5726) (di:complement) AE000320 AE000320 g1788653 Escherichia coli 562 -11536626 5000692842 (de:(ecoli_2263) (pn:dedd protein) (gn:dedd) (gtcfc:13.7:14.1) (ec:) (dedd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2263 ECOLI_2263 Escherichia coli 562 10010767

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873249	13592	35748	678	225

Description

6500732769 deda:b2317 deda protein:dsg-1 protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2317 b2317 Escherichia coli 562 -11536627 68173 deda (de:deda protein (dsg-1 protein)) (db:swissprot) DEDA_ECOLI P09548 ESCHERICHIA COLI 562 -11536627 131115 deda deda protein (cl:deda protein) (db:pir1.dat) (mp:50 min) XMECAD B29803 Escherichia coli 562 -11536627 224861 deda deda protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to (pir accession number b29803)) (le:4724) (re:5383) (di:complement) D90863 D90863 g1799710 Escherichia coli 562 -11536627 7500880127 deda (sr:e.coli (strain k12) dna, clone psi210) (db:genpept-bct1) (de:e.coli histidine (hist, 3' end), deda, dedb (acetyl-coa carboxylasebeta subunit) complete cds, dedc, dedd, dede (complete cds.), andamidophosphoribosyltransferase (purf), segment 1.) (le:... ECOHISPUR1 M68934 g146363 Escherichia coli 562 -11536627 234658 deda orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 210 of 400 of the completegenome.) (nt:f219; 100 pct identical to deda_ecoli sw: p09548) (le:8151) (re:8810) (di:complement) AE000320 AE000320 g1788656 Escherichia coli 562 -11536627 5000692843 (de:(ecoli_2266) (pn:deda protein:dsg-1 protein) (gn:deda) (gtcfc:13.7:14.1) (ec:) (deda_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2266 ECOLI_2266 Escherichia coli 562 10010766

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873251	13593	35749	321	106

Description

6500732770 trua:hist:asuc:leuk:b2318 pseudouridylate synthase
i:pseudouridine synthase i:uracil hydrolyase (gtcfc:14.3) (ec:4.2.1.70)
(keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2318 b2318
Escherichia coli 562 -11536628 7500893515 trua:hist:asuc:leuk (ec:4.2.1.70)
(de:i) (pseudouridine synthase i) (uracil hydrolyase) (psu-i))
(db:swissprot) TRUA_ECOLI P07649 ESCHERICHIA COLI 562 -11536628 125680
trua:hist trna-pseudouridine synthase i::pseudouridine synthase:uracil
hydrolyase (cl:trna-pseudouridine synthase i) (ec:5.4.99.12) (db:pir1.dat)
(mp:50 min) SYECZ1 B23792 Escherichia coli 562 -11536628 224862 asuc
pseudouridylate synthase i ec 4.2.1.70 (sr:escherichia coli (strain:k12)
dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic
dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to (swissprot accession
number p07649)) (le:5466) (re:6278) (di:complement) D90863 D90863 g1799711
Escherichia coli 562 -11536628 5000692844 (db:genpept-bct1) (de:e. coli k12
pdx, gene usg, gene hist for pseudouridine synthase land gene usg.)
(nt:pseudouridine synthase 1 (hist) (aa 1-270)) (le:1402) (re:2214)
(di:direct) ECHIST1 X02743 g41718 Escherichia coli 562 -11536628 233111
trua pseudouridylate synthase i (fn:enzyme; aminoacyl trna synthetases,
trna) (db:genpept-bct2) (ec:4.2.1.70) (de:escherichia coli k-12 mg1655
section 210 of 400 of the completegenome.) (nt:f270; 100 pct identical to
trua_ecoli sw: p07649) (le:8893) (re:9705) (di:complement) AE000320 AE000320
g1788657 Escherichia coli 562 -11536628 102497 trua:hist:asuc:leuk
(ec:4.2.1.70) (de:(uracil hydrolyase)) (db:swissprot) TRUA_ECOLI P07649
ESCHERICHIA COLI 562 -11536628

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873255	13594	35750	204	67

Description

6500732771 usg:b2319 1 protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0)
(db:gtc-escherichia coli) b2319 b2319 Escherichia coli 562 -11536629
7500893867 usg (de:usg-1 protein) (db:swissprot) USG_ECOLI P08390
ESCHERICHIA COLI 562 -11536629 136436 usg:usg1 usg1 protein
(cl:aspartate-semialdehyde dehydrogenase) (db:pir2.dat) (mp:50 min) QQECH3
A23792 Escherichia coli 562 -11536629 224863 usg1 usg1 protein
(sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
(db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8
min.)) (nt:similar to (pir accession number a23792)) (le:6278) (re:7291)
(di:complement) D90863 D90863 g1799712 Escherichia coli 562 -11536629
5000692845 (db:genpept-bct1) (de:e. coli k12 pdxb, gene usg, gene hist for
pseudouridine synthase land gene usg.) (nt:usg protein (aa 1-337)) (le:389)
(re:1402) (di:direct) ECHIST1 X02743 g41717 Escherichia coli 562 -11536629
233110 usg putative pts system enzyme ii a component (fn:putative
transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 210 of 400 of the completegenome.) (nt:f337; 100 pct
identical to usg_ecoli sw: p08390) (le:9705) (re:10718) (di:complement)
AE000320 AE000320 g1788658 Escherichia coli 562 -11536629 104004 usg
(de:usg-1 protein) (db:swissprot) USG_ECOLI P08390 ESCHERICHIA COLI 562
-11536629

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873259	13595	35751	438	145

Description

6500732772 div:b2321 div protein:protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2321 b2321 Escherichia coli 562 -11536630 68721 div (de:div protein) (db:swissprot) DIV_ECOLI P15286 ESCHERICHIA COLI 562 -11536630 7000685059 div div protein (db:pir2.dat) G65004 G65004 Escherichia coli 562 -11536630 224865 div div protein fragment . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #407(52.4-52.8 min.)) (nt:similar to (swissprot accession number p15286)) (le:8592) (re:9587) (di:direct) D90863 D90863 g1799714 Escherichia coli 562 -11536630 7500880342 div div (fn:unknown) (db:genpept-bct1) (de:escherichia coli beta-ketoacyl-acp synthase i (fabB) gene, partialcds, div (div) and 4-phosphoerythronate dehydrogenase (pdxB) genes,complete cds.) (nt:gene transcribed divergently to pdxB) (le:1461) (re:2456) (di:com... ECU76961 U76961 g1684787 Escherichia coli 562 -11536630 240030 div cell division protein (fn:factor; cell division) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 211 of 400 of the completegenome.) (nt:o331; 100 pct identical to fragment div_ecoli) (le:1298) (re:2293) (di:direct) AE000321 AE000321 g1788661 Escherichia coli 562 -11536630 5000692846 (de:(ecoli_2270) (pn:protein:fragment) (gn:div) (gtcfc:13.7:14.1) (ec:)) (div_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2270 ECOLI_2270 Escherichia coli 562 10120117

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873261	13596	35752	915	304

Description

6500732773 vacj:b2346 vacj lipoprotein precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2346 b2346 Escherichia coli 562 -11536631 1500686819 vacj (de:vacj lipoprotein precursor) (db:swissprot) VACJ_ECOLI P76506 ESCHERICHIA COLI 562 -11536631 7000686934 vacj vacj lipoprotein precursor (cl:vacj lipoprotein) (db:pir2.dat) H65007 H65007 Escherichia coli 562 -11536631 7500893953 vacj lipoprotein precursor (fn:membrane; macromolecule synthesis,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 213 of 400 of the completegenome.) (nt:f251; 99 pct identical to vacj_shif1 sw: p43262) (le:3723) (re:4478) (di:complement) AE000323 AE000323 g1788688 Escherichia coli 562 -11536631 5000692867 (de:(ecoli_2295) (pn:vacj lipoprotein precursor) (gn:vacj) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2295 ECOLI_2295 Escherichia coli 562 10062700

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873266	13597	35753	1416	472

Description

6500732774 yfdb:b2349 putative prophage sf6-like integrase in argw
3region:putative prophage sf6-like integrase in argw-dsdc intergenic region
(gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2349
b2349 Escherichia coli 562 -11536632 111836 intc (de:putative prophage
sf6-like integrase) (db:swissprot) INTC_ECOLI P37326 ESCHERICHIA COLI 562
-11536632 163928 yfdb prophage sf6-like integrase argw 3region
(cl:satellite phage p4 integrase) (db:pir2.dat) (mp:51 min) I84552 I84552
Escherichia coli 562 -11536632 224895 yfdb putative prophage sf6-like
integrage in argw (sr:escherichia coli (strain:k12) dna, clone_lib:kohara
lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone
#410(53.0-53.4 min.)) (nt:similar to (swissprot accession number p37326))
(le:11044) (re:12201) (di:direct) D90865 D90865 g1799746 Escherichia coli
562 -11536632 7500884180 (db:genpept-bct1) (de:escherichia coli k12
trnaarg5 (argw) gene, complete sequence, andputative integrase gene,
complete cds.) (nt:putative integrase, similiar to integrase of) (le:1548)
(re:2705) (di:direct) ECU11296 U11296 g508280 Escherichia coli 562 -11536632
238598 intc putative prophage sf6-like integrase (fn:is, phage, tn; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 213
of 400 of the completegenome.) (nt:o385; formerly designated yfdb) (le:6016)
(re:7173) (di:direct) AE000323 AE000323 g1788690 Escherichia coli 562
-11536632 5000692869 (de:(ecoli_2297) (pn:putative prophage sf6-like
integrage in argw:3"region) (gn:yfdb) (gtcfc:13.7:14.1) (ec:) (yfdb_ecoli)
(keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2297
ECOLI_2297 Escherichia coli 562 10053564

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873273	13598	35754	1875	624
<u>Description</u>				
6500732775 dsdx:b2365 dsdx permease (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2365 b2365 Escherichia coli 562 -11536633 7500880675 dsdx (de:dsdx permease) (db:swissprot) DSDX_ECOLI P08555 ESCHERICHIA COLI 562 -11536633 130696 dsdx:dcdc d-serine permease (cl:d-serine permease) (db:pir1.dat) (mp:51 min) S54140 S54140 Escherichia coli 562 -11536633 224912 dsdx dsdx permease. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #411(53.2-53.6 min.)) (nt:similar to (swissprot accession number p08555)) (le:10856) (re:12193) (di:direct) D90866 D90866 g1799764 Escherichia coli 562 -11536633 224920 dsdx dsdx permease. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #412(53.4-53.8 min.)) (nt:similar to (swissprot accession number p08555)) (le:1615) (re:2952) (di:direct) D90867 D90867 g1799773 Escherichia coli 562 -11536633 232711 dsdc d-serine permease (db:genpept-bct1) (de:e.coli dsdc & dsda genes.) (le:377) (re:1714) (di:direct) ECDNADSD X86379 g784980 Escherichia coli 562 -11536633 5000692884 dsdx (db:genpept-bct1) (de:e.coli dsdx and dsdc genes.) (le:21) (re:1358) (di:complement) ECDSDXC X91821 g1050467 Escherichia coli 562 -11536633 232693 dsdx transport system permease serine? (fn:transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 214 of 400 of the completegenome.) (nt:o445; 100 pct identical to dsdx_ecoli sw: p08555) (le:7266) (re:8603) (di:direct) AE000324 AE000324 g1788707 Escherichia coli 562 -11536633 69320 dsdx (de:dsdx permease) (db:swissprot) DSDX_ECOLI P08555 ESCHERICHIA COLI 562 -11536633				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873278	13599	35755	1041	346

Description

6500732776 emry:b2367 multidrug resistance protein y (gtcfc:13.3)
 (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2367 b2367
 Escherichia coli 562 -11536634 70136 emry (de:multidrug resistance protein
 y) (db:swissprot) EMRY_ECOLI P52600 ESCHERICHIA COLI 562 -11536634
 7000685156 emry multidrug resistance protein y (db:pir2.dat) D65010 D65010
 Escherichia coli 562 -11536634 224917 emry multidrug resistance protein y.
 (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise)
 (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #411(53.2-53.6
 min.)) (nt:similar to (swissprot accession number p52600)) (le:13647)
 (re:15185) (di:complement) D90866 D90866 g1799769 Escherichia coli 562
 -11536634 224925 emry multidrug resistance protein y. (sr:escherichia coli
 (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1)
 (de:e.coli genomic dna, kohara clone #412(53.4-53.8 min.)) (nt:similar to
 (swissprot accession number p52600)) (le:4406) (re:5944) (di:complement)
 D90867 D90867 g1799778 Escherichia coli 562 -11536634 301441 emry (fn:emry
 is homologous to the multidrug resistace) (sr:escherichia coli dna)
 (db:genpept-bct1) (de:escherichia coli dna for emrk and emry, complete cds.)
 (le:1592) (re:3130) (di:direct) ECOEMRK D78168 g1060877 Escherichia coli 562
 -11536634 234234 emry multidrug resistance protein y (fn:putative
 transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli
 k-12 mg1655 section 215 of 400 of the completegenome.) (nt:f512; 100 pct
 identical to emry_ecoli sw: p52600) (le:84) (re:1622) (di:complement)
 AE000325 AE000325 g1788710 Escherichia coli 562 -11536634 5000692885
 (de:(ecoli_2315) (pn:multidrug resistance protein y) (gn:emry)
 (gtcfc:13.7:14.1) (ec:) (emry_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli)) ECOLI_2315 ECOLI_2315 Escherichia coli 562
 10012713

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873301	13600	35756	828	275

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873312	13601	35757	1017	338

Description

6500732777 emrk:b2368 multidrug resistance protein k (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2368 b2368 Escherichia coli 562 -11536635 70134 emrk (de:multidrug resistance protein k) (db:swissprot) EMRK_ECOLI P52599 ESCHERICHIA COLI 562 -11536635 7000685155 emrk multidrug resistance protein k (cl:multidrug resistance protein a:lipoyl/biotin-binding homology) (db:pir2.dat) E65010 E65010 Escherichia coli 562 -11536635 7500881008 emrk multidrug resistance protein k (fn:putative transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 215 of 400 of the completegenome.) (nt:f387; 100 pct identical to 387 residues from) (le:1622) (re:2785) (di:complement) AE000325 AE000325 g1788711 Escherichia coli 562 -11536635 5000692886 (de:(ecoli_2316) (pn:multidrug resistance protein k) (gn:emrk) (gtcfc:13.7:14.1) (ec:) (emrk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2316 ECOLI_2316 Escherichia coli 562 10123656

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873319	13602	35758	996	331

Description

6500732778 xapb:b2406 xanthosine permease:xanthosine transporter (gtcfc:12.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2406 b2406 Escherichia coli 562 -11536636 108071 xapb (de:xanthosine permease (xanthosine transporter)) (db:swissprot) XAPB_ECOLI P45562 ESCHERICHIA COLI 562 -11536636 7000687020 xapb xanthosine permease (db:pir2.dat) E65014 E65014 Escherichia coli 562 -11536636 224961 xapb xanthosine permease xanthosine transporter . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #416(54.1-54.5 min.)) (nt:similar to (swissprot accession number p45562)) (le:15573) (re:16829) (di:complement) D90869 D90869 g1799816 Escherichia coli 562 -11536636 224964 xapb xanthosine permease xanthosine transporter . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #417(54.4-54.6 min.)) (nt:similar to (swissprot accession number p45562)) (le:2055) (re:3311) (di:complement) D90870 D90870 g1799820 Escherichia coli 562 -11536636 7500894431 xapb xanthosine permease (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 218 of 400 of the completegenome.) (nt:f418; 94 pct identical to xapb_ecoli sw: p45562) (le:4418) (re:5674) (di:complement) AE000328 AE000328 g1788745 Escherichia coli 562 -11536636 5000692911 (de:(ecoli_2347) (pn:xanthosine permease) (gn:xapb) (gtcfc:13.7:14.1) (ec:) (xapb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2347 ECOLI_2347 Escherichia coli 562 10120179

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873330	13603	35759	198	65

Description

6500732779 euth:b2452 ethanolamine utilization protein euth:putative ethanolamine transporter (gtcfc:12.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2452 b2452 Escherichia coli 562 -11536637 1500686929 euth (de:transporter)) (db:swissprot) EUTH_ECOLI P76552 ESCHERICHIA COLI 562 -11536637 7000685195 euth ethanolamine utilization protein euth (db:pir2.dat) C65020 C65020 Escherichia coli 562 -11536637 7500881207 euth ethanolamine utilization:homolog of salmonella (fn:putative transport; degradation of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:f408; this 408 aa orf is 94 pct identical (1 gap)) (le:3564) (re:4790) (di:complement) AE000332 AE000332 g1788794 Escherichia coli 562 -11536637 5000692941 (de:(ecoli_2392) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2392 ECOLI_2392 Escherichia coli 562 10063066

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873332	13604	35760	633	210

Description

6500732780 eutg:b2453 ethanolamine utilization protein eutg (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2453 b2453 Escherichia coli 562 -11536638 7000690874 eutg ethanolamine utilization protein eutg (cl:lactaldehyde reductase:lactaldehyde reductase homology) (db:pir2.dat) D65020 D65020 Escherichia coli 562 -11536638 7500959732 eutg ethanolamine utilization:homolog of salmonella (fn:putative enzyme; degradation of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:f404; 80 pct identical (4 gaps) to 394 residues) (le:5007) (re:6221) (di:complement) AE000332 AE000332 g1788795 Escherichia coli 562 -11536638 5000692942 (de:(ecoli_2393) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2393 ECOLI_2393 Escherichia coli 562 10123694

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873333	13605	35761	624	207

Description

GTC ORF with score 525 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 0604.) (nt:similar to saccharomyces serevisiae hypothetical) (le:<1) (re:1121) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873337	13606	35762	582	193

Description

6500732781 eutj:b2454 ethanolamine utilization protein eutj (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2454 b2454 Escherichia coli 562 -11536639 1500686930 eutj (de:ethanolamine utilization protein eutj) (db:swissprot) EUTJ_ECOLI P77277 ESCHERICHIA COLI 562 -11536639 7000685197 eutj ethanolamine utilization protein eutj (db:pir2.dat) E65020 E65020 Escherichia coli 562 -11536639 225020 eutj ethanolamine utilization protein eutj. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #421(55.1-55.5 min.)) (nt:similar to (swissprot accession number p41794)) (le:9545) (re:10381) (di:complement) D90874 D90874 g1799880 Escherichia coli 562 -11536639 7500881209 eutj ethanolamine utilization:homolog of salmonella (fn:putative enzyme; degradation of small) (db:genpept-bct2) (de:escherichia coli k-12 mgl655 section 222 of 400 of the completegenome.) (nt:f278; 89 pct identical (1 gap) to eutj_salty) (le:6184) (re:7020) (di:complement) AE000332 AE000332 g1788796 Escherichia coli 562 -11536639 5000692943 (de:(ecoli_2394) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2394 ECOLI_2394 Escherichia coli 562 10063067

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873345	13607	35763	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873354	13608	35764	639	212

Description

GTC ORF with score 153 to: (sr:thale cress) (db:genpept-pln1) (ec:3.6.1.3) (de:arabidopsis thaliana mgatp-energized glutathione s-conjugate pump(mrp2) gene, complete cds.) (nt:atp-binding cassette transport protein) (le:141:564:829:991:1313) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873368	13609	35765	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873372	13610	35766	2313	770

Description

6500732782 eute:b2455 ethanolamine utilization protein eute (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2455 b2455 Escherichia coli 562 -11536640 1500686928 eute (de:ethanolamine utilization protein eute) (db:swissprot) EUTE_ECOLI P77445 ESCHERICHIA COLI 562 -11536640 7000685194 eute ethanolamine utilization protein eute (db:pir2.dat) F65020 F65020 Escherichia coli 562 -11536640 225021 eute ethanolamine utilization protein eute. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #421(55.1-55.5 min.)) (nt:similar to (swissprot accession number p41793)) (le:10392) (re:11795) (di:complement) D90874 D90874 g1799881 Escherichia coli 562 -11536640 7500881206 eute ethanolamine utilization:similar to (fn:putative enzyme; degradation of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:f467; 93 pct identical to eute_salty sw: p41793) (le:7031) (re:8434) (di:complement) AE000332 AE000332 g1788797 Escherichia coli 562 -11536640 5000692944 (de:(ecoli_2395) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2395 ECOLI_2395 Escherichia coli 562 10063065

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873382	13611	35767	1410	469

Description

6500732783 euti:b2458 ethanolamine utilization protein euti (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2458 b2458 Escherichia coli 562 -11536641 1500687200 euti (de:ethanolamine utilization protein euti) (db:swissprot) EUTI_ECOLI P77218 ESCHERICHIA COLI 562 -11536641 7000685196 euti ethanolamine utilization protein euti (cl:phosphate acetyltransferase) (db:pir2.dat) A65021 A65021 Escherichia coli 562 -11536641 225024 euti ethanolamine utilization protein euti (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #421(55.1-55.5 min.)) (nt:similar to (swissprot accession number p41790)) (le:12533) (re:13549) (di:complement) D90874 D90874 g1799884 Escherichia coli 562 -11536641 7500881208 euti ethanolamine utilization:homolog of salmonella (fn:putative enzyme; degradation of small) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 222 of 400 of the completegenome.) (nt:f338; 91 pct identical to 242 residues of) (le:9172) (re:10188) (di:complement) AE000332 AE000332 g1788800 Escherichia coli 562 -11536641 5000692947 (de:(ecoli_2398) (pn:function not assigned) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2398 ECOLI_2398 Escherichia coli 562 10064200

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501873386	13612	35768	594	197

Description

6500732784 bcp:b2480 bacterioferritin comigratory protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2480 b2480 Escherichia coli 562 -11536642 61509 bcp (de:bacterioferritin comigratory protein) (db:swissprot) BCP_ECOLI P23480 ESCHERICHIA COLI 562 -11536642 162772 bcp bacterioferritin comigratory protein (cl:bacterioferritin comigratory protein:alkyl hydroperoxidase c22 protein homology) (db:pir2.dat) B49749 B49749 Escherichia coli 562 -11536642 225046 bacterioferritin comigratory protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #423(55.7-56.1 min.)) (nt:similar to (pir accession number b49749)) (le:11428) (re:11898) (di:direct) D90876 D90876 g1799908 Escherichia coli 562 -11536642 225056 bacterioferritin comigratory protein (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #424(55.9-56.3 min.)) (nt:similar to (pir accession number b49749)) (le:4168) (re:4638) (di:direct) D90877 D90877 g1805539 Escherichia coli 562 -11536642 7000684689 bcp bacterioferritin comigratory protein (db:genpept-bct1) (de:escherichia coli p177 (o177), bacterioferritin comigratory protein(bcp), putative hydrogenase-4 complex (hyfabcdefghijr), andputative formate transporter (focb) gene, complete cds and putativepermease p75 (perm) gene partial cds.)... ECOORF123 M63654 g2668495 Escherichia coli 562 -11536642 235284 bcp bacterioferritin comigratory protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 225 of 400 of the completegenome.) (nt:o156; 100 pct identical to bcp_ecoli sw: p23480) (le:2784) (re:3254) (di:direct) AE000335 AE000335 g1788825 Escherichia coli 562 -11536642 5000692963 (de:(ecoli_2420) (pn:bacterioferritin comigratory protein) (gn:bcp) (gtcfc:13.7:14.1) (ec:) (bcp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2420 ECOLI_2420 Escherichia coli 562 10004218

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873387	13613	35769	540	179

Description

6500732785 gcpe:b2515 gcpe protein:protein e (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2515 b2515 Escherichia coli 562 -11536643 7500882260 gcpe (de:gcpe protein (protein e)) (db:swissprot) GCPE_ECOLI P27433 ESCHERICHIA COLI 562 -11536643 163093 gcpe gcpe protein (cl:gcpe protein) (db:pir2.dat) S23058 S23058 Escherichia coli 562 -11536643 5000692988 gcpe (db:genpept-bct1) (de:e.coli gcpe gene.) (le:535) (re:1653) (di:direct) ECGCPE X64451 g41542 Escherichia coli 562 -11536643 232977 gcpe orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 228 of 400 of the completegenome.) (nt:f372; 100 pct identical to gcpe_ecoli sw: p27433) (le:86) (re:1204) (di:complement) AE000338 AE000338 g1788863 Escherichia coli 562 -11536643 73421 gcpe (de:gcpe protein (protein e)) (db:swissprot) GCPE_ECOLI P27433 ESCHERICHIA COLI 562 -11536643

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873401	13614	35770	585	194

Description

6500732786 sseb:b2522 sseb protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2522 b2522 Escherichia coli 562 -11536644 99541 sseb (de:ss eb protein) (db:swissprot) SSEB_ECOLI P31143 ESCHERICHIA COLI 562 -11536644 7000686684 sseb rhodanese-like protein sseb (db:pir2.dat) A65029 A65029 Escherichia coli 562 -11536644 7500892126 sseb enhanced serine sensitivity (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 229 of 400 of the completegenome.) (nt:f261; 98 pct identical to sseb_ecoli sw: p31143 but) (le:439) (re:1224) (di:complement) AE000339 AE000339 g1788871 Escherichia coli 562 -11536644 5000692993 (de:(ecoli_2462) (pn:enhanced serine sensitivity) (gn:ss eb) (gtcfc:13.7:14.1) (ec:) (sseb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2462 ECOLI_2462 Escherichia coli 562 10123719

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873404	13615	35771	1905	635
<u>Description</u>				
6500732787 suhb:ssya:b2533 extragenic suppressor protein suhb (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2533 b2533 Escherichia coli 562 -11536645 99828 suhb:ssya (de:extragenic suppressor protein suhb) (db:swissprot) SUHB_ECOLI P22783 ESCHERICHIA COLI 562 -11536645 7000686698 suhb suppressor protein suhb (cl:suppressor protein suhb) (db:pir2.dat) D65030 D65030 Escherichia coli 562 -11536645 225116 ssya extragenic suppressor protein suhb. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #430(57.2-57.5 min.)) (nt:similar to (swissprot accession number p22783)) (le:7205) (re:8008) (di:direct) D90883 D90883 g1799941 Escherichia coli 562 -11536645 225124 ssya extragenic suppressor protein suhb. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p22783)) (le:666) (re:1469) (di:direct) D90884 D90884 g1799950 Escherichia coli 562 -11536645 7500892240 suhb enhances synthesis of sigma32 in mutant (fn:phenotype; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 229 of 400 of the completegenome.) (nt:o267; 99 pct identical to suhb_ecoli sw: p22783) (le:9724) (re:10527) (di:direct) AE000339 AE000339 g1788882 Escherichia coli 562 -11536645 5000693002 (de:(ecoli_2473) (pn:enhances synthesis of sigma32 in mutant extragenic suppressor protein suhb) (gn:suhb) (gtcfc:13.7:14.1) (ec:) (suhb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2473 ECOLI_2473 Escherichia coli 562 10120252				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873406	13616	35772	981	326
<u>Description</u>				
6500732788 csie:b2535 stationary phase inducible protein csie (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2535 b2535 Escherichia coli 562 -11536646 66640 csie (de:stationary phase inducible protein csie) (db:swissprot) CSIE_ECOLI P54901 ESCHERICHIA COLI 562 -11536646 7000684921 csie stationary phase inducible protein csie (db:pir2.dat) F65030 F65030 Escherichia coli 562 -11536646 7500879460 csie orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:o433; 99 pct identical to 433 aa of gb:) (le:1140) (re:2441) (di:direct) AE000340 AE000340 g1788885 Escherichia coli 562 -11536646 5000693004 (de:(ecoli_2475) (pn:csie protein) (gn:csie) (gtcfc:13.7:14.1) (ec:) (csie_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2475 ECOLI_2475 Escherichia coli 562 10123722				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873408	13617	35773	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873410	13618	35774	381	126

Description

6500732789 yfhu:b2538 digoxigenin beta subunit:digoxigenin alpha subunit (gtcfc:14.3) (ec:1.14.1.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2538 b2538 Escherichia coli 562 -11536647 4000707869 hcaa:hcaal (ec:1.14.1.-) (de:digoxigenin alpha subunit,) (db:swissprot) HCAA_ECOLI Q47139 ESCHERICHIA COLI 562 -11536647 7000685025 dioxygenase beta chain (cl:toluene dioxygenase terminal oxygenase component large chain) (db:pir2.dat) A65031 A65031 Escherichia coli 562 -11536647 225130 bedc1 benzene 1:2-dioxygenase alpha subunit ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number q07944)) (le:6256) (re:7617) (di:direct) D90884 D90884 g1799956 Escherichia coli 562 -11536647 7500883070 hcaal large terminal subunit of phenylpropionate (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:o453; 99 pct identical to 383 aa of gb: ecdigoxab_2) (le:4758) (re:6119) (di:direct) AE000340 AE000340 g1788888 Escherichia coli 562 -11536647 5000693007 (de:(ecoli_2478) (pn:digoxigenin beta subunit) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2478 ECOLI_2478 Escherichia coli 562 10120260

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873425	13619	35775	237	78

Description

6500732790 yfhv:b2539 digoxigenin alpha subunit:digoxigenin beta subunit (gtcfc:14.3) (ec:1.14.1.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2539 b2539 Escherichia coli 562 -11536648 4000707870 hcab:hcaa2 (ec:1.14.1.-) (de:digoxigenin beta subunit,) (db:swissprot) HCAB_ECOLI Q47140 ESCHERICHIA COLI 562 -11536648 7000685026 biphenyl dioxygenase:terminal oxygenase component alpha chain:digoxigenin alpha chain (cl:toluene dioxygenase terminal oxygenase component small chain) (ec:1.14.-.-) (db:pir2.dat) B65031 B65031 Escherichia coli 562 -11536648 225131 bnzb benzene 1:2-dioxygenase beta subunit ec (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #431(57.3-57.7 min.)) (nt:similar to (swissprot accession number p08085)) (le:7614) (re:8132) (di:direct) D90884 D90884 g1799957 Escherichia coli 562 -11536648 7500883071 hcaa2 small terminal subunit of phenylpropionate (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 230 of 400 of the completegenome.) (nt:o172; 96 pct identical to 49 aa fragment) (le:6116) (re:6634) (di:direct) AE000340 AE000340 g1788889 Escherichia coli 562 -11536648 5000693008 (de:(ecoli_2479) (pn:digoxigenin alpha subunit) (gtcfc:13.7:14.1) (ec:) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2479 ECOLI_2479 Escherichia coli 562 10120261

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873426	13620	35776	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873429	13621	35777	405	134

Description

6500732791 rsec:b2570 sigma-e factor regulatory protein rsec (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2570 b2570 Escherichia coli 562 -11536649 97461 rsec (de:sigma-e factor regulatory protein rsec) (db:swissprot) RSEC_ECOLI P46187 ESCHERICHIA COLI 562 -11536649 164583 rsec sigma-e factor regulatory protein rsec (db:pir2.dat) I83299 I83299 Escherichia coli 562 -11536649 239527 hypothetical protein in mcla 3region (sr:escherichia coli (strain k12) (library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli ribonuclease iii and other genes, complete cds.) (le:14784) (re:15263) (di:complement) ECOK12RIII D64044 g987645 Escherichia coli 562 -11536649 234895 rsec sigma-e factor:negative regulatory protein (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 233 of 400 of the completegenome.) (nt:f159; 100 pct identical to rsec_ecoli sw: p46187) (le:7082) (re:7561) (di:complement) AE000343 AE000343 g1788923 Escherichia coli 562 -11536649 239531 rsec rsec (db:genpept-bct2) (de:escherichia coli heat shock sigma factor (rpoe) gene, and rsea,rseb and rsec genes, complete cds.) (nt:regulator of rpoe; integral inner membrane protein) (le:2545) (re:3024) (di:direct) ECU37089 U37089 g1045631 Escherichia coli 562 -11536649 7500891148 rsec rsec (db:genpept-bct2) (de:escherichia coli regulators of sigma e rsea gene, partial cds, andrseb and rsec genes, complete cds.) (nt:regulator of sigma e) (le:985) (re:1464) (di:direct) ECU37455 U37455 g1050877 Escherichia coli 562 -11536649 5000693028 (de:(ecoli_2510) (pn:sigma-e factor, negative regulatory protein) (gn:rsec) (gtcfc:13.7:14.1) (ec:) (rsec_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2510 ECOLI_2510 Escherichia coli 562 10039353

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873432	13622	35778	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873469	13623	35779	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873471	13624	35780	315	104

Description

6500732792 rseb:b2571 sigma-e factor regulatory protein rseb precursor (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2571 b2571 Escherichia coli 562 -11536650 97459 rseb (de:sigma-e factor regulatory protein rseb precursor) (db:swissprot) RSEB_ECOLI P46186 ESCHERICHIA COLI 562 -11536650 164582 rseb sigma-e factor regulatory protein rseb precursor (cl:conserved hypothetical protein hi0630) (db:pir2.dat) I83298 I83298 Escherichia coli 562 -11536650 239526 orf1 protein (sr:escherichia coli (strain k12) (library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli ribonuclease iii and other genes, complete cds.) (le:15260) (re:16216) (di:complement) ECOK12RIII D64044 g987646 Escherichia coli 562 -11536650 234896 rseb regulates activity of sigma-e factor (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 233 of 400 of the completegenome.) (nt:f318; 100 pct identical to rseb_ecoli sw: p46186) (le:7558) (re:8514) (di:complement) AE000343 AE000343 g1788924 Escherichia coli 562 -11536650 239530 rseb rseb (db:genpept-bct2) (de:escherichia coli heat shock sigma factor (rpoe) gene, and rsea,rseb and rsec genes, complete cds.) (nt:regulator of rpoe; periplasmic protein) (le:1592) (re:2548) (di:direct) ECU37089 U37089 g1045630 Escherichia coli 562 -11536650 7500891146 rseb rseb (db:genpept-bct2) (de:escherichia coli regulators of sigma e rsea gene, partial cds, andrseb and rsec genes, complete cds.) (nt:regulator of sigma e) (le:32) (re:988) (di:direct) ECU37455 U37455 g1050876 Escherichia coli 562 -11536650 5000693029 (de:(ecoli_2511) (pn:regulates activity of sigma-e factor) (gn:rseb) (gtcfc:13.7:14.1) (ec:) (rseb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2511 ECOLI_2511 Escherichia coli 562 10039351

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501873478	13625	35781	840	280
<u>Description</u> 6500732793 rsea:mcla:b2572 sigma-e factor negative regulatory protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2572 b2572 Escherichia coli 562 -11536651 97457 rsea:mcla (de:sigma-e factor negative regulatory protein) (db:swissprot) RSEA_ECOLI P38106 ESCHERICHIA COLI 562 -11536651 164043 rsea:mcla sigma-e factor negative regulatory protein mcla:rsea protein (db:pir2.dat) B57255 B57255 Escherichia coli 562 -11536651 238590 mcla protein (sr:escherichia coli (strain k12) (library: kohara) dna, clone 7g4) (db:genpept-bct1) (de:escherichia coli ribonuclease iii and other genes, complete cds.) (le:16216) (re:16866) (di:complement) ECOK12RIII D64044 g987647 Escherichia coli 562 -11536651 239525 mcla mcla (fn:mcla is a putative negative regulator of rpoe) (db:genpept-bct1) (de:escherichia coli rpoe (rpoe) gene, partial cds and negativeregulator mcla (mcla) gene, complete cds.) (nt:mcla is similar to muca, pir accession number) (le:101) (re:751) (di:direct) ECU10148 U10148 g994818 Escherichia coli 562 -11536651 234897 rsea sigma-e factor:negative regulatory protein (fn:regulator; global regulatory functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 233 of 400 of the completgenome.) (nt:f216; 100 pct identical to rsea_ecoli sw: p38106) (le:8514) (re:9164) (di:complement) AE000343 AE000343 g1788925 Escherichia coli 562 -11536651 7500891144 rsea rsea (db:genpept-bct2) (de:escherichia coli heat shock sigma factor (rpoe) gene, and rsea,rseb and rsec genes, complete cds.) (nt:inhibitor of rpoe; integral inner membrane protein) (le:942) (re:1592) (di:direct) ECU37089 U37089 g1045629 Escherichia coli 562 -11536651 5000693030 (de:(ecoli_2512) (pn:sigma-e factor, negative regulatory protein) (gn:rsea) (gtcfc:13.7:14.1) (ec:) (rsea_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2512 ECOLI_2512 Escherichia coli 562 10039349				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873488	13626	35782	945	314

Description

6500732794 sfhb:b2594 ftsh suppressor protein sfhb:sfhb protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2594 b2594 Escherichia coli 562 -11536652 111951 rlud:sfhb (ec:4.2.1.70) (de:(pseudouridylate synthase) (uracil hydrolyase)) (db:swissprot) RLUD_ECOLI P33643 ESCHERICHIA COLI 562 -11536652 7000686591 sfhb ftsh suppressor protein sfhb (cl:conserved hypothetical protein hi0176) (db:pir2.dat) E65037 E65037 Escherichia coli 562 -11536652 7500891566 sfhb sfhb (sr:escherichia coli strain=k-12, w3110) (db:genpept-bct1) (de:escherichia coli ftsh suppressor protein (sfhb) gene and (yfi)gene, complete cds, and clpb gene, partial cds.) (nt:the sfhb mutation suppresses the) (le:262) (re:1242) (di:direct) ECU50134 U50134 g1236631 Escherichia coli 562 -11536652 239636 sfhb suppressor of ftsh mutation (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 236 of 400 of the completegenome.) (nt:f326; 100 pct identical to gb: ecu50134_1 (sfhb);) (le:823) (re:1803) (di:complement) AE000346 AE000346 g1788946 Escherichia coli 562 -11536652 5000693041 (de:(ecoli_2530) (pn:ftsh suppressor protein sfhb) (gn:sfhb) (gtcfc:13.7:14.1) (ec:)) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2530 ECOLI_2530 Escherichia coli 562 10123741

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873489	13627	35783	318	105

Description

6500732795 smpb:b2620 small protein b:18.3 kd protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2620 b2620 Escherichia coli 562 -11536653 164632 smpb small protein b:smpb (cl:small protein smpb) (db:pir2.dat) (mp:56.5 min) JS0701 JS0701 Escherichia coli 562 -11536653 239482 smpb small protein (sr:escherichia coli (strain k12) (library: kohara's library) dna) (db:genpept-bct1) (de:e.coli gene for small stable rna (10sa rna).) (le:658) (re:1140) (di:direct) ECOSRNA D12501 g216668 Escherichia coli 562 -11536653 7500960462 smpb (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (le:3850) (re:4332) (di:direct) ECU36840 U36840 g1033116 Escherichia coli 562 -11536653 236034 smpb small protein b (fn:orf; unknown function) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the completegenome.) (nt:o160; 100 pct identical to smpb_ecoli sw: p32052) (le:8618) (re:9100) (di:direct) AE000347 AE000347 g1788973 Escherichia coli 562 -11536653 5000693056 (de:(ecoli_2556) (pn:small protein b:18) (gn:smpb) (gtcfc:13.7:14.1) (ec:)) (smpb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2556 ECOLI_2556 Escherichia coli 562 10087407

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873490	13628	35784	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873491	13629	35785	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873496	13630	35786	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873503	13631	35787	1038	346

Description

6500732796 inta:slpa:intx:b2622 slpa integrase:prophage cp4-57 integrase (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2622 b2622 Escherichia coli 562 -11536654 79552 inta:slpa:intx (de:prophage cp4-57 integrase) (db:swissprot) INTA_ECOLI P32053 ESCHERICHIA COLI 562 -11536654 7000685637 inta:intx slpa integrase:prophage cp4-57 integrase (cl:satellite phage p4 integrase) (db:pir2.dat) (mp:56.5 min) H65040 H65040 Escherichia coli 562 -11536654 239483 slpa slpa integrase (db:genpept-bct1) (de:escherichia coli k12 10sa stable rna (ssra) gene, partial sequence, and cryptic prophage cp4-57 slpa integrase (slpa) and alpatranscriptional regulator (alpa) genes, complete cds.) (nt:int protein of cp4-57) (le:296) (re:1537) (di:... ECOALPA U03737 g433349 Escherichia coli 562 -11536654 7500884178 slpa slpa integrase (db:genpept-bct1) (de:escherichia coli k-12 genome, approximately 57 minutes.) (nt:int protein of cp4-57; alternate name intx; orf of) (le:5113) (re:6354) (di:direct) ECU36840 U36840 g1033117 Escherichia coli 562 -11536654 233764 inta prophage cp4-57 integrase (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 237 of 400 of the complete genome.) (nt:o413; 100 pct identical to inta_ecoli sw:) (le:9881) (re:11122) (di:direct) AE000347 AE000347 g1788974 Escherichia coli 562 -11536654 5000693057 (de:(ecoli_2557) (pn:prophage cp4-57 integrase) (gn:inta) (gtcfc:13.7:14.1) (ec:) (inta_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2557 ECOLI_2557 Escherichia coli 562 10021869

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873507	13632	35788	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873522	13633	35789	1089	362

Description

6500732797 mpra:emrr:b2684 transcriptional repressor mpra:emrr protein (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2684 b2684 Escherichia coli 562 -11536655 307575 mpra:emrr (de:transcriptional repressor mpra (emrr protein)) (db:swissprot) MPRA_ECOLI P24201 ESCHERICHIA COLI 562 -11536655 164476 emrr:mpra regulatory protein mpra:emrr protein (cl:regulatory protein mpra) (db:pir2.dat) (mp:58 min) S14473 S14473 Escherichia coli 562 -11536655 225236 emrr emrr protein. (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #445(60.2-60.6 min.)) (nt:similar to (swissprot accession number p24201)) (le:14243) (re:14773) (di:direct) D90891 D90891 g1800069 Escherichia coli 562 -11536655 5000693107 mpra (db:genpept-bct1) (de:e. coli mpra gene.) (le:98) (re:628) (di:direct) ECPRA X54151 g42014 Escherichia coli 562 -11536655 233401 emrr regulator of plasmid mcrb operon microcin b17 (fn:regulator; plasmid-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 243 of 400 of the completegenome.) (nt:o176; 100 pct identical to emrr_ecoli sw: p24201;) (le:1245) (re:1775) (di:direct) AE000353 AE000353 g1789040 Escherichia coli 562 -11536655 70135 mpra:emrr (de:transcriptional repressor mpra (emrr protein)) (db:swissprot) MPRA_ECOLI P24201 ESCHERICHIA COLI 562 -11536655

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873525	13634	35790	411	136

Description

6500732798 oraa:recx:b2698 regulatory protein recx:oraa protein (gtcfc:10.2:12.13:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2698 b2698 Escherichia coli 562 -11536656 93835 oraa:recx (de:regulatory protein recx (oraa protein)) (db:swissprot) RECX_ECOLI P33596 ESCHERICHIA COLI 562 -11536656 7000686292 oraa:recx regulatory protein recx:oraa protein (cl:recx protein) (db:pir2.dat) F65049 F65049 Escherichia coli 562 -11536656 225250 oraa regulatory protein recx oraa protein . (sr:escherichia coli (strain:k12) dna, clone_lib:kohara lambda minise) (db:genpept-bct1) (de:e.coli genomic dna, kohara clone #446(60.5-60.9 min.)) (nt:similar to (swissprot accession number p33596)) (le:11045) (re:11545) (di:complement) D90892 D90892 g1800084 Escherichia coli 562 -11536656 7500889601 oraa regulator:oraa protein (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 244 of 400 of the completegenome.) (nt:f166; 98 pct identical to recx_ecoli sw: p33596; cg) (le:95) (re:595) (di:complement) AE000354 AE000354 g1789050 Escherichia coli 562 -11536656 5000693111 (de:(ecoli_2626) (pn:regulatory protein recx:oraa protein) (gn:oraa) (gtcfc:13.7:14.1) (ec:) (recx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2626 ECOLI_2626 Escherichia coli 562 10120330

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873539	13635	35791	510	169

Description

6500732799 sure:b2744 stationary-phase survival protein sure:survival protein sure (gtcfc:13.2:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2744 b2744 Escherichia coli 562 -11536657 99888 sure (de:survival protein sure) (db:swissprot) SURE_ECOLI P36664 ESCHERICHIA COLI 562 -11536657 164672 sure stationary-phase survival protein sure (cl:stationary-phase survival protein sure) (db:pir2.dat) I69732 I69732 Escherichia coli 562 -11536657 7500892276 sure (sr:escherichia coli (strain mp180) dna) (db:genpept-bct1) (de:escherichia coli sure gene, complete cds and l-isoaspartylproteinmethyltransferase (pcm) gene, partial cds.) (nt:orf2) (le:1826) (re:2587) (di:direct) ECOPCMORFS L07942 g1036739 Escherichia coli 562 -11536657 235369 sure survival protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 248 of 400 of the completegenome.) (nt:f253; 100 pct identical to pir: i69732; alternate) (le:4487) (re:5248) (di:complement) AE000358 AE000358 g1789101 Escherichia coli 562 -11536657 5000693129 (de:(ecoli_2673) (pn:survival protein sure) (gn:sure) (gtcfc:13.7:14.1) (ec:) (sure_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2673 ECOLI_2673 Escherichia coli 562 10041743

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873551	13636	35792	1206	401

Description

6500732800 chpa:mazf:chpak:b2782 pemk-like protein 1:mazf protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2782 b2782 Escherichia coli 562 -11536658 64412 chpa:mazf:chpak (de:pemk-like protein 1 (mazf protein)) (db:swissprot) CHPA_ECOLI P33645 ESCHERICHIA COLI 562 -11536658 162810 chpa cell growth regulatory protein chpak (db:pir2.dat) B49339 B49339 Escherichia coli 562 -11536658 235741 chpa chpak (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e. coli chpa gene for chpai and chpak, complete cds.) (le:335) (re:670) (di:direct) ECOCHPA D16450 g506194 Escherichia coli 562 -11536658 239356 mazf (sr:escherichia coli dna) (db:genpept-bct1) (de:e. coli rela gene encoding atp:gtp 3'-pyrophosphotransferase,complete cds.) (nt:homologous to plasmid r100 pemk gene) (le:2840) (re:3175) (di:direct) ECORELA J04039 g416197 Escherichia coli 562 -11536658 7500878696 mazf pemk-like protein 1 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 62 minute region.) (nt:cg site no. 33287; alternate gene names chpa,) (le:8621) (re:8956) (di:complement) ECU29580 U29580 g882676 Escherichia coli 562 -11536658 233995 chpa probable growth inhibitor:pemk-like (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 252 of 400 of the completegenome.) (nt:f111; 100 pct identical to chpa_ecoli sw: p33645;) (le:1006) (re:1341) (di:complement) AE000362 AE000362 g1789145 Escherichia coli 562 -11536658 5000693160 (de:(ecoli_2713) (pn:probable growth inhibitor, pemk-like, autoregulated) (gn:chpa) (gtcfc:13.7:14.1) (ec:) (chpa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2713 ECOLI_2713 Escherichia coli 562 10007075

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873555	13637	35793	783	261

Description

6500732801 chpr:maze:chpai:b2783 pemi-like protein 1:maze protein
 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2783
 b2783 Escherichia coli 562 -11536659 64414 chpr:maze:chpai (de:pemi-like
 protein 1 (maze protein)) (db:swissprot) CHPR_ECOLI P18534 ESCHERICHIA COLI
 562 -11536659 131116 chpr:chpai:maze cell growth regulatory protein
 maze:pemi-like protein 1 (cl:maze protein) (db:pir1.dat) (mp:60 min) BVECZE
 B31996 Escherichia coli 562 -11536659 235740 chpa chpai (sr:escherichia
 coli (strain:k-12) dna) (db:genpept-bct1) (de:e. coli chpa gene for chpai
 and chpak, complete cds.) (le:87) (re:335) (di:direct) ECOCHPA D16450
 g506193 Escherichia coli 562 -11536659 239357 maze (sr:escherichia coli
 dna) (db:genpept-bct1) (de:e. coli rela gene encoding atp:gtp
 3'-pyrophosphotransferase,complete cds.) (nt:homologous to plasmid r100 pemi
 gene) (le:2592) (re:2840) (di:direct) ECORELA J04039 g416196 Escherichia
 coli 562 -11536659 7500878698 maze pemi-like protein 1 (db:genpept-bct1)
 (de:escherichia coli k-12 genome; approximately 62 minute region.) (nt:cg
 site no. 33283; alternate gene names chpr,) (le:8956) (re:9204)
 (di:complement) ECU29580 U29580 g882677 Escherichia coli 562 -11536659
 233994 chpr suppressor of inhibitory function of chpa (fn:phenotype; not
 classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 252
 of 400 of the completegenome.) (nt:f82; 100 pct identical to chpr_ecoli sw:
 p18534; cg) (le:1341) (re:1589) (di:complement) AE000362 AE000362 g1789146
 Escherichia coli 562 -11536659 5000693161 (de:(ecoli_2714) (pn:suppressor
 of inhibitory function of chpa, pemi-like, autoregulated) (gn:chpr)
 (gtcfc:13.7:14.1) (ec:) (chpr_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli)) ECOLI_2714 ECOLI_2714 Escherichia coli 562
 10007077

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873559	13638	35794	348	115

Description

6500732802 exo:b2798 potential 5-3 nuclease (gtcfc:10.10:14.3) (ec:3.1.11.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2798 b2798 Escherichia coli 562 -11536660 70850 xni:exo (ec:3.1.11.-) (de:exodeoxyribonuclease ix, (exonuclease ix) (exo ix)) (db:swissprot) EX9_ECOLI P38506 ESCHERICHIA COLI 562 -11536660 7000685210 exo potential 5-3 exonuclease (ec:3.1.11.-) (db:pir2.dat) B65062 B65062 Escherichia coli 562 -11536660 7500881229 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:ttg start; orf_o281) (le:12520) (re:13365) (di:direct) ECU29581 U29581 g882693 Escherichia coli 562 -11536660 239372 exo 5-3 exonuclease (fn:enzyme; degradation of dna) (db:genpept-bct2) (ec:3.1.11.-) (de:escherichia coli k-12 mg1655 section 253 of 400 of the completegenome.) (nt:o281; 99 pct identical to exo_ecoli sw: p38506 but) (le:8678) (re:9523) (di:direct) AE000363 AE000363 g1789162 Escherichia coli 562 -11536660 5000693171 (de:(ecoli_2729) (pn:potential:5"-3" nuclease:potential 5"-3" nuclease) (gn:exo) (gtcfc:13.7:14.1) (ec:3.1.11.-) (exo_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2729 ECOLI_2729 Escherichia coli 562 10123840

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873566	13639	35795	423	140

Description

6500732803 fucu:b2804 fucose operon protein:fucose operon fucu protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2804 b2804 Escherichia coli 562 -11536661 72514 fucu (de:fucose operon fucu protein) (db:swissprot) FUCU_ECOLI P11555 ESCHERICHIA COLI 562 -11536661 7000685332 fucu fucose operon u protein (cl:fucose operon u protein) (db:pir1.dat) (mp:60 min) Q4ECKR H65062 Escherichia coli 562 -11536661 7500881910 fucu (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (le:20443) (re:20865) (di:direct) ECU29581 U29581 g882699 Escherichia coli 562 -11536661 239378 fucu protein of fucose operon (fn:phenotype; degradation of small molecules.) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 254 of 400 of the completegenome.) (nt:o140; 100 pct identical to fucu_ecoli sw: p11555) (le:4957) (re:5379) (di:direct) AE000364 AE000364 g1789169 Escherichia coli 562 -11536661 5000693172 (de:(ecoli_2735) (pn:fucose operon fucu protein) (gn:fucu) (gtcfc:13.7:14.1) (ec:) (fucu_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2735 ECOLI_2735 Escherichia coli 562 10123841

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873567	13640	35796	285	94

Description

6500732804 ptr:b2821 protease iii precursor:pitrilysin:protease pi (gtcfc:10.11) (ec:3.4.24.55) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2821 b2821 Escherichia coli 562 -11536662 7500889003 ptr (ec:3.4.24.55) (de:protease iii precursor, (pitrilysin) (protease pi)) (db:swissprot) PTR_ECOLI P05458 ESCHERICHIA COLI 562 -11536662 7000686232 ptr pitrilysin:precursor:endopeptidase pi:proteinase iii (cl:insulinase) (ec:3.4.99.44) (db:pir1.dat) (mp:61) SNECPI F65064 Escherichia coli 562 -11536662 7502852316 preprotease iii aa -23 to 939 (db:genpept-bct1) (de:e. coli ptr gene for protease iii.) (le:206) (re:3094) (di:direct) ECPTR X06227 g42561 Escherichia coli 562 -11536662 237949 ptr protease iii (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.24.55) (de:escherichia coli k-12 mg1655 section 255 of 400 of the completegenome.) (nt:f962; 99 pct identical to ptr_ecoli sw: p05458; cg) (le:10065) (re:12953) (di:complement) AE000365 AE000365 g2367164 Escherichia coli 562 -11536662 92313 ptr (ec:3.4.24.55) (de:protease iii precursor, (pitrilysin) (protease pi)) (db:swissprot) PTR_ECOLI P05458 ESCHERICHIA COLI 562 -11536662

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873592	13641	35797	825	274

Description

6500732805 ppdc:b2823 prepilin peptidase dependent protein c precursor (gtcfc:10.11:12.8) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2823 b2823 Escherichia coli 562 -11536663 239394 ppdc (de:prepilin peptidase dependent protein c precursor) (db:swissprot) PPDC_ECOLI P08372 ESCHERICHIA COLI 562 -11536663 135191 ppdc prepilin peptidase dependent protein c precursor (cl:prepilin peptidase dependent protein c precursor) (db:pir1.dat) (mp:61 min) QQEC12 E24137 Escherichia coli 562 -11536663 5000693181 (db:genpept-bct1) (de:e. coli recc gene and thya-recc intergenic region including urf1-3.) (nt:urf3 (aa 1-107)) (le:2206) (re:2529) (di:direct) ECRECC X03966 g42688 Escherichia coli 562 -11536663 7500888356 ppdc prepilin peptidase dependent protein c (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:alternate name urf3; orf of x03966) (le:43996) (re:44319) (di:complement) ECU29581 U29581 g882715 Escherichia coli 562 -11536663 238033 ppdc prepilin peptidase dependent protein c (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 256 of 400 of the completegenome.) (nt:f107; 100 pct identical to ppdc_ecoli sw: p08372;) (le:3499) (re:3822) (di:complement) AE000366 AE000366 g1789187 Escherichia coli 562 -11536663 90762 ppdc (de:prepilin peptidase dependent protein c precursor) (db:swissprot) PPDC_ECOLI P08372 ESCHERICHIA COLI 562 -11536663

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873602	13642	35798	921	306

Description

6500732806 ppdb:b2825 prepilin peptidase dependent protein b precursor (gtcfc:10.11:12.8) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2825 b2825 Escherichia coli 562 -11536664 90761 ppdb (de:prepilin peptidase dependent protein b precursor) (db:swissprot) PPDB_ECOLI P08371 ESCHERICHIA COLI 562 -11536664 7000686163 ppdb prepilin peptidase dependent protein b precursor (cl:prepilin peptidase dependent protein b precursor) (db:pir1.dat) (mp:61 min) QQEC30 B65065 Escherichia coli 562 -11536664 7500888355 ppdb prepilin peptidase dependent protein b (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:alternate name urf1; orf of x03966) (le:44708) (re:45271) (di:complement) ECU29581 U29581 g882717 Escherichia coli 562 -11536664 239396 ppdb prepilin peptidase dependent protein b (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 256 of 400 of the completegenome.) (nt:f187; 100 pct identical to ppdb_ecoli sw: p08371;) (le:4211) (re:4774) (di:complement) AE000366 AE000366 g1789189 Escherichia coli 562 -11536664 5000693183 (de:(ecoli_2753) (pn:prepilin peptidase dependent protein b precursor) (gn:ppdb) (gtcfc:13.7:14.1) (ec: (ppdb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2753 ECOLI_2753 Escherichia coli 562 10032876

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873609	13643	35799	429	142

Description

6500732807 ppda:b2826 prepilin peptidase dependent protein a precursor (gtcfc:10.11:12.8) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2826 b2826 Escherichia coli 562 -11536665 7000691890 ppda prepilin peptidase dependent protein a precursor (db:pir2.dat) C65065 C65065 Escherichia coli 562 -11536665 7500960418 ppda prepilin peptidase dependent protein a (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (le:45262) (re:45732) (di:complement) ECU29581 U29581 g882718 Escherichia coli 562 -11536665 239397 ppda prepilin peptidase dependent protein a (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 256 of 400 of the completegenome.) (nt:f156; 99 pct identical to ppda_ecoli sw: p33554) (le:4765) (re:5235) (di:complement) AE000366 AE000366 g1789190 Escherichia coli 562 -11536665 5000693184 (de:(ecoli_2754) (pn:prepilin peptidase dependent protein a precursor function unknown) (gn:ppda) (gtcfc:13.7:14.1) (ec: (ppda_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2754 ECOLI_2754 Escherichia coli 562 10123849

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873639	13644	35800	504	167

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873656	13645	35801	1206	401

Description

6500732808 ptsp:b2829 phosphoenolpyruvate-protein
phosphotransferase:phosphoenolpyruvate-protein phosphotransferase
ptsp:phosphotransferase system:enzyme i:enzyme i-ntr (gtcfc:14.3)
(ec:2.7.3.9) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2829
b2829 Escherichia coli 562 -11536666 92082 ptsp (ec:2.7.3.9)
(de:(phosphotransferase system, enzyme i) (enzyme i-ntr)) (db:swissprot)
PT1P_ECOLI P37177 ESCHERICHIA COLI 562 -11536666 7000686205 ptsp
phosphotransferase system enzyme i (cl:phosphotransferase system enzyme i
homology) (ec:2.7.3.9) (db:pir2.dat) F65065 F65065 Escherichia coli 562
-11536666 7500888902 ptsp enzyme i ntr (fn:pts related carbon and organic
nitrogen) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately
63 to 64 minutes.) (nt:orf_f748; previously orf_f113 and orf_f629 before)
(le:47743) (re:49989) (di:complement) ECU29581 U29581 g1255724 Escherichia
coli 562 -11536666 239400 ptsp pts system:enzyme i:transcriptional
regulator (fn:enzyme; transport of small molecules: other) (db:genpept-bct2)
(ec:2.7.3.9) (de:escherichia coli k-12 mg1655 section 256 of 400 of the
completegenome.) (nt:f748; 100 pct identical to ptlp_ecoli sw: p37177;)
(le:7246) (re:9492) (di:complement) AE000366 AE000366 g1789193 Escherichia
coli 562 -11536666 5000693185 (de:(ecoli_2757)
(pn:phosphoenolpyruvate-protein phosphotransferase ptphosphotransferase
system, enzyme i:enzyme i-ntr) (gn:ptsp) (gtcfc:13.7:14.1) (ec:2.7.3.9)
(ptlp_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)
ECOLI_2757 ECOLI_2757 Escherichia coli 562 10034116

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873658	13646	35802	570	189

Description

6500732809 kdud:b2842 2-deoxy-d-gluconate
3-dehydrogenase:2-keto-3-deoxygluconate oxydoreductase (gtcfc:14.3)
(ec:1.1.1.125) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2842
b2842 Escherichia coli 562 -11536667 80606 kdud (ec:1.1.1.125)
(de:deoxygluconate oxidoreductase)) (db:swissprot) KDUD_ECOLI P37769
ESCHERICHIA COLI 562 -11536667 7000685677 kdud 2-deoxy-d-gluconate
3-dehydrogenase (cl:ribitol dehydrogenase:short-chain alcohol dehydrogenase
homology) (ec:1.1.1.125) (db:pir2.dat) C65067 C65067 Escherichia coli 562
-11536667 7500884580 (db:genpept-bct1) (de:escherichia coli k-12 genome;
approximately 63 to 64 minutes.) (nt:orf_f253) (le:64052) (re:64813)
(di:complement) ECU29581 U29581 g882735 Escherichia coli 562 -11536667
239413 kdud 2-deoxy-d-gluconate 3-dehydrogenase (fn:enzyme; central
intermediary metabolism: pool,) (db:genpept-bct2) (ec:1.1.1.125)
(de:escherichia coli k-12 mg1655 section 258 of 400 of the completegenome.)
(nt:f253; 100 pct identical to kdud_ecoli sw: p37769) (le:1828) (re:2589)
(di:complement) AE000368 AE000368 gl789208 Escherichia coli 562 -11536667
5000693192 (de:(ecoli_2770) (pn:2-deoxy-d-gluconate
3-dehydrogenase:2-keto-3- deoxygluconate oxydoreductase) (gn:kdud)
(gtcfc:13.7:14.1) (ec:1.1.1.125) (kdud_ecoli) (keggfc:11.1) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_2770 ECOLI_2770 Escherichia coli 562
10022848

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873661	13647	35803	261	86

Description

6500732810 kdui:b2843 5-keto-4-deoxyuronate isomerase (gtcfc:14.3) (ec:5.3.1.17) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2843 b2843 Escherichia coli 562 -11536668 5500685457 kdui (ec:5.3.1.17) (de:(5-keto-4-deoxyuronate isomerase) (dki isomerase)) (db:swissprot) KDUI_ECOLI_Q46938 ESCHERICHIA COLI 562 -11536668 7000685679 kdui 4-deoxyl-1-threo-5-hexosulose-uronate ketol-isomerase (cl:erwinia chrysanthemi kdui protein) (ec:5.3.1.17) (db:pir2.dat) D65067 D65067 Escherichia coli 562 -11536668 7500884582 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 63 to 64 minutes.) (nt:orf_f278) (le:64843) (re:65679) (di:complement) ECU29581 U29581 g882736 Escherichia coli 562 -11536668 239414 kdui homolog of pectin degrading enzyme 5-keto (fn:enzyme; degradation of small molecules: carbon) (db:genpept-bct2) (ec:5.3.1.17) (de:escherichia coli k-12 mg1655 section 258 of 400 of the completegenome.) (nt:f278; 74 pct identical to kdui_erwch sw: q05529) (le:2619) (re:3455) (di:complement) AE000368 AE000368 g1789209 Escherichia coli 562 -11536668 5000693193 (de:(ecoli_2771) (pn:5-keto-4-deoxyuronate isomerase) (gn:kdui) (gtcfc:13.7:14.1) (ec:5.3.1.17) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2771 ECOLI_2771 Escherichia coli 562 10123857

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873664	13648	35804	366	121

Description

6500732811 fldb:b2895 flavodoxin ii:flavodoxin 2 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2895 b2895 Escherichia coli 562 -11536669 7000690882 fldb flavodoxin ii:flavodoxin b (cl:flavodoxin:flavodoxin homology) (db:pir2.dat) G65073 G65073 Escherichia coli 562 -11536669 7500953768 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 64 to 65 minutes.) (nt:orf_o173) (le:49669) (re:50190) (di:direct) ECU28375 U28375 g887845 Escherichia coli 562 -11536669 239108 fldb flavodoxin 2 (fn:enzyme; energy metabolism, carbon: aerobic) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 263 of 400 of the completegenome.) (nt:o173; 99 pct identical to flaw_ecoli sw: p41050) (le:3558) (re:4079) (di:direct) AE000373 AE000373 g1789262 Escherichia coli 562 -11536669 5000693235 (de:(ecoli_2819) (pn:flavodoxin 2) (gn:fldb) (gtcfc:13.7:14.1) (ec:) (flaw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2819 ECOLI_2819 Escherichia coli 562 10123900

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873669	13649	35805	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873682	13650	35806	441	146

Description

6500732812 gsp:b2988 glutathionylspermidine synthetase/amidase (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b2988 b2988 Escherichia coli 562 -11536670 74783 gsp (ec:6.3.1.8:3.5.1.78) (de:(spermidine-forming)) (gsp amidase)) (db:swissprot) GSP_ECOLI P43675 ESCHERICHIA COLI 562 -11536670 163134 gsp glutathionylspermidine synthetase/amidase (db:pir2.dat) A57538 A57538 Escherichia coli 562 -11536670 239201 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f619) (le:91054) (re:92913) (di:complement) ECU28377 U28377 g882517 Escherichia coli 562 -11536670 238772 gsp glutathionylspermidine synthetase/amidase (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 271 of 400 of the completegenome.) (nt:f619; 100 pct identical to gsp_ecoli sw: p43675) (le:8547) (re:10406) (di:complement) AE000381 AE000381 g1789361 Escherichia coli 562 -11536670 7500882817 gsp glutathionylspermidine synthetase/amidase (fn:catalyzes formation of an amide bond between) (db:genpept-bct2) (de:escherichia coli glutathionylspermidine synthetase/amidase (gsp)gene, complete cds.) (nt:c-terminal similar to e. coli yjfc, swiss-prot) (le:408) (re:2267) (di:direct) ECU23148 U23148 g861186 Escherichia coli 562 -11536670 5000693294 (de:(ecoli_2910) (pn:glutathionylspermidine synthetase) (gn:gsp) (gtcfc:13.7:14.1) (ec:) (gsp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2910 ECOLI_2910 Escherichia coli 562 10017296

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873686	13651	35807	1143	381

Description

6500732813 sufi:b3017 sufi protein precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3017 b3017 Escherichia coli 562 -11536671 99811 sufi (de:sufi protein precursor) (db:swissprot) SUFI_ECOLI P26648 ESCHERICHIA COLI 562 -11536671 7000686697 sufi sufi protein precursor (db:pir2.dat) G65088 G65088 Escherichia coli 562 -11536671 7500892236 periplasmic protein (fn:suppresses ftsi mutation) (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_f470; alternate name sufi; 16aoh-c in m63491) (le:115644) (re:117056) (di:complement) ECU28377 U28377 g882547 Escherichia coli 562 -11536671 239231 sufi suppressor of ftsi (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 274 of 400 of the completegenome.) (nt:f470; 100 pct identical to sufi_ecoli sw: p26648) (le:86) (re:1498) (di:complement) AE000384 AE000384 g1789394 Escherichia coli 562 -11536671 5000693314 (de:(ecoli_2940) (pn:sufi protein precursor involved in cell division, supresses a ftsi mutation:sufi protein precursor, involved in cell division, supresses a ftsi mutation) (gn:sufi) (gtcfc:13.7:14.1) (ec:) (sufi_ecoli) (keggfc) ECOLI_2940 ECOLI_2940 Escherichia coli 562 10041666

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873687	13652	35808	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873714	13653	35809	1389	462

Description

6500732814 mdab:mda66:b3028 modulator of drug activity b (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3028 b3028 Escherichia coli 562 -11536672 83273 mdab:mda66 (de:modulator of drug activity b) (db:swissprot) MDAB_ECOLI P40717 ESCHERICHIA COLI 562 -11536672 164049 mdab drug activity modulator b (db:pir2.dat) I80319 I80319 Escherichia coli 562 -11536672 239242 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 65 to 68 minutes.) (nt:orf_o193) (le:126918) (re:127499) (di:direct) ECU28377 U28377 g882558 Escherichia coli 562 -11536672 238753 mdab modulator of drug activity b (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 275 of 400 of the completegenome.) (nt:o193; 100 pct identical to mdab_ecoli sw: p40717) (le:190) (re:771) (di:direct) AE000385 AE000385 g1789406 Escherichia coli 562 -11536672 7500885414 mda66 (db:genpept-bct2) (de:escherichia coli modulator of drug activity (mda66) and orf1 genes,complete cds.) (nt:orf2; encodes a 22 kda protein) (le:447) (re:1028) (di:complement) ECU18656 U18656 g609328 Escherichia coli 562 -11536672 5000693323 (de:(ecoli_2951) (pn:modulator of drug activity b) (gn:mdab) (gtcfc:13.7:14.1) (ec:) (mdab_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2951 ECOLI_2951 Escherichia coli 562 10025492

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873727	13654	35810	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873734	13655	35811	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873738	13656	35812	1008	335

Description

6500732815 aer:air:b3072 aerotaxis receptor protein:aerotaxis receptor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3072 b3072 Escherichia coli 562 -11536673 59013 aer:air (de:aerotaxis receptor) (db:swissprot) AER_ECOLI P50466 ESCHERICHIA COLI 562 -11536673 7000684532 air aerotaxis receptor protein (db:pir2.dat) E65095 E65095 Escherichia coli 562 -11536673 7500876631 (db:genpept-bct1) (de:escherichia coli k-12 genome; approximately 68 minutes.) (nt:orf_f506) (le:22351) (re:23871) (di:complement) ECU28379 U28379 g882594 Escherichia coli 562 -11536673 239276 aer aerotaxis sensor receptor:flavoprotein (fn:regulator; degradation of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 279 of 400 of the completegenome.) (nt:f506; alternate gene name air) (le:951) (re:2471) (di:complement) AE000389 AE000389 g1789453 Escherichia coli 562 -11536673 5000693352 (de:(ecoli_2994) (pn:aerotaxis receptor) (gn:air) (gtcfc:13.7:14.1) (ec:) (air_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_2994 ECOLI_2994 Escherichia coli 562 10001757

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873746	13657	35813	810	269

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873750	13658	35814	225	74

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501873755	13659	35815	606	201

Description

6500732816 ygjl:b3081 probable nadh-dependent flavin oxidoreductase (gtcfc:14.3) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3081 b3081 Escherichia coli 562 -11536674 7000687872 ygjl probable nadh-dependent flavin oxidoreductase (cl:nadh oxidase) (ec:1.-.-.-) (db:pir2.dat) F65096 F65096 Escherichia coli 562 -11536674 5500684807 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o672) (le:12418) (re:14436) (di:direct) ECOUW67 U18997 g606019 Escherichia coli 562 -11536674 7500881318 fadh 2:4-dienoyl-coa reductase (db:genpept-bct1) (ec:1.3.1.34) (de:escherichia coli 2,4-dienoyl-coa reductase (fadh) gene, completecds.) (le:118) (re:2136) (di:direct) ECU93405 U93405 g2584857 Escherichia coli 562 -11536674 236318 ygjl putative nadph dehydrogenase (fn:orf; not classified) (db:genpept-bct2) (ec:1.-.-.-) (de:escherichia coli k-12 mg1655 section 280 of 400 of the completegenome.) (nt:o672; 100 pct identical amino acid sequence and) (le:3961) (re:5979) (di:direct) AE000390 AE000390 g1789463 Escherichia coli 562 -11536674 112424 fadh (ec:1.3.1.34) (de:a reductase) (db:swissprot) FADH_ECOLI P42593 ESCHERICHIA COLI 562 -11536674 5000693356 (de:(ecoli_3003) (pn:probable nadh-dependent flavin oxidoreductase) (gn:ygjl) (gtcfc:13.7:14.1) (ec:1.-.-.-) (ygjl_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3003 ECOLI_3003 Escherichia coli 562 10054152

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501873769	13660	35816	354	117

Description

6500732817 agar:b3131 putative aga operon transcriptional repressor (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3131 b3131 Escherichia coli 562 -11536675 58933 agar (de:putative aga operon transcriptional repressor) (db:swissprot) AGAR_ECOLI P42902 ESCHERICHIA COLI 562 -11536675 7000684535 agar probable transcription repressor of aga operon (cl:regulatory protein gutr) (db:pir2.dat) G65102 G65102 Escherichia coli 562 -11536675 7500876662 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f269) (le:58609) (re:59418) (di:complement) ECOUW67 U18997 g606071 Escherichia coli 562 -11536675 236370 agar putative deor-type transcriptional regulator of (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:f269; 100 pct identical amino acid sequence and) (le:8254) (re:9063) (di:complement) AE000394 AE000394 g1789519 Escherichia coli 562 -11536675 5000693396 (de:(ecoli_3055) (pn:putative aga operon transcriptional repressor) (gn:agar) (gtcfc:13.7:14.1) (ec:) (agar_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3055 ECOLI_3055 Escherichia coli 562 10001677

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873772	13661	35817	642	213

Description

6500732818 agaw:b3134 pts system:n-acetylgalactosamine-specific iic component 2:eiic-aga:n-acetylgalactosamine-permease iic component 2 (gtcfc:11.4:12.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3134 b3134 Escherichia coli 562 -11536676 92295 agaw (de:(n-acetylgalactosamine-permease iic component 2)) (db:swissprot) PTPW_ECOLI P42905 ESCHERICHIA COLI 562 -11536676 7000686229 agaw pts system:n-acetylgalactosamine-specific iic component 2 (db:pir2.dat) B65103 B65103 Escherichia coli 562 -11536676 7500888996 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o133) (le:61454) (re:61855) (di:direct) ECOUW67 U18997 g606074 Escherichia coli 562 -11536676 236373 agaw pts system n-acetylgalactosamine-specific iic (fn:enzyme; central intermediary metabolism: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 284 of 400 of the completegenome.) (nt:o133; 100 pct identical amino acid sequence and) (le:11099) (re:11500) (di:direct) AE000394 AE000394 g1789522 Escherichia coli 562 -11536676 5000693397 (de:(ecoli_3058) (pn:pts system, n-acetylgalactosamine-specific iic component 2:eiic-aga":n-acetylgalactosamine-permease iic component 2) (gn:agaw) (gtcfc:13.7:14.1) (ec:) (ptpw_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-esche) ECOLI_3058 ECOLI_3058 Escherichia coli 562 10034327

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873782	13662	35818	786	261

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873787	13663	35819	870	289

Description

6500732819 agas:b3136 protein:agas protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3136 b3136 Escherichia coli 562 -11536677 58935 agas (de:agas protein) (db:swissprot) AGAS_ECOLI P42907 ESCHERICHIA COLI 562 -11536677 7000684536 agas agas protein (db:pir2.dat) D65103 D65103 Escherichia coli 562 -11536677 7500876663 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o384) (le:62728) (re:63882) (di:direct) ECOUW67 U18997 g606076 Escherichia coli 562 -11536677 236375 agas putative tagatose-6-phosphate aldose/ketose (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 285 of 400 of the completegenome.) (nt:o384; 100 pct identical amino acid sequence and) (le:211) (re:1365) (di:direct) AE000395 AE000395 g1789525 Escherichia coli 562 -11536677 5000693398 (de:(ecoli_3060) (pn:agas protein) (gn:agas) (gtcfc:13.7:14.1) (ec:) (agas_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3060 ECOLI_3060 Escherichia coli 562 10001679

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873788	13664	35820	1113	370

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873810	13665	35821	345	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873833	13666	35822	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873846	13667	35823	2628	875

Description

6500732820 agac:b3139 pts system:n-acetylgalactosamine-specific iic component 1:eiic-aga:n-acetylgalactosamine-permease iic component 1 (gtcfc:11.4:12.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3139 b3139 Escherichia coli 562 -11536678 92279 agac (de:(n-acetylgalactosamine-permease iic component 1)) (db:swissprot) PTPC_ECOLI P42910 ESCHERICHIA COLI 562 -11536678 7000686226 agac pts system:n-acetylgalactosamine-specific iic component 1 (db:pir2.dat) G65103 G65103 Escherichia coli 562 -11536678 7500888989 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o267) (le:65437) (re:66240) (di:direct) ECOUW67 U18997 g606079 Escherichia coli 562 -11536678 236378 agac pts system n-acetylgalactosamine-specific iic (fn:enzyme; central intermediary metabolism: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 285 of 400 of the completegenome.) (nt:o267; 100 pct identical amino acid sequence and) (le:2920) (re:3723) (di:direct) AE000395 AE000395 g1789528 Escherichia coli 562 -11536678 5000693399 (de:(ecoli_3063) (pn:pts system, n-acetylgalactosamine-specific iic component 1:eiic-aga:n-acetylgalactosamine-permease iic component 1) (gn:agac) (gtcfc:13.7:14.1) (ec:) (ptpc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escher) ECOLI_3063 ECOLI_3063 Escherichia coli 562 10034311

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873847	13668	35824	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873863	13669	35825	444	147

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873865	13670	35826	576	191

Description

6500732821 agad:b3140 pts system:n-acetylgalactosamine-specific iid
 component:eiid-aga:n-acetylgalactosamine-permease iid
 component:phosphotransferase enzyme ii:d component (gtcfc:11.4:12.2)
 (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3140 b3140
 Escherichia coli 562 -11536679 92280 agad (de:enzyme ii, d component)
 (db:swissprot) PTPD_ECOLI P42911 ESCHERICHIA COLI 562 -11536679 7000686227
 agad pts system:n-acetylgalactosamine-specific iid component
 (cl:phosphotransferase system mannose-specific enzyme ii, factor ii-m)
 (db:pir2.dat) H65103 H65103 Escherichia coli 562 -11536679 7500888990 agad
 pts system:n-acetylglucosamine enzyme iid (fn:enzyme; central intermediary
 metabolism: amino) (db:genpept-bct2) (de:escherichia coli k-12 mg1655
 section 285 of 400 of the completegenome.) (nt:o263; 100 pct identical to
 ptpd_ecoli sw: p42911) (le:3713) (re:4504) (di:direct) AE000395 AE000395
 g1789529 Escherichia coli 562 -11536679 5000693400 (de:(ecoli_3064) (pn:pts
 system, n-acetylgalactosamine-specific iid
 component:eiid-aga:n-acetylgalactosamine-permease iid
 component:phosphotransferase enzyme ii, d component) (gn:agad)
 (gtcfc:13.7:14.1) (ec:) (ptpd_ecoli) (keggfc) ECOLI_3064 ECOLI_3064
 Escherichia coli 562 10034312

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873866	13671	35827	387	129

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873870	13672	35828	417	138

Description

6500732822 trub:p35:b3166 trna pseudouridine 55 synthase:psi55 synthase:p35 protein (gtcfc:10.6:4.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3166 b3166 Escherichia coli 562 -11536680 7500893523 trub:p35 (ec:4.2.1.70) (de:hydrolyase) (p35 protein)) (db:swissprot) TRUB_ECOLI P09171 ESCHERICHIA COLI 562 -11536680 135154 trub trna pseudouridine 55 synthase:p35 protein:psi55 synthase (cl:escherichia coli protein p35) (db:pir1.dat) (mp:69 min) Q9EC35 S01916 Escherichia coli 562 -11536680 237665 p35 gene product aa 1 -314 (db:genpept-bct1) (de:e. coli gene p15b and p35 (between infb and rpso).) (le:649) (re:1593) (di:direct) ECP15B X13775 g42219 Escherichia coli 562 -11536680 7502852317 (db:genpept-bct1) (de:e. coli p15b and p35 genes.) (nt:p35 gene product (aa 1 - 314)) (le:649) (re:1593) (di:direct) ECP15B35 X13270 g42223 Escherichia coli 562 -11536680 237662 trub trna pseudouridine 5s synthase (fn:enzyme; aminoacyl trna synthetases, trna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 287 of 400 of the completegenome.) (nt:f314; 99 pct identical amino acid sequence and) (le:8456) (re:9400) (di:complement) AE000397 AE000397 g2367200 Escherichia coli 562 -11536680 102500 trub:p35 (de:trna pseudouridine 55 synthase (psi55 synthase) (p35 protein)) (db:swissprot) TRUB_ECOLI P09171 ESCHERICHIA COLI 562 -11536680

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873871	13673	35829	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873878	13674	35830	189	62

Description

6500732823 rbfa:p15b:b3167 ribosome-binding factor a:p15b protein (gtcfc:10.4) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3167 b3167 Escherichia coli 562 -11536681 135153 rbfa ribosome-binding factor rbfa:protein p15b (cl:escherichia coli protein p15b) (db:pir1.dat) (mp:69 min) Q9EC15 S01915 Escherichia coli 562 -11536681 237661 yhbb p15b (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:93529) (re:93930) (di:complement) ECOUW67 U18997 g606107 Escherichia coli 562 -11536681 237664 p15b gene product aa 1 -133 (db:genpept-bct1) (de:e. coli gene p15b and p35 (between infb and rpso).) (le:248) (re:649) (di:direct) ECP15B X13775 g42218 Escherichia coli 562 -11536681 7500953690 (db:genpept-bct1) (de:e. coli p15b and p35 genes.) (nt:p15b gene product (aa 1 - 133)) (le:248) (re:649) (di:direct) ECP15B35 X13270 g42222 Escherichia coli 562 -11536681 236406 rbfa ribosome-binding factor a (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 287 of 400 of the completegenome.) (nt:f133; 100 pct identical amino acid sequence and) (le:9400) (re:9801) (di:complement) AE000397 AE000397 g1789558 Escherichia coli 562 -11536681 5000693421 (de:(ecoli_3091) (pn:ribosome-binding factor a) (gn:rbfa) (gtcfc:13.7:14.1) (ec:) (rbfa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3091 ECOLI_3091 Escherichia coli 562 10035172

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873879	13675	35831	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873886	13676	35832	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873891	13677	35833	1494	497

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873893	13678	35834	378	125

Description

6500732824 mrna:b3176 mrna protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3176 b3176 Escherichia coli 562 -11536682 84246 mrna (de:mrna protein) (db:swissprot) MRSA_ECOLI P31120 ESCHERICHIA COLI 562 -11536682 164844 mrna:yhbf mrna protein (cl:probable phosphorylating protein urec) (db:pir2.dat) I41215 I41215 Escherichia coli 562 -11536682 236413 yhbf (sr:escherichia coli (sub_strain w3110, strain k-12) (library: kohar) (db:genpept-bct1) (de:escherichia coli dihydropteroate synthase (folp) gene; and yhbfgene, complete cds's.) (nt:putative) (le:1042) (re:2379) (di:complement) ECOFOLPA L12968 g290443 Escherichia coli 562 -11536682 7500885894 yhbf (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:103485) (re:104822) (di:complement) ECOUW67 U18997 g606114 Escherichia coli 562 -11536682 234391 mrna similar to phosphoglucomutases and (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 288 of 400 of the completegenome.) (nt:f445; 100 pct identical amino acid sequence and) (le:4594) (re:5931) (di:complement) AE000398 AE000398 g1789566 Escherichia coli 562 -11536682 5000693424 (de:(ecoli_3098) (pn:similar to phosphoglucomutases and phosphomannomutases) (gn:mrna) (gtcfc:13.7:14.1) (ec:) (mrna_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3098 ECOLI_3098 Escherichia coli 562 10026447

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873900	13679	35835	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873902	13680	35836	426	141

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873918	13681	35837	2370	789

Description

6500732825 hflb:ftsh:mrsc:b3178 cell division protein ftsh (gtcfc:12.8) (ec:3.4.24.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3178 b3178 Escherichia coli 562 -11536683 72447 hflb:ftsh:mrsc:tolz (ec:3.4.24.-) (de:cell division protein ftsh,) (db:swissprot) FTSH_ECOLI P28691 ESCHERICHIA COLI 562 -11536683 163085 hflb:ftsh cell division protein ftsh (cl:cell division protein ftsh:ftsh/sec18/cdc48-type atp-binding domain homology) (ec:3.4.24.-) (db:pir2.dat) S35109 S35109 Escherichia coli 562 -11536683 236415 ftsh (sr:escherichia coli (sub_strain w3110, strain k-12) dna) (db:genpept-bct1) (de:e.coli ftsh and ftsj genes, complete cds.) (le:867) (re:2801) (di:direct) ECOFTSHJA M83138 g146028 Escherichia coli 562 -11536683 7500881821 ftsh (fn:cell division) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:cg site no. 735) (le:105753) (re:107687) (di:complement) ECOUW67 U18997 g606116 Escherichia coli 562 -11536683 234406 hflb degrades sigma32:integral membrane peptidase (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.24.-) (de:escherichia coli k-12 mg1655 section 288 of 400 of the completengenome.) (nt:f644; cg site no. 735; 100 pct identical) (le:6862) (re:8796) (di:complement) AE000398 AE000398 g1789568 Escherichia coli 562 -11536683 5000693425 (de:(ecoli_3100) (pn:integral membrane peptidase, requires zn, degrades sigma32) (gn:hflb) (gtcfc:13.7:14.1) (ec:3.4.24.-) (ftsh_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3100 ECOLI_3100 Escherichia coli 562 10014998

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873934	13682	35838	255	84

Description

6500732826 yhbn:b3200 17.3 kd protein in rpon 5region precursor:17.3 kd protein in mura-rpon intergenic region precursor:orf185 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3200 b3200 Escherichia coli 562 -11536684 112642 yhbn (de:17.3 kd protein in mura-rpon intergenic region precursor (orf185)) (db:swissprot) YHBN_ECOLI P38685 ESCHERICHIA COLI 562 -11536684 7000687902 yhbn 17.3 kd protein in rpon 5region precursor orf185 (db:pir2.dat) B65111 B65111 Escherichia coli 562 -11536684 238602 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_ol85) (le:124131) (re:124688) (di:direct) ECOUW67 U18997 g606139 Escherichia coli 562 -11536684 7500936775 (fn:unknown) (db:genpept-bct1) (de:escherichia coli rpon operon and adjoining regions includingorf185, orf241, sigma-54 (rpon), orf95, iiantr (ptsn), orf284, andnpr (npr) genes, complete cds.) (nt:orf185) (le:141) (re:698) (di:direct) ECU12684 U12684 g551336 Escherichia coli 562 -11536684 236438 yhbn orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:ol85; 100 pct identical amino acid sequence and) (le:14653) (re:15210) (di:direct) AE000399 AE000399 gl789592 Escherichia coli 562 -11536684 5000693440 (de:(ecoli_3123) (pn:17) (gn:yhbn) (gtcfc:13.7:14.1) (ec:) (yhbn_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3123 ECOLI_3123 Escherichia coli 562 10054370

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873942	13683	35839	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873948	13684	35840	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873951	13685	35841	573	191

Description

6500732827 yhbg:b3201 probable abc transporter in ntra/rpon 5region:probable abc transporter atp-binding protein in mura-rpon intergenic region:orf1:orf241 (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3201 b3201 Escherichia coli 562 -11536685
7000689376 yhbg probable abc transporter ntra/rpon 5region (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) C65111 C65111 Escherichia coli 562 -11536685 7500955269 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o241) (le:124695) (re:125420) (di:direct) ECOUW67 U18997 g606140 Escherichia coli 562 -11536685 236439 yhbg putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:o241; 98 pct identical amino acid sequence and) (le:15217) (re:15942) (di:direct) AE000399 AE000399 g1789593 Escherichia coli 562 -11536685
5000693441 (de:(ecoli_3124) (pn:probable abc transporter atp-binding protein in ntra) (gn:yhbg) (gtcfc:13.7:14.1) (ec:) (yhbg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3124 ECOLI_3124 Escherichia coli 562 10123991

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501873965	13686	35842	201	66

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501873975	13687	35843	459	153

Description

6500732828 yhbh:b3203 probable sigma:54 modulation protein:orf3:orf95 (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3203 b3203 Escherichia coli 562 -11536686 238605 yhbh (de:probable sigma(54) modulation protein (orf3) (orf95)) (db:swissprot) RP5M_ECOLI P31221 ESCHERICHIA COLI 562 -11536686 163486 yhbh hypothetical protein 3 rpon 3 region:probable sigma 54 modulation protein orf3 orf95 (db:pir2.dat) I76719 I76719 Escherichia coli 562 -11536686 236441 rpon orf3 (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e. coli rpon gene.) (le:2519) (re:2806) (di:direct) ECORPON D12938 g285782 Escherichia coli 562 -11536686 238257 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o95) (le:126924) (re:127211) (di:direct) ECOUW67 U18997 g606142 Escherichia coli 562 -11536686 5000693442 (db:genpept-bct1) (de:e.coli(k12) rpon gene for sigma factor 54.) (nt:orfii) (le:1549) (re:1836) (di:direct) ECSIG540 Z27094 g414886 Escherichia coli 562 -11536686 7500890509 (fn:unknown) (db:genpept-bct1) (de:escherichia coli rpon operon and adjoining regions includingorf185, orf241, sigma-54 (rpon), orf95, iiantr (ptsn), orf284, andnpr (npr) genes, complete cds.) (nt:orf95) (le:2934) (re:3221) (di:direct) ECU12684 U12684 g551339 Escherichia coli 562 -11536686 235892 yhbh probable sigma-54 modulation protein (fn:putative regulator; global regulatory) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 289 of 400 of the completegenome.) (nt:o95; 100 pct identical amino acid sequence and) (le:17446) (re:17733) (di:direct) AE000399 AE000399 g1789595 Escherichia coli 562 -11536686 95981 yhbh (de:probable sigma(54) modulation protein (orf3) (orf95)) (db:swissprot) RP5M_ECOLI P31221 ESCHERICHIA COLI 562 -11536686

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501873980	13688	35844	840	279

Description

6500732829 ptso:npr:rpor:b3206 phosphocarrier protein npr:nitrogen related hpr (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3206 b3206 Escherichia coli 562 -11536687 238608 ptso:npr:rpor (de:phosphocarrier protein npr (nitrogen related hpr)) (db:swissprot) PTSO_ECOLI P33996 ESCHERICHIA COLI 562 -11536687 163886 ptso phosphocarrier protein npr nitrogen related hpr (cl:phosphotransferase system phosphohistidine-containing protein:phosphotransferase system phosphohistidine-containing protein homology) (db:pir2.dat) I76722 I76722 Escherichia coli 562 -11536687 238260 npr (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:similar to nitrogen-related hpr phosphocarrier) (le:128717) (re:128989) (di:direct) ECOUW67 U18997 g606145 Escherichia coli 562 -11536687 5000693444 (db:genpept-bct1) (de:e.coli(k12) rpon gene for sigma factor 54.) (nt:orf) (le:3342) (re:3614) (di:direct) ECSIG540 Z27094 g414889 Escherichia coli 562 -11536687 7500889008 npr npr (fn:similar to hpr of the phosphotransferase system) (db:genpept-bct1) (de:escherichia coli rpon operon and adjoining regions includingorf185, orf241, sigma-54 (rpon), orf95, iiantr (ptsn), orf284, andnpr (npr) genes, complete cds.) (le:4727) (re:4999)... ECU12684 U12684 g551342 Escherichia coli 562 -11536687 236444 ptso phosphocarrier protein hpr-like npr:nitrogen (fn:transport; transport of small molecules: other) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 290 of 400 of the completengenome.) (nt:o90; similar to nitrogen-related hpr phosphocarrier) (le:1496) (re:1768) (di:direct) AE000400 AE000400 g1789599 Escherichia coli 562 -11536687 92330 ptso:npr:rpor (de:phosphocarrier protein npr (nitrogen related hpr)) (db:swissprot) PTSO_ECOLI P33996 ESCHERICHIA COLI 562 -11536687

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874001	13689	35845	207	68

Description

6500732830 yhbl:b3209 sigma cross-reacting protein 27a:scrp-27a (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3209 b3209
 Escherichia coli 562 -11536688 7000691915 yhbl sigma cross-reacting protein 27a (cl:sigma cross-reacting protein 27a) (db:pir2.dat) C65112 C65112
 Escherichia coli 562 -11536688 7500960458 sigma cross-reacting protein 27a (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f220) (le:130557) (re:131219) (di:complement) ECOUW67 U18997 g606148 Escherichia coli 562 -11536688 236447 yhbl sigma cross-reacting protein 27a scrp-27a (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 290 of 400 of the completegenome.) (nt:f220; 100 pct identical to 217 amino acids of) (le:3336) (re:3998) (di:complement) AE000400 AE000400 g1789602 Escherichia coli 562 -11536688 5000693447 (de:(ecoli_3132) (pn:sigma cross-reacting protein 27a:scrp-27a) (gn:yhbl) (gtcfc:13.7:14.1) (ec:) (s27a_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3132
 ECOLI_3132 Escherichia coli 562 10123992

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874011	13690	35846	246	81

Description

6500732831 nant:b3224 putative sialic acid transporter (gtcfc:12.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3224 b3224
 Escherichia coli 562 -11536689 7000691897 nant probable sialic acid transporter (db:pir2.dat) B65114 B65114 Escherichia coli 562 -11536689 7500960431 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f506) (le:151829) (re:153349) (di:complement) ECOUW67 U18997 g606163 Escherichia coli 562 -11536689 236462 nant sialic acid transporter (fn:transport; murein sacculus, peptidoglycan) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 291 of 400 of the completegenome.) (nt:f506; 100 pct identical to 496 amino acids) (le:10371) (re:11891) (di:complement) AE000401 AE000401 g1789618 Escherichia coli 562 -11536689 5000693457 (de:(ecoli_3147) (pn:putative sialic acid transporter) (gn:nant) (gtcfc:13.7:14.1) (ec:) (nant_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3147
 ECOLI_3147 Escherichia coli 562 10123995

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874013	13691	35847	1995	664

Description

6500732832 degq:hhoa:b3234 protease precursor:protease degq precursor (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3234 b3234 Escherichia coli 562 -11536690 76963 degq:hhoa (ec:3.4.21.-) (de:protease degq precursor,) (db:swissprot) DEQO_ECOLI P39099 ESCHERICHIA COLI 562 -11536690 164780 hhoa trypsin-like proteinase:hhoa precursor (ec:3.4.21.-) (db:pir2.dat) JC6051 JC6051 Escherichia coli 562 -11536690 238715 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o455) (le:161488) (re:162855) (di:direct) ECOUW67 U18997 g606173 Escherichia coli 562 -11536690 236472 degq serine endoprotease (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.21.-) (de:escherichia coli k-12 mg1655 section 292 of 400 of the completegenome.) (nt:o455; 100 pct identical amino acid sequence and) (le:8130) (re:9497) (di:direct) AE000402 AE000402 g1789629 Escherichia coli 562 -11536690 239432 hhoa hhoa (db:genpept-bct2) (de:escherichia coli serine protease (hhoa and hhob) genes, completecds, and malate dehydrogenase (mdh) gene, partial cds.) (nt:putative serine protease) (le:534) (re:1901) (di:direct) ECU15661 U15661 g558912 Escherichia coli 562 -11536690 7500880149 degq degq (db:genpept-bct2) (de:escherichia coli putative serine protease (degq and degs) genes,complete cds.) (nt:serine protease in vitro) (le:136) (re:1503) (di:direct) ECU32495 U32495 g984379 Escherichia coli 562 -11536690 5000693462 (de:(ecoli_3157) (pn:protease hhoa precursor) (gn:hhoa) (gtcfc:13.7:14.1) (ec:3.4.21.-) (hhoa_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3157 ECOLI_3157 Escherichia coli 562 10019325

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874024	13692	35848	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874048	13693	35849	423	140

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874078	13694	35850	504	167

Description

GTC ORF with score 485 to: (sr:rattus sp. brain) (db:genpept-rod) (de:rab geranylgeranyl transferase component b beta subunit (rats,brain, mrna, 1344 nt).) (nt:method: conceptual translation with partial peptide) (le:13) (re:1008) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874084	13695	35851	462	153

Description

GTC ORF with score 260 to: (de:(ypr176c) (pn:type ii proteins geranylgeranyltransferase beta subunit:type ii protein geranyl-geranyltransferase beta subunit:ggase-ii-beta:pggt:ypt1:geranylgeranyltransferase type ii beta subunit) (gn:p9705:bet2) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874085	13696	35852	237	78

Description

GTC ORF with score 145 to: (or:Candida albicans) (sr:candida albicans (strain:atcc10231) dna) (db:genpept) (de:candida albicans gene for beta subunit of geranylgeranyltransferase type2, complete cds, strain atcc10231.) (le:364) (re:1389) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874102	13697	35853	741	246

Description

6500732833 degs:hhob:htrh:b3235 protease precursor:protease degs precursor (gtcfc:10.11) (ec:3.4.21.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3235 b3235 Escherichia coli 562 -11536691 76964 degs:hhob:htrh (ec:3.4.21.-) (de:protease degs precursor,) (db:swissprot) DEGS_ECOLI P31137 ESCHERICHIA COLI 562 -11536691 164781 hhob trypsin-like proteinase:hhob:hhob protein (ec:3.4.21.-) (db:pir2.dat) JC6052 JC6052 Escherichia coli 562 -11536691 238716 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o355) (le:162945) (re:164012) (di:direct) ECOUW67 U18997 g606174 Escherichia coli 562 -11536691 236473 degs protease (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.21.-) (de:escherichia coli k-12 mg1655 section 292 of 400 of the completegenome.) (nt:o355; 100 pct identical amino acid sequence and) (le:9587) (re:10654) (di:direct) AE000402 AE000402 g1789630 Escherichia coli 562 -11536691 239433 hhob hhob (db:genpept-bct2) (de:escherichia coli serine protease (hhoa and hhob) genes, completecds, and malate dehydrogenase (mdh) gene, partial cds.) (nt:putative serine protease) (le:1991) (re:3058) (di:direct) ECU15661 U15661 g558913 Escherichia coli 562 -11536691 7500880152 degs degs (db:genpept-bct2) (de:escherichia coli putative serine protease (degq and degs) genes,complete cds.) (nt:putative serine protease) (le:1593) (re:2660) (di:direct) ECU32495 U32495 g984380 Escherichia coli 562 -11536691 5000693463 (de:(ecoli_3158) (pn:protease hhob precursor) (gn:hhob) (gtcfc:13.7:14.1) (ec:3.4.21.-) (hhob_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3158 ECOLI_3158 Escherichia coli 562 10019326

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874110	13698	35854	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874127	13699	35855	333	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874129	13700	35856	1512	503

Description

GTC ORF with score 555 to: (fn:activities of formation of isobutene and)
(sr:rhodotorula minuta (strain:ifol1102) dna) (db:genpept-pln1)
(de:rhodotorula minuta dna for isobutene-forming enzyme and
benzoate4-hydroxylase, complete cds.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874150	13701	35857	627	208

Description

6500732834 tldd:b3244 tldd protein (gtcfc:14.3) (keggfc:14.2)
(rileyfc:5.8.0) (db:gtc-escherichia coli) b3244 b3244 Escherichia coli 562
-11536692 101636 tldd (de:tldd protein) (db:swissprot) TLDD_ECOLI P46473
ESCHERICHIA COLI 562 -11536692 7000686802 tldd tldd protein (db:pir2.dat)
F65116 F65116 Escherichia coli 562 -11536692 236482 tldd tldd protein
(fn:modulator of interaction between letd protein) (sr:escherichia coli
(strain:k12, isolate:kp4714) dna, clone:pkp1846) (db:genpept-bct1)
(de:escherichia coli dna for tldd protein, complete cds.) (le:662) (re:2107)
(di:direct) ECOTLDD1 D44451 g1732437 Escherichia coli 562 -11536692
7500893212 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region
from 67.4 to 76.0 minutes.) (nt:orf_f481) (le:171327) (re:172772)
(di:complement) ECOUW67 U18997 g606183 Escherichia coli 562 -11536692
236104 tldd suppresses inhibitory activity of csra (fn:phenotype; not
classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 293
of 400 of the completengenome.) (nt:f481; 100 pct identical to tldd_ecoli sw:
p46473) (le:7315) (re:8760) (di:complement) AE000403 AE000403 g1789640
Escherichia coli 562 -11536692 5000693470 (de:(ecoli_3167) (pn:tldd
protein) (gn:tldd) (gtcfc:13.7:14.1) (ec:) (tldd_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3167 ECOLI_3167 Escherichia
coli 562 10043468

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874154	13702	35858	459	152
<u>Description</u>				
6500732835 envr:b3264 potential acref/envcd operon repressor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3264 b3264 Escherichia coli 562 -11536693 236504 envr (de:potential acref/envcd operon repressor) (db:swissprot) ENVR_ECOLI P31676 ESCHERICHIA COLI 562 -11536693 7000685166 envr potential acref/envcd operon repressor (cl:probable transcription repressor mtrr) (db:pir2.dat) B65119 B65119 Escherichia coli 562 -11536693 5000693483 potential repressor envr (db:genpept-bct1) (de:e.coli envc, envd and envr genes.) (nt:in vitro and in vivo expression of cloned envr) (le:42) (re:704) (di:complement) ECENVCD X57948 g510828 Escherichia coli 562 -11536693 7500881067 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f220) (le:193549) (re:194211) (di:complement) ECOUW67 U18997 g606205 Escherichia coli 562 -11536693 232769 envr putative transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 295 of 400 of the completegenome.) (nt:f220; 100 pct identical amino acid sequence and) (le:2599) (re:3261) (di:complement) AE000405 AE000405 g1789664 Escherichia coli 562 -11536693 70248 envr (de:potential acref/envcd operon repressor) (db:swissprot) ENVR_ECOLI P31676 ESCHERICHIA COLI 562 -11536693				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874160	13703	35859	411	136
<u>Description</u>				
6500732836 secy:prla:b3300 preprotein translocase secy subunit (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3300 b3300 Escherichia coli 562 -11536694 7500891491 secy:prla (de:preprotein translocase secy subunit) (db:swissprot) SECY_ECOLI P03844 ESCHERICHIA COLI 562 -11536694 135226 prla:secy preprotein translocase secy (cl:preprotein translocase secy) (db:pir1.dat) (mp:73 min) QQECSY A04473 Escherichia coli 562 -11536694 238292 secy (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:223514) (re:224845) (di:complement) ECOUW67 U18997 g606234 Escherichia coli 562 -11536694 5000693500 (db:genpept-bct1) (de:escherichia coli spc ribosomal protein operon.) (nt:secy (prla) polypeptide (aa 1-443)) (le:4294) (re:5625) (di:direct) ECSPC X01563 g42989 Escherichia coli 562 -11536694 236533 prla putative atpase subunit of translocase (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 298 of 400 of the completegenome.) (nt:f443; 100 pct identical amino acid sequence and) (le:293) (re:1624) (di:complement) AE000408 AE000408 g1789696 Escherichia coli 562 -11536694 98348 secy:prla (de:preprotein translocase secy subunit) (db:swissprot) SECY_ECOLI P03844 ESCHERICHIA COLI 562 -11536694				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874184	13704	35860	786	261

Description

GTC ORF with score 243 to: (db:genpept-bct2) (de:myxococcus xanthus saframycin mx1 synthetase b (safb), saframycinmx1 synthetase a (safa), and safc genes, complete cds.) (nt:contains two putative amino acid activating (le:5491) (re:13308) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874188	13705	35861	2370	789

Description

6500732837 yhed:b3323 putative general secretion pathway protein b (gtcfc:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3323 b3323 Escherichia coli 562 -11536695 74687 gspa (de:probable general secretion pathway protein a) (db:swissprot) GSPA_ECOLI P45756 ESCHERICHIA COLI 562 -11536695 7000685462 yhed probable general secretion pathway protein b (db:pir2.dat) F65125 F65125 Escherichia coli 562 -11536695 7500882805 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f489) (le:234677) (re:236146) (di:complement) ECOUW67 U18997 g606257 Escherichia coli 562 -11536695 236556 yhed putative export protein a for general secretion (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completegenome.) (nt:f489; 100 pct identical amino acid sequence and) (le:570) (re:2039) (di:complement) AE000409 AE000409 g1789720 Escherichia coli 562 -11536695 5000693501 (de:(ecoli_3241) (pn:putative general secretion pathway protein b) (gn:yhed) (gtcfc:13.7:14.1) (ec:) (gspa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3241 ECOLI_3241 Escherichia coli 562 10017200

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874191	13706	35862	273	90

Description

6500732838 yhee:b3324 putative general secretion pathway protein c (gtcfc:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3324 b3324 Escherichia coli 562 -11536696 74693 gspc (de:probable general secretion pathway protein c) (db:swissprot) GSPC_ECOLI P45757 ESCHERICHIA COLI 562 -11536696 7000685463 yhee probable general secretion pathway protein c (db:pir2.dat) G65125 G65125 Escherichia coli 562 -11536696 7500882806 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o271) (le:236326) (re:237141) (di:direct) ECOUW67 U18997 g606258 Escherichia coli 562 -11536696 236557 yhee putative general secretion pathway for protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completegenome.) (nt:o271; 100 pct identical amino acid sequence and) (le:2219) (re:3034) (di:direct) AE000409 AE000409 g1789721 Escherichia coli 562 -11536696 5000693502 (de:(ecoli_3242) (pn:putative general secretion pathway protein c) (gn:yhee) (gtcfc:13.7:14.1) (ec:) (gspc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3242 ECOLI_3242 Escherichia coli 562 10017206

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874199	13707	35863	465	154

Description

6500732839 yhef:b3325 putative general secretion pathway protein d precursor (gtcfc:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3325 b3325 Escherichia coli 562 -11536697 74700 gspd (de:probable general secretion pathway protein d precursor) (db:swissprot) GSPD_ECOLI P45758 ESCHERICHIA COLI 562 -11536697 7000685464 yhef probable general secretion pathway protein d precursor (db:pir2.dat) H65125 H65125 Escherichia coli 562 -11536697 7500882807 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o654) (le:237113) (re:239077) (di:direct) ECOUW67 U18997 g606259 Escherichia coli 562 -11536697 236558 yhef putative general protein secretion protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completegenome.) (nt:o654; 100 pct identical amino acid sequence and) (le:3006) (re:4970) (di:direct) AE000409 AE000409 g1789722 Escherichia coli 562 -11536697 5000693503 (de:(ecoli_3243) (pn:putative general secretion pathway protein d precursor) (gn:yhef) (gtcfc:13.7:14.1) (ec:) (gspd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3243 ECOLI_3243 Escherichia coli 562 10017213

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874200	13708	35864	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874203	13709	35865	303	100

Description

6500732840 yheg:b3326 type ii traffic:putative general secretion pathway protein e:type ii traffic warden atpase (gtcfc:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3326 b3326 Escherichia coli 562 -11536698 74708 gspe (de:atpase)) (db:swissprot) GSPE_ECOLI P45759 ESCHERICHIA COLI 562 -11536698 7000685465 yheg probable general secretion pathway protein e (cl:secretion protein xcpr) (db:pir2.dat) A65126 A65126 Escherichia coli 562 -11536698 7500882808 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o493) (le:239087) (re:240568) (di:direct) ECOUW67 U18997 g606260 Escherichia coli 562 -11536698 236559 yheg putative general secretion pathway for protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completegenome.) (nt:o493; 100 pct identical amino acid sequence and) (le:4980) (re:6461) (di:direct) AE000409 AE000409 g1789723 Escherichia coli 562 -11536698 5000693504 (de:(ecoli_3244) (pn:putative general secretion pathway protein e:type ii traffic warden atpase) (gn:yheg) (gtcfc:13.7:14.1) (ec:) (gspe_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3244 ECOLI_3244 Escherichia coli 562 10017221

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874204	13710	35866	636	211

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874219	13711	35867	189	62

Description

6500732841 hoff:hopf:b3327 putative general secretion pathway protein
f:protein transport protein hoff (gtcfc:12.6:12.10) (keggfc:14.2)
(rileyfc:5.8.0) (db:gtc-escherichia coli) b3327 b3327 Escherichia coli 562
-11536699 74716 hoff:hopf (de:protein hoff)) (db:swissprot) GSPF_ECOLI
P41441 ESCHERICHIA COLI 562 -11536699 7000685466 hoff:hopf probable general
secretion pathway protein f:hopf protein (cl:secretion protein xcps)
(db:pir2.dat) B65126 B65126 Escherichia coli 562 -11536699 7500882809
(db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to
76.0 minutes.) (nt:orf_o398) (le:240565) (re:241761) (di:direct) ECOUW67
U18997 g606261 Escherichia coli 562 -11536699 236560 hoff putative general
protein secretion protein (fn:putative transport; not classified)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the
completegenome.) (nt:o398; 100 pct identical amino acid sequence and)
(le:6458) (re:7654) (di:direct) AE000409 AE000409 g1789724 Escherichia coli
562 -11536699 5000693505 (de:(ecoli_3245) (pn:putative general secretion
pathway protein f:protein transport protein hoff) (gn:hoff)
(gtcfc:13.7:14.1) (ec:) (gspf_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
(db:gtc-escherichia coli)) ECOLI_3245 ECOLI_3245 Escherichia coli 562
10017229

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874223	13712	35868	327	108
<u>Description</u>				
6500732842 hofg:hofg:b3328 putative general secretion pathway protein g precursor:protein transport protein hofg (gtcfc:12.6:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3328 b3328 Escherichia coli 562 -11536700 74724 hofg:hofg (de:transport protein hofg)) (db:swissprot) GSPG_ECOLI P41442 ESCHERICHIA COLI 562 -11536700 153080 hofg probable general secretion pathway protein g precursor:hofg protein (cl:secretion protein xcpt) (db:pir2.dat) B56150 B56150 Escherichia coli 562 -11536700 238766 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_ol45) (le:241771) (re:242208) (di:direct) ECUW67 U18997 g606262 Escherichia coli 562 -11536700 7500882810 hopg hopg (db:genpept-bct1) (de:escherichia coli type ii export system (hopg) gene, complete cds,and (hopf) and (hoph) genes, partial cds.) (le:625) (re:1062) (di:direct) ECU20786 U20786 g693706 Escherichia coli 562 -11536700 236561 hofg putative general protein secretion protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completegenome.) (nt:ol45; 100 pct identical amino acid sequence and) (le:7664) (re:8101) (di:direct) AE000409 AE000409 g1789725 Escherichia coli 562 -11536700 5000693506 (de:(ecoli_3246) (pn:putative general secretion pathway protein g precursor:protein transport protein hofg) (gn:hofg) (gtcfc:13.7:14.1) (ec:) (gspg_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3246 ECOLI_3246 Escherichia coli 562 10017237				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874226	13713	35869	345	114

Description

6500732843 hofh:hoph:b3329 putative general secretion pathway protein h precursor:protein transport protein hofh (gtcfc:12.6:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3329 b3329 Escherichia coli 562 -11536701 74732 hofh:hoph (de:transport protein hofh) (db:swissprot) GSPH_ECOLI P41443 ESCHERICHIA COLI 562 -11536701 7000685467 hofh:hoph probable general secretion pathway protein h precursor:hoph protein (db:pir2.dat) D65126 D65126 Escherichia coli 562 -11536701 7500882811 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o169) (le:242216) (re:242725) (di:direct) ECOUW67 U18997 g606263 Escherichia coli 562 -11536701 236562 hofh putative general protein secretion protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completegenome.) (nt:o169; 100 pct identical amino acid sequence and) (le:8109) (re:8618) (di:direct) AE000409 AE000409 g1789726 Escherichia coli 562 -11536701 5000693507 (de:(ecoli_3247) (pn:putative general secretion pathway protein h precursor:protein transport protein hofh) (gn:hofh) (gtcfc:13.7:14.1) (ec:) (gsph_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3247 ECOLI_3247 Escherichia coli 562 10017245

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874243	13714	35870	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874244	13715	35871	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874252	13716	35872	687	228

Description

6500732844 yheh:b3330 putative general secretion pathway protein i precursor (gtcfc:12.6:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3330 b3330 Escherichia coli 562 -11536702 7000685468 yheh probable general secretion pathway protein i precursor (db:pir2.dat) E65126 E65126 Escherichia coli 562 -11536702 236563 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_ol38) (le:242683) (re:243099) (di:direct) ECOUW67 U18997 g606264 Escherichia coli 562 -11536702 7500960424 yheh putative export protein for general secretion (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completgenome.) (nt:ol38; 100 pct identical amino acid sequence and) (le:8576) (re:8992) (di:direct) AE000409 AE000409 g1789727 Escherichia coli 562 -11536702 74740 gspi_ecoli (de:putative general secretion pathway protein i precursor.) P45760 P45760 Escherichia coli 562 -11536702 5000693508 (de:(ecoli_3248) (pn:putative general secretion pathway protein i precursor) (gn:yheh) (gtcfc:13.7:14.1) (ec:) (gspi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3248 ECOLI_3248 Escherichia coli 562 10017253

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874268	13717	35873	243	80

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874276	13718	35874	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874280	13719	35875	315	104

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874297	13720	35876	2691	897

Description

6500732845 yhei:b3331 putative general secretion pathway protein j precursor (gtcfc:12.6:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3331 b3331 Escherichia coli 562 -11536703 74748 gspj (de:probable general secretion pathway protein j precursor) (db:swissprot) GSPJ_ECOLI P45761 ESCHERICHIA COLI 562 -11536703 7000685469 yhei probable general secretion pathway protein j precursor (db:pir2.dat) F65126 F65126 Escherichia coli 562 -11536703 7500882813 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o195) (le:243092) (re:243679) (di:direct) ECOUW67 U18997 g606265 Escherichia coli 562 -11536703 236564 yhei putative export protein i for general secretion (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completgenome.) (nt:o195; 100 pct identical amino acid sequence and) (le:8985) (re:9572) (di:direct) AE000409 AE000409 gl789728 Escherichia coli 562 -11536703 5000693509 (de:(ecoli_3249) (pn:putative general secretion pathway protein j precursor) (gn:yhei) (gtcfc:13.7:14.1) (ec:) (gspj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3249 ECOLI_3249 Escherichia coli 562 10017261

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874299	13721	35877	396	131

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874309	13722	35878	969	322

Description

6500732846 yhej:b3332 putative general secretion pathway protein k (gtcfc:12.6:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3332 b3332 Escherichia coli 562 -11536704 74756 gspk (de:probable general secretion pathway protein k) (db:swissprot) GSPK_ECOLI P45762 ESCHERICHIA COLI 562 -11536704 7000685470 yhej probable general secretion pathway protein k (cl:outk protein) (db:pir2.dat) G65126 G65126 Escherichia coli 562 -11536704 7500882814 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o327) (le:243672) (re:244655) (di:direct) ECOUW67 U18997 g606266 Escherichia coli 562 -11536704 236565 yhej putative export protein j for general secretion (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completengenome.) (nt:o327; 100 pct identical amino acid sequence and) (le:9565) (re:10548) (di:direct) AE000409 AE000409 g1789729 Escherichia coli 562 -11536704 5000693510 (de:(ecoli_3250) (pn:putative general secretion pathway protein k) (gn:yhej) (gtcfc:13.7:14.1) (ec:) (gspk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3250 ECOLI_3250 Escherichia coli 562 10017269

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874319	13723	35879	846	281

Description

6500732847 yhek:b3333 putative general secretion pathway protein l (gtcfc:12.6:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3333 b3333 Escherichia coli 562 -11536705 74764 gspl (de:probable general secretion pathway protein l) (db:swissprot) GSPL_ECOLI P45763 ESCHERICHIA COLI 562 -11536705 7000685471 yhek probable general secretion pathway protein l (db:pir2.dat) H65126 H65126 Escherichia coli 562 -11536705 7500882815 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o388) (le:244667) (re:245833) (di:direct) ECOUW67 U18997 g606267 Escherichia coli 562 -11536705 236566 yhek putative general secretion protein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completengenome.) (nt:o388; 100 pct identical amino acid sequence and) (le:10560) (re:11726) (di:direct) AE000409 AE000409 g1789730 Escherichia coli 562 -11536705 5000693511 (de:(ecoli_3251) (pn:putative general secretion pathway protein l) (gn:yhek) (gtcfc:13.7:14.1) (ec:) (gspl_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3251 ECOLI_3251 Escherichia coli 562 10017277

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874335	13724	35880	1107	368

Description

6500732848 pshm:hopz:b3334 putative general secretion pathway protein m:transport protein pshm (gtcfc:12.6:12.10) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3334 b3334 Escherichia coli 562 -11536706 7000685472 pshm probable general secretion pathway protein m (db:pir2.dat) A65127 A65127 Escherichia coli 562 -11536706 236567 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_o161) (le:245806) (re:246291) (di:direct) ECOUW67 U18997 g606268 Escherichia coli 562 -11536706 234680 pshm putative general secretion (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completegenome.) (nt:o161; 100 pct identical amino acid sequence and) (le:11699) (re:12184) (di:direct) AE000409 AE000409 g1789731 Escherichia coli 562 -11536706 7500882816 pshm (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:escherichia coli pshm gene; leader peptidase (hopd) gene;bacterioferritin (bfr) gene.) (nt:homologous to xcpz of pseudomonas aeruginosa) (le:153) (re:638) (di:direct) ECOHOPSHM L28106 g451904 Escherichia coli 562 -11536706 74772 pshm:hopz (de:putative general secretion pathway protein m (transport protein pshm)) (db:swissprot) GSPM_ECOLI P36678 ESCHERICHIA COLI 562 -11536706 5000693512 (de:(ecoli_3252) (pn:putative general secretion pathway protein m:transport protein pshm) (gn:pshm) (gtcfc:13.7:14.1) (ec:) (gspm_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3252 ECOLI_3252 Escherichia coli 562 10017285

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874336	13725	35881	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874347	13726	35882	861	287

Description

6500732849 hofd:hopd:hopo:b3335 type 4 prepilin-like protein specific leader peptidase (gtcfc:11.1:10.11) (ec:3.4.99.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3335 b3335 Escherichia coli 562 -11536707 81878 hofd:hopd:hopo (ec:3.4.99.-) (de:type 4 prepilin-like protein specific leader peptidase,) (db:swissprot) LEP3_ECOLI P25960 ESCHERICHIA COLI 562 -11536707 7000685726 hofd type 4 prepilin-like protein specific leader peptidase (db:pir2.dat) B65127 B65127 Escherichia coli 562 -11536707 234681 hofd leader peptidase:integral membrane protein (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 299 of 400 of the completegenome.) (nt:o225; 98 pct identical amino acid sequence and) (le:12184) (re:12861) (di:direct) AE000409 AE000409 g1789732 Escherichia coli 562 -11536707 7500884916 hopd leader peptidase (sr:escherichia coli (strain k-12) dna) (db:genpept-bct2) (de:escherichia coli pshm gene; leader peptidase (hopd) gene;bacterioferritin (bfr) gene.) (nt:homologous to pild of pseudomonas aeruginosa) (le:638) (re:1315) (di:direct) ECOHOPSHM L28106 g451905 Escherichia coli 562 -11536707 5000693513 (de:(ecoli_3253) (pn:leader peptidase, integral membrane protein) (gn:hofd) (gtcfc:13.7:14.1) (ec:3.4.99.-) (lep3_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3253 ECOLI_3253 Escherichia coli 562 10024112

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874353	13727	35883	393	130

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874361	13728	35884	696	231

Description

GTC ORF with score 384 to: (sr:humicola grisea var. thermoidea (sub_species:ifo9854) dna) (db:genpept) (de:humicola grisea var. thermoidea bgl4 gene for beta-glucosidase,complete cds.) (le:289:437) (re:332:1823) (di:directjoin)

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501874364	13729	35885	1062	353

Description

6500732850 fkpa:b3347 fkbp-type peptidyl-prolyl cis-trans isomerase:fkbp-type peptidyl-prolyl cis-trans isomerase fkpa precursor:ppiase:rotamase (gtcfc:14.3) (ec:5.2.1.8) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3347 b3347 Escherichia coli 562 -11536708 71774 fkpa (ec:5.2.1.8) (de:(ec 5.2.1.8) (ppiase) (rotamase)) (db:swissprot) FKBA_ECOLI P45523 ESCHERICHIA COLI 562 -11536708 163056 fkpa fkbp-type peptidyl-prolyl cis-trans isomerase fkpa (cl:bkbp-type peptidylprolyl isomerase homology) (ec:5.2.1.-) (db:pir2.dat) I65035 I65035 Escherichia coli 562 -11536708 236580 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (nt:orf_f270) (le:257355) (re:258167) (di:complement) ECOUW67 U18997 g606281 Escherichia coli 562 -11536708 235995 fkpa fkbp-type peptidyl-prolyl cis-trans isomerase (fn:enzyme; proteins - translation and) (db:genpept-bct2) (ec:5.2.1.-) (de:escherichia coli k-12 mgl655 section 300 of 400 of the completegenome.) (nt:f270; 100 pct identical amino acid sequence and) (le:9876) (re:10688) (di:complement) AE000410 AE000410 g1789745 Escherichia coli 562 -11536708 7500881497 fkpa (sr:escherichia coli (strain cs109) dna) (db:genpept-bct2) (de:escherichia coli (slyd) gene, complete cds, (fkpa) gene, completedcds.) (le:1129) (re:1941) (di:direct) ECOSLYD L28082 g862300 Escherichia coli 562 -11536708 5000693520 (de:(ecoli_3265) (pn:peptidyl-prolyl cis-trans isomerase; in protein folding) (gn:fkpa) (gtcfc:13.7:14.1) (ec:5.2.1.8) (fkba_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3265 ECOLI_3265 Escherichia coli 562 10014331

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874373	13730	35886	291	96

Description

6500732851 hofq:hofq:b3391 protein transport protein hofq precursor (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3391 b3391 Escherichia coli 562 -11536709 77455 hofq:hofq (de:protein transport protein hofq precursor) (db:swissprot) HOFQ_ECOLI P34749 ESCHERICHIA COLI 562 -11536709 7000685549 hofq protein transport protein hofq precursor (cl:hypothetical protein hi0435) (db:pir2.dat) B65134 B65134 Escherichia coli 562 -11536709 7500883454 hopq (fn:encodes hypothetical protein with a sequence) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 67.4 to 76.0 minutes.) (le:300213) (re:301451) (di:complement) ECOUW67 U18997 g606325 Escherichia coli 562 -11536709 236624 hofq putative transport portein (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 304 of 400 of the completegenome.) (nt:f412; 100 pct identical amino acid sequence and) (le:8477) (re:9715) (di:complement) AE000414 AE000414 g1789793 Escherichia coli 562 -11536709 5000693545 (de:(ecoli_3309) (pn:protein transport protein hofq precursor) (gn:hofq) (gtcfc:13.7:14.1) (ec:) (hofq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3309 ECOLI_3309 Escherichia coli 562 10019815

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874395	13731	35887	582	193

Description

6500732852 rhsb:b3482 rhsb core protein with unique extension:rhsb protein precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3482 b3482 Escherichia coli 562 -11536710 7000691907 rhsb rhsb protein precursor (cl:rhsf protein) (db:pir2.dat) (mp:77 min) E65145 E65145 Escherichia coli 562 -11536710 7500960450 rhsb rhsb protein in rhs element (fn:orf; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 314 of 400 of the completegenome.) (nt:ol1411; 99 pct identical amino acid sequence and) (le:65) (re:4300) (di:direct) AE000424 AE000424 g1789894 Escherichia coli 562 -11536710 5000693588 (de:(ecoli_3400) (pn:rhsb protein precursor) (gn:rhsb) (gtcfc:13.7:14.1) (ec:) (rhsb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3400 ECOLI_3400 Escherichia coli 562 10124039

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874418	13732	35888	1254	418

Description

6500732853 yhhi:b3484 h repeat-associated protein in rhsb-pit intergenic region:orf-h (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3484 b3484 Escherichia coli 562 -11536711 112822 yhhi (de:h repeat-associated protein in rhsb-pit intergenic region (orf-h)) (db:swissprot) YHHI_ECOLI P28912 ESCHERICHIA COLI 562 -11536711 164850 yhhi h repeat-associated protein-like protein b3484:yhhi protein (db:pir2.dat) S47703 S47703 Escherichia coli 562 -11536711 236719 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate gene name yhhi) (le:38640) (re:39776) (di:direct) ECUW76 U00039 g466620 Escherichia coli 562 -11536711 235810 yhhi putative receptor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 314 of 400 of the completegenome.) (nt:o378; 100 pct identical amino acid sequence and) (le:5251) (re:6387) (di:direct) AE000424 AE000424 g1789896 Escherichia coli 562 -11536711 300041 h repeat-associated protein (db:genpept-bct2) (de:escherichia coli rhs core protein, rhsb accessory element-encodedprotein (rhsb), and h repeat-associated protein genes, completedcds; and unknown genes.) (nt:orf-h) (le:5912) (re:7048) (di:direct) ECORHSBAA L02370 g147628 Escherichia coli 562 -11536711 5000693590 (de:(ecoli_3402) (pn:h repeat-associated protein in rhsb-pit intergenic region:orf-h) (gn:yhhi) (gtcfc:13.7:14.1) (ec:) (yhhi_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3402 ECOLI_3402 Escherichia coli 562 10054550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874444	13733	35889	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874449	13734	35890	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874461	13735	35891	588	195

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874462	13736	35892	786	261

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874481	13737	35893	1149	382

Description

6500732854 arsr:b3501 arsenical resistance operon arsefg repressor (gtcfc:10.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3501 b3501 Escherichia coli 562 -11536712 236737 arsr:arse (de:arsenical resistance operon repressor) (db:swissprot) ARSR_ECOLI P37309 ESCHERICHIA COLI 562 -11536712 154745 arsr arsenical resistance operon arsefg repressor (cl:arsenical resistance operon repressor) (db:pir2.dat) (mp:77.5 min) A56269 A56269 Escherichia coli 562 -11536712 5000693604 arsr arsenic-inducible repressor (db:genpept-bct1) (de:e.coli genes arsr, arsb, arsc.) (le:708) (re:1061) (di:direct) ECARSRBC X80057 g510825 Escherichia coli 562 -11536712 7500877214 arse (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:62787) (re:63140) (di:direct) ECOUW76 U00039 g466638 Escherichia coli 562 -11536712 232401 arsr transcriptional repressor of chromosomal ars (fn:regulator; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 316 of 400 of the completegenome.) (nt:o117; 100 pct identical amino acid sequence and) (le:7827) (re:8180) (di:direct) AE000426 AE000426 g1789916 Escherichia coli 562 -11536712 60292 arsr:arse (de:arsenical resistance operon repressor) (db:swissprot) ARSR_ECOLI P37309 ESCHERICHIA COLI 562 -11536712

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874482	13738	35894	600	199

Description

6500732855 arsb:b3502 arsenical pump membrane protein (gtcfc:11.1:12.6) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3502 b3502 Escherichia coli 562 -11536713 153044 arsb arsenite efflux pump::arsenical pump membrane protein (cl:arsenical pump membrane protein) (ec:1.-.-.) (db:pir2.dat) S47723 S47723 Escherichia coli 562 -11536713 7500955280 arsf (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:63173) (re:64483) (di:direct) ECOUW76 U00039 g912466 Escherichia coli 562 -11536713 236738 arsb arsenical pump membrane protein (fn:transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 316 of 400 of the completegenome.) (nt:o436; 100 pct identical to 429 amino acids) (le:8213) (re:9523) (di:direct) AE000426 AE000426 g1789917 Escherichia coli 562 -11536713 5000693605 (de:(ecoli_3421) (pn:arsenical pump membrane protein) (gn:arsb) (gtcfc:13.7:14.1) (ec:) (arsb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3421 ECOLI_3421 Escherichia coli 562 10080743

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874486	13739	35895	348	115

Description

6500732856 arsc:b3503 arsenate reductase:arsenical pump modifier (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3503 b3503 Escherichia coli 562 -11536714 236739 arsc:arsg (de:arsenate reductase (arsenical pump modifier)) (db:swissprot) ARSC_ECOLI P37311 ESCHERICHIA COLI 562 -11536714 122664 arsc arsenate reductase::arsenical pump modifier (cl:escherichia coli arsenate reductase) (ec:1.-.-.) (db:pir1.dat) (mp:80 min) C56269 C56269 Escherichia coli 562 -11536714 5000693606 arsc arsenate reductase (db:genpept-bct1) (de:e.coli genes arsr, arsb, arsc.) (le:2417) (re:2842) (di:direct) ECARSRBC X80057 g516212 Escherichia coli 562 -11536714 7500877212 arsg (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:64496) (re:64921) (di:direct) ECOUW76 U00039 g466640 Escherichia coli 562 -11536714 232403 arsc arsenate reductase (fn:enzyme; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 316 of 400 of the completegenome.) (nt:o141; 100 pct identical amino acid sequence and) (le:9536) (re:9961) (di:direct) AE000426 AE000426 g1789918 Escherichia coli 562 -11536714 60285 arsc:arsg (de:arsenate reductase (arsenical pump modifier)) (db:swissprot) ARSC_ECOLI P37311 ESCHERICHIA COLI 562 -11536714

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874487	13740	35896	360	119

Description

6500732857 hdeb:b3509 protein precursor:protein hdeb precursor:10k-1 protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3509 b3509 Escherichia coli 562 -11536715 162584 hdeb protein hdeb precursor:hypothetical protein b (db:pir2.dat) S30269 S30269 Escherichia coli 562 -11536715 236745 10k-s protein (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e. coli gene for 10k-1 and 10k-s protein.) (le:1009) (re:1347) (di:direct) ECO10KLS D11109 g216432 Escherichia coli 562 -11536715 7500883119 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate name 10k-s of d11109) (le:70225) (re:70563) (di:complement) ECOUW76 U00039 g466646 Escherichia coli 562 -11536715 233543 hdeb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 317 of 400 of the completegenome.) (nt:f112; 100 pct identical amino acid sequence and) (le:5083) (re:5421) (di:complement) AE000427 AE000427 g1789925 Escherichia coli 562 -11536715 76408 hdeb (de:protein hdeb precursor (10k-1 protein)) (db:swissprot) HDEB_ECOLI P26605 ESCHERICHIA COLI 562 -11536715 5000693611 (de:(ecoli_3428) (pn:protein hdeb precursor:10k-1 protein) (gn:hdeb) (gtcfc:13.7:14.1) (ec:) (hdeb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3428 ECOLI_3428 Escherichia coli 562 10018771

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874488	13741	35897	273	90

Description

6500732858 hdea:b3510 protein precursor:protein hdea precursor:10k-s protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3510 b3510 Escherichia coli 562 -11536716 76407 hdea (de:protein hdea precursor (10k-s protein)) (db:swissprot) HDEA_ECOLI P26604 ESCHERICHIA COLI 562 -11536716 162585 hdea protein hdea precursor:10k s protein precursor:hypothetical protein a (db:pir2.dat) S30268 S30268 Escherichia coli 562 -11536716 236746 10k-l protein (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e. coli gene for 10k-l and 10k-s protein.) (le:574) (re:906) (di:direct) ECO10KLS D11109 g216431 Escherichia coli 562 -11536716 7500883118 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate name 10k-l of d11109) (le:70667) (re:70999) (di:complement) ECOUW76 U00039 g466647 Escherichia coli 562 -11536716 233542 hdea orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 317 of 400 of the completegenome.) (nt:f110; 100 pct identical amino acid sequence and) (le:5525) (re:5857) (di:complement) AE000427 AE000427 g1789926 Escherichia coli 562 -11536716 5000693612 (de:(ecoli_3429) (pn:protein hdea precursor:10k-s protein) (gn:hdea) (gtcfc:13.7:14.1) (ec:) (hdea_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3429 ECOLI_3429 Escherichia coli 562 10018770

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874494	13742	35898	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874498	13743	35899	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874499	13744	35900	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874503	13745	35901	405	134

Description

GTC ORF with score 188 to: (sr:aspergillus fumigatus (library: cbs 144.89) (clone: fp4) myceliu) (db:genpept-pln1) (de:aspergillus fumigatus 88 kda secreted dipetidyl peptidase gene,complete cds.) (nt:putative) (le:326:461:571:860:1922) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874504	13746	35902	189	62

Description

GTC ORF with score 115 to: (sr:aspergillus fumigatus (library: cbs 144.89) (clone: fp4) myceliu) (db:genpept-pln1) (de:aspergillus fumigatus 88 kda secreted dipetidyl peptidase gene,complete cds.) (nt:putative) (le:326:461:571:860:1922) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874523	13747	35903	2466	822

Description

6500732859 hded:b3511 hded protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3511 b3511 Escherichia coli 562 -11536717 76409 hded (de:hded protein) (db:swissprot) HDED_ECOLI P26603 ESCHERICHIA COLI 562 -11536717 163755 hded probable membrane protein hded:protein b3511:protein o190 (db:pir2.dat) S47731 S47731 Escherichia coli 562 -11536717 7500883120 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:alternate name orfd of 123635) (le:71254) (re:71826) (di:direct) ECOUW76 U00039 g466648 Escherichia coli 562 -11536717 234701 hded orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 317 of 400 of the completegenome.) (nt:o190; 100 pct identical amino acid sequence and) (le:6112) (re:6684) (di:direct) AE000427 AE000427 g1789927 Escherichia coli 562 -11536717 236747 (sr:escherichia coli (strain:k-12) dna, clone:lambda-4d9) (db:genpept-bct2) (de:escherichia coli dna, complete cds (orf-d).) (nt:orf-d) (le:62) (re:634) (di:direct) ECOHSND D11389 g216573 Escherichia coli 562 -11536717 5000693613 (de:(ecoli_3430) (pn:hded protein) (gn:hded) (gtcfc:13.7:14.1) (ec:) (hded_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3430 ECOLI_3430 Escherichia coli 562 10018772

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874528	13748	35904	1539	512

Description

6500732860 yhya:b3518 probable cytochrome c peroxidase (gtcfc:12.12:2.8) (ec:1.11.1.5) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3518 b3518 Escherichia coli 562 -11536718 112899 yhya (ec:1.11.1.5) (de:probable cytochrome c peroxidase,) (db:swissprot) YHJA_ECOLI P37197 ESCHERICHIA COLI 562 -11536718 123011 yhya cytochrome-c peroxidase (cl:escherichia coli cytochrome-c peroxidase:pseudomonas cytochrome-c peroxidase homology) (ec:1.11.1.5) (db:pir1.dat) S47738 S47738 Escherichia coli 562 -11536718 7500937021 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:82050) (re:83447) (di:complement) ECOUW76 U00039 g466655 Escherichia coli 562 -11536718 236754 yhya putative cytochrome c peroxidase ec 1.11.1 (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:1.11.1.5) (de:escherichia coli k-12 mg1655 section 318 of 400 of the completegenome.) (nt:f465; 100 pct identical amino acid sequence and) (le:4113) (re:5510) (di:complement) AE000428 AE000428 g1789935 Escherichia coli 562 -11536718 5000693619 (de:(ecoli_3437) (pn:probable cytochrome c peroxidase) (gn:yhya) (gtcfc:13.7:14.1) (ec:1.11.1.5) (yhja_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3437 ECOLI_3437 Escherichia coli 562 10054627

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874543	13749	35905	645	214

Description

6500732861 yhj:b3527 53.1 kd protein in kdgk-dcta intergenic region precursor:f498 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3527 b3527 Escherichia coli 562 -11536719 112908 yhj (de:53.1 kd protein in kdgk-dcta intergenic region precursor) (db:swissprot) YHJJ_ECOLI P37648 ESCHERICHIA COLI 562 -11536719 163672 yhj 53.1k protein kdgk-dcta intergenic region precursor:hypothetical protein f498 (db:pir2.dat) S47748 S47748 Escherichia coli 562 -11536719 7500937032 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:94700) (re:96196) (di:complement) ECOUW76 U00039 g466665 Escherichia coli 562 -11536719 236764 yhj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 319 of 400 of the completegenome.) (nt:f498; 100 pct identical amino acid sequence and) (le:5930) (re:7426) (di:complement) AE000429 AE000429 g1789946 Escherichia coli 562 -11536719 5000693627 (de:(ecoli_3447) (pn:53) (gn:yhj) (gtcfc:13.7:14.1) (ec:) (yhj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3447 ECOLI_3447 Escherichia coli 562 10054636

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874555	13750	35906	366	121

Description

6500732862 yhjw:b3546 64.9 kd protein in prok-tag intergenic region (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3546 b3546 Escherichia coli 562 -11536720 7500937046 yhjw (de:64.9 kd protein in prok-tag intergenic region) (db:swissprot) YHJW_ECOLI P37661 ESCHERICHIA COLI 562 -11536720 7000690842 yhjw 64.9 kd protein in prok-tag intergenic region:hypothetical protein f589 (db:pir2.dat) D65153 D65153 Escherichia coli 562 -11536720 7500937048 yhjw orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 322 of 400 of the completegenome.) (nt:f574; sequence change shortens and) (le:1023) (re:2747) (di:complement) AE000432 AE000432 g2367242 Escherichia coli 562 -11536720

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874556	13751	35907	1071	356

Description

6500732863 yiae:b3553 putative 2-hydroxyacid dehydrogenase in bisc-cspa intergenic region (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3553 b3553 Escherichia coli 562 -11536721 7000691891 yiae probable 2-hydroxyacid dehydrogenase in bisc-cspa intergenic region:hypothetical protein o365 (db:pir2.dat) C65154 C65154 Escherichia coli 562 -11536721 7500937287 yiae putative dehydrogenase (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 322 of 400 of the completegenome.) (nt:o328; sequence change shortens and) (le:9537) (re:10523) (di:direct) AE000432 AE000432 g2367243 Escherichia coli 562 -11536721 7500937285 yiae (de:putative 2-hydroxyacid dehydrogenase in bisc-cspa intergenic region) (db:swissprot) YIAE_ECOLI P37666 ESCHERICHIA COLI 562 -11536721

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874557	13752	35908	876	291

Description

6500732864 rhsa:b3593 rhsa protein precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3593 b3593 Escherichia coli 562 -11536722 94321 rhsa (de:rhsa protein precursor) (db:swissprot) RHSA_ECOLI P16916 ESCHERICHIA COLI 562 -11536722 7000686322 rhsa rhsa protein precursor (cl:rhsf protein) (db:pir2.dat) C65159 C65159 Escherichia coli 562 -11536722 236830 rhsa core protein (db:genpept-bct1) (de:escherichia coli core protein (rhsa), orf-a2 and orf-a3, plantstress protein homologue, apre protein homologue genes, completecds.) (nt:extension at carboxy terminus) (le:952) (re:5085) (di:direct) ECORHSA L19044 g304934 Escherichia coli 562 -11536722 245396 rhsa (fn:repetitive sequence responsible for chromosomal) (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:176435) (re:180568) (di:direct) ECOUW76 U00039 g466731 Escherichia coli 562 -11536722 300026 (sr:e.coli (k12) cell line ch923 dna, clone prl276) (db:genpept-bct1) (de:e.coli rhsa locus encoding rsha protein, complete cds.) (nt:rhsa protein) (le:759) (re:4892) (di:direct) M29716 M29716 g147614 Escherichia coli 562 -11536722 235799 rhsa rhsa protein in rhs element (fn:orf; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 327 of 400 of the completegenome.) (nt:o1377; 100 pct identical amino acid sequence and) (le:164) (re:4297) (di:direct) AE000437 AE000437 g1790020 Escherichia coli 562 -11536722 5000693674 rhsa core protein rhsa (db:genpept) (de:escherichia coli core protein rhsa (rhsa) gene, complete cds; andunknown genes.) (nt:extension at carboxy terminus) (le:952) (re:5085) (di:direct) ECORHSA L19044 g304934 Escherichia coli 562 -11536722

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874559	13753	35909	285	94

Description

6500732865 lldp:lctp:b3603 l-lactate permease (gtcfc:1.1:1.2) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3603 b3603 Escherichia coli 562 -11536723 82264 lldp:lctp (de:l-lactate permease) (db:swissprot) LLDP_ECOLI P33231 ESCHERICHIA COLI 562 -11536723 163982 lldp:lctp l-lactate permease:lctp protein (cl:l-lactate permease) (db:pir2.dat) A49904 A49904 Escherichia coli 562 -11536723 236840 lctp l-lactate permease (fn:uptake of l-lactate) (sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia coli lct operon encoding l-lactate permease (lctp)gene, (lctr) gene, and l-lactate dehydrogenase (lctd) gene,complete cds.) (nt:hydrophobicity plot and t... ECOLCTPRD L13970 g404693 Escherichia coli 562 -11536723 7500885082 lctp (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (nt:aug is 3rd start) (le:191649) (re:193304) (di:direct) ECOUW76 U00039 g466741 Escherichia coli 562 -11536723 234959 lldp l-lactate permease (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 328 of 400 of the completegenome.) (nt:o551; 100 pct identical amino acid sequence and) (le:5195) (re:6850) (di:direct) AE000438 AE000438 g1790031 Escherichia coli 562 -11536723 5000693681 (de:(ecoli_3523) (pn:l-lactate permease) (gn:lldp) (gtcfc:13.7:14.1) (ec:) (lldp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3523 ECOLI_3523 Escherichia coli 562 10024494

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501874570	13754	35910	204	67

Description

6500732866 mutm:fpg:b3635 formamidopyrimidine-dna glycosylase:fapy-dna glycosylase (gtcfc:4.2) (ec:3.2.2.23) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3635 b3635 Escherichia coli 562 -11536724 236872 mutm:fpg (ec:3.2.2.23) (de:glycosylase)) (db:swissprot) FPG_ECOLI P05523 ESCHERICHIA COLI 562 -11536724 124699 mutm:fpg formamidopyrimidine-dna glycosidase::2-6-diamino-4-hydroxy-5n-methyl-formamidopyrimidine:fapy-dna glycosylase (cl:formamidopyrimidine dna glycosylase) (ec:3.2.2.23) (db:pir1.dat) (mp:82 min) DGEFCF A30254 Escherichia coli 562 -11536724 5000693688 (db:genpept-bct1) (de:e. coli fpg gene for fapy-dna glycosylase.) (nt:fapy-dna glycosylase (aa 1 - 269)) (le:126) (re:935) (di:direct) ECFPG X06036 g41481 Escherichia coli 562 -11536724 7500881727 fpg formamidopyrimidine-dna glycosylase (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 76.0 to 81.5 minutes.) (le:224607) (re:225416) (di:complement) ECOUW76 U00039 g466773 Escherichia coli 562 -11536724 232910 mutm formamidopyrimidine dna glycosylase (fn:enzyme; dna - replication, repair,) (db:genpept-bct2) (ec:3.2.2.-) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:f269; 100 pct identical amino acid sequence and) (le:2238) (re:3047) (di:complement) AE000441 AE000441 g1790066 Escherichia coli 562 -11536724 72260 mutm:fpg (ec:3.2.2.23) (de:glycosylase)) (db:swissprot) FPG_ECOLI P05523 ESCHERICHIA COLI 562 -11536724

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874582	13755	35911	615	204

Description

6500732867 yicc:b3644 33.2 kd protein in dind-rph intergenic region:orf x (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3644 b3644 Escherichia coli 562 -11536725 113183 yicc (de:33.2 kd protein in dind-rph intergenic region (orf x)) (db:swissprot) YICC_ECOLI P23839 ESCHERICHIA COLI 562 -11536725 7000688012 yicc 33.2 kd protein in dind-rph intergenic region orf x (cl:hypothetical protein hi0467) (db:pir2.dat) F65165 F65165 Escherichia coli 562 -11536725 7500937336 o287 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:6068) (re:6931) (di:direct) ECOUW82 L10328 g290494 Escherichia coli 562 -11536725 236882 yicc putative alpha helix protein (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:100 pct identical amino acid sequence and equal) (le:8571) (re:9434) (di:direct) AE000441 AE000441 g1790075 Escherichia coli 562 -11536725 5000693690 (de:(ecoli_3564) (pn:33) (gn:yicc) (gtcfc:13.7:14.1) (ec:) (yicc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3564 ECOLI_3564 Escherichia coli 562 10054911

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874584	13756	35912	609	202

Description

6500732868 dind:pcsa:b3645 dna-damage-inducible protein d (gtcfc:13.4:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3645 b3645 Escherichia coli 562 -11536726 7000690871 dind dna-damage-inducible protein d:hypothetical protein y (db:pir2.dat) G65165 G65165 Escherichia coli 562 -11536726 7500959726 o278 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (le:7140) (re:7976) (di:direct) ECOUW82 L10328 g290495 Escherichia coli 562 -11536726 236883 dind dna-damage-inducible protein (fn:phenotype; dna - replication, repair,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 331 of 400 of the completegenome.) (nt:100 pct identical to 274 amino acids of) (le:9643) (re:10479) (di:direct) AE000441 AE000441 g1790076 Escherichia coli 562 -11536726 5000693691 (de:(ecoli_3565) (pn:dna-damage-inducible protein d) (gn:dind) (gtcfc:13.7:14.1) (ec:) (dind_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3565 ECOLI_3565 Escherichia coli 562 10124051

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874608	13757	35913	450	149

Description

6500732869 emrd:b3673 multidrug resistance protein d (gtcfc:13.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3673 b3673 Escherichia coli 562 -11536727 70132 emrd (de:multidrug resistance protein d) (db:swissprot) EMRD_ECOLI P31442 ESCHERICHIA COLI 562 -11536727 7000685154 emrd multidrug resistance protein d (cl:bicyclomycin resistance protein) (db:pir2.dat) B65169 B65169 Escherichia coli 562 -11536727 7500881006 o396 (fn:unknown) (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to drug resistance translocases) (le:43310) (re:44500) (di:direct) ECOUW82 L10328 g290522 Escherichia coli 562 -11536727 236910 emrd 2-module integral membrane pump:multidrug (fn:transport; drug/analog sensitivity) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 335 of 400 of the completegenome.) (nt:o396; 100 pct identical amino acid sequence and) (le:1091) (re:2281) (di:direct) AE000445 AE000445 g1790107 Escherichia coli 562 -11536727 5000693703 (de:(ecoli_3592) (pn:integral membrane pump; multidrug resistance) (gn:emrd) (gtcfc:13.7:14.1) (ec:)(emrd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3592 ECOLI_3592 Escherichia coli 562 10012709

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874631	13758	35914	216	71

Description

6500732870 yidc:b3705 60 kd protein:60 kd inner-membrane protein (gtcfc:11.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3705 b3705 Escherichia coli 562 -11536728 57612 yidc (de:60 kd inner-membrane protein) (db:swissprot) 60IM_ECOLI P25714 ESCHERICHIA COLI 562 -11536728 7000684468 yidc probable 60k inner membrane protein (cl:probable 60k inner membrane protein:stage iii sporulation protein homology) (db:pir2.dat) B65173 B65173 Escherichia coli 562 -11536728 7500876132 o548 60 kd protein (sr:escherichia coli k12 strain mg1655; lambda clones ec14-52) (db:genpept-bct1) (de:e. coli; the region from 81.5 to 84.5 minutes.) (nt:similar to 60k protein from other bacteria) (le:74474) (re:76120) (di:direct) ECOUW82 L10328 g290553 Escherichia coli 562 -11536728 236941 yidc 60 kd inner-membrane protein (fn:membrane; inner membrane) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 337 of 400 of the completegenome.) (nt:o548; 100 pct identical to 60im_ecoli sw:) (le:8090) (re:9736) (di:direct) AE000447 AE000447 g1790140 Escherichia coli 562 -11536728 5000693725 (de:(ecoli_3623) (pn:60 kd inner-membrane protein) (gn:yidc) (gtcfc:13.7:14.1) (ec:)(60im_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3623 ECOLI_3623 Escherichia coli 562 10000395

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874632	13759	35915	1827	608

Description

6500732871 ppic:parva:b3775 peptidyl-prolyl cis-trans isomerase c:ppiase
c:rotamase c:parvulin (gtcfc:5.10:6.6) (ec:5.2.1.8) (keggfc:14.1)
(rileyfc:5.8.0) (db:gtc-escherichia coli) b3775 b3775 Escherichia coli 562
-11536729 164239 ppic peptidylprolyl isomerase::parvulin:ppiase
(ec:5.2.1.8) (db:pir2.dat) S48658 S48658 Escherichia coli 562 -11536729
258760 ppic peptidyl-prolyl cis-trans isomerase c (fn:accelerates the
folding of proteins) (db:genpept-bct1) (ec:5.2.1.8) (de:e. coli genomic
sequence of the region from 84.5 to 86.5 minutes.) (le:12663) (re:12944)
(di:complement) ECOUW85 M87049 g836657 Escherichia coli 562 -11536729
7500960409 parva parvulin (sr:escherichia coli k-12 hb101)
(db:genpept-bct1) (de:parva=parvulin (escherichia coli, k-12 hb101, genomic,
1135 nt).) (nt:putative member of new third ppiase family_.) (le:560)
(re:841) (di:direct) S73874 S73874 g693800 Escherichia coli 562 -11536729
237006 ppic peptidyl-prolyl cis-trans isomerase c rotamase (fn:enzyme;
proteins - translation and) (db:genpept-bct2) (ec:5.2.1.8) (de:escherichia
coli k-12 mg1655 section 344 of 400 of the completegenome.) (nt:f93; 100 pct
identical to cypc_ecoli sw: p39159) (le:1620) (re:1901) (di:complement)
AE000454 AE000454 g1790211 Escherichia coli 562 -11536729 5000693745
(de:(ecoli_3687) (pn:peptidyl-prolyl cis-trans isomerase c:rotamase c)
(gn:ppic) (gtcfc:13.7:14.1) (ec:5.2.1.8) (cypc_ecoli) (keggfc:11.1)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3687 ECOLI_3687 Escherichia
coli 562 10087243

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874635	13760	35916	216	71

Description

6500732872 yifk:b3795 probable transport protein yifk:o461 (gtcfc:12.6)
(keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3795 b3795
Escherichia coli 562 -11536730 7500937425 yifk (de:probable transport
protein yifk) (db:swissprot) YIFK_ECOLI P27837 ESCHERICHIA COLI 562
-11536730 7000691899 yifk probable transport protein yifk o461 (cl:arginine
permease) (db:pir2.dat) H65183 H65183 Escherichia coli 562 -11536730
7500937427 yifk putative amino acid/amine transport protein (fn:putative
transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12
mg1655 section 345 of 400 of the completegenome.) (nt:o461; 99 pct identical
to yifk_ecoli sw:) (le:10805) (re:12190) (di:direct) AE000455 AE000455
g2367290 Escherichia coli 562 -11536730

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874636	13761	35917	1311	436

Description

6500732873 hemy:b3802 hemy protein (gtcfc:14.3) (keggfc:14.2)
(rileyfc:5.8.0) (db:gtc-escherichia coli) b3802 b3802 Escherichia coli 562
-11536731 237026 hemy (de:hemy protein) (db:swissprot) HEMY_ECOLI P09128
ESCHERICHIA COLI 562 -11536731 163186 hemy hemy protein (db:pir2.dat)
(mp:85 min) S01694 S01694 Escherichia coli 562 -11536731 5000693751
(db:genpept-bct1) (de:e. coli genes hemc and hemd for porphobilinogen
deaminase (ec4.3.1.8) and uroporphyrinogen iii cosynthetase (ec 4.2.1.75).)
(nt:orf y (aa 1 - 398)) (le:3004) (re:4200) (di:direct) ECHEMCD X12614
g41669 Escherichia coli 562 -11536731 7500883204 hemy (fn:unknown)
(db:genpept-bct1) (de:e. coli genomic sequence of the region from 84.5 to
86.5 minutes.) (le:39798) (re:40994) (di:complement) ECOUW85 M87049 g148201
Escherichia coli 562 -11536731 233074 hemy a late step of protoheme ix
synthesis (fn:enzyme; biosynthesis of cofactors, carriers:)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 346 of 400 of the
completeness.) (nt:f398; 100 pct identical to hemy_ecoli sw: p09128)
(le:3828) (re:5024) (di:complement) AE000456 AE000456 g1790234 Escherichia
coli 562 -11536731 76772 hemy (de:hemy protein) (db:swissprot) HEMY_ECOLI
P09128 ESCHERICHIA COLI 562 -11536731

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874656	13762	35918	1323	440

Description

6500732874 cyay:b3807 cyay protein (gtcfc:14.3) (keggfc:14.2)
(rileyfc:5.8.0) (db:gtc-escherichia coli) b3807 b3807 Escherichia coli 562
-11536732 237031 cyay (de:cyay protein) (db:swissprot) CYAY_ECOLI P27838
ESCHERICHIA COLI 562 -11536732 162586 cyay hypothetical 11k protein
cyaa-dapf intergenic region:cyay protein (db:pir2.dat) (mp:86 min) S30697
S30697 Escherichia coli 562 -11536732 5000693752 cyay (db:genpept-bct1)
(de:e.coli hemc, cya, cyay and dapf genes for uroporphyrinogen isynthase,
adenylate cyclase, an unknown protein, anddiaminopimelate epimerase.)
(le:3240) (re:3560) (di:complement) ECCYALOC X66782 g41188 Escherichia coli
562 -11536732 7500879651 f106 (fn:unknown) (db:genpept-bct1) (de:e. coli
genomic sequence of the region from 84.5 to 86.5 minutes.) (le:46851)
(re:47171) (di:complement) ECOUW85 M87049 g148206 Escherichia coli 562
-11536732 232612 cyay orf:hypothetical protein (fn:orf; unknown)
(db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 346 of 400 of the
completeness.) (nt:f106; 100 pct identical to cyay_ecoli sw: p27838)
(le:10881) (re:11201) (di:complement) AE000456 AE000456 g1790239 Escherichia
coli 562 -11536732 67095 cyay (de:cyay protein) (db:swissprot) CYAY_ECOLI
P27838 ESCHERICHIA COLI 562 -11536732

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874667	13763	35919	627	208

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874682	13764	35920	306	101

Description

6500732875 hemn:b3867 oxygen-independent coproporphyrinogen iii oxidase:coproporphyrinogenase:coprogen oxidase (gtcfc:9.10) (ec:1.-.-.) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3867 b3867 Escherichia coli 562 -11536733 7000691878 hemn coproporphyrinogen oxidase:iii:oxygen-independent:hypothetical protein o459 (cl:oxygen-independent coproporphyrinogen oxidase) (ec:1.3.3.3) (db:pir2.dat) F65191 F65191 Escherichia coli 562 -11536733 7500953845 hemn o2-independent coproporphyrinogen iii oxidase (fn:enzyme; biosynthesis of cofactors, carriers:) (db:genpept-bct2) (ec:1.-.-.) (de:escherichia coli k-12 mg1655 section 352 of 400 of the completegenome.) (nt:o459; 99 pct identical to 457 amino acids) (le:1972) (re:3351) (di:direct) AE000462 AE000462 g1790298 Escherichia coli 562 -11536733 5000693785 (de:(ecoli_3766) (pn:oxygen-independent coproporphyrinogen iii oxidase) (gn:hemn) (gtcfc:13.7:14.1) (ec:1.-.-.) (hemn_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3766 ECOLI_3766 Escherichia coli 562 10124117

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874689	13765	35921	384	127

Description

GTC ORF with score 360 to: (sr:human) (db:genpept-pri3) (de:homo sapiens nitrilase homolog 1 (nit1) gene, alternatively splicedproduct, complete cds.) (nt:nit1; alternatively spliced) (le:679:1288:1636:2011:2321) (re:680:1383:1890:2114:2454) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874695	13766	35922	555	185

Description

6500732876 yihk:b3871 65.4 kd gtp-binding protein in glna-fdhe intergenic region:65.4 kd gtp-binding protein in glna-rbn intergenic region (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3871 b3871 Escherichia coli 562 -11536734 113325 typa:bipa (de:gtp-binding protein typa/bipa (tyrosine phosphorylated protein a)) (db:swissprot) TYPA_ECOLI P32132 ESCHERICHIA COLI 562 -11536734 163862 yihk 65.4k gtp-binding protein glna-fdhe intergenic region:hypothetical protein o591 (cl:translation elongation factor tu homology) (db:pir2.dat) S40816 S40816 Escherichia coli 562 -11536734 7500893596 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (nt:matches ps00017: atp_gtp_a and ps00301:) (le:20047) (re:21822) (di:direct) ECOUW87 L19201 g304976 Escherichia coli 562 -11536734 237090 yihk putative gtp-binding factor (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 352 of 400 of the completegenome.) (nt:o591; 100 pct identical to yihk_ecoli sw:) (le:8340) (re:10115) (di:direct) AE000462 AE000462 g1790302 Escherichia coli 562 -11536734 5000693786 (de:(ecoli_3770) (pn:65) (gn:yihk) (gtcfc:13.7:14.1) (ec: (yihk_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3770 ECOLI_3770 Escherichia coli 562 10055053

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874716	13767	35923	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874732	13768	35924	546	181

Description

GTC ORF with score 217 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c2d10.) (nt:spbc2d10.20, len:198, similarity:saccharomyces) (le:38739:38929:39087:39182) (re:38781:38976:39118:39185) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874733	13769	35925	510	169

Description

6500732877 frvx:b3898 putative frv operon protein frvx (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3898 b3898 Escherichia coli 562 -11536735 72377 frvx (de:putative frv operon protein frvx) (db:swissprot) FRVX_ECOLI P32153 ESCHERICHIA COLI 562 -11536735 163644 frvx probable frv operon protein frvx:hypothetical protein f356 (cl:thermophilic aminopeptidase i alpha chain) (db:pir2.dat) S40842 S40842 Escherichia coli 562 -11536735 7500881765 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:51495) (re:52565) (di:complement) ECOUW87 L19201 g305002 Escherichia coli 562 -11536735 237116 frvx frv operon protein (fn:orf; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 355 of 400 of the completengenome.) (nt:f356; 100 pct identical amino acid sequence and) (le:4033) (re:5103) (di:complement) AE000465 AE000465 g1790332 Escherichia coli 562 -11536735 5000693807 (de:(ecoli_3797) (pn:putative frv operon protein frvx) (gn:frvx) (gtcfc:13.7:14.1) (ec:) (frvx_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3797 ECOLI_3797 Escherichia coli 562 10014928

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874734	13770	35926	972	323

Description

6500732878 glpx:b3925 glpx protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3925 b3925 Escherichia coli 562 -11536736 237142 glpx (de:glpx protein) (db:swissprot) GLPX_ECOLI P28860 ESCHERICHIA COLI 562 -11536736 163109 glpx glpx protein (db:pir2.dat) (mp:88 min) A45248 A45248 Escherichia coli 562 -11536736 5000693817 glpx protein (db:genpept-bct1) (de:e.coli glpx gene.) (nt:unknown function; third gene in glpfx operon) (le:141) (re:1151) (di:direct) ECGLPXG Z11767 g41589 Escherichia coli 562 -11536736 7500882523 glpx (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2 minutes.) (le:76202) (re:77212) (di:complement) ECOUW87 L19201 g305028 Escherichia coli 562 -11536736 233014 glpx unknown function in glycerol metabolism (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357 of 400 of the completengenome.) (nt:f336; 100 pct identical amino acid sequence and) (le:1695) (re:2705) (di:complement) AE000467 AE000467 g1790360 Escherichia coli 562 -11536736 74056 glpx (de:glpx protein) (db:swissprot) GLPX_ECOLI P28860 ESCHERICHIA COLI 562 -11536736

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874752	13771	35927	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874755	13772	35928	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874758	13773	35929	489	163

Description

6500732879 meng:b3929 menaquinone biosynthesis protein
meng:s-adenosylmethionine:2-demethylmenaquinone methyltransferase
(gtcfc:9.12) (ec:2.1.-.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia
coli) b3929 b3929 Escherichia coli 562 -11536737 83453 meng (ec:2.1.-.-)
(de:(ec 2.1.-.-)) (db:swissprot) MENG_ECOLI P32165 ESCHERICHIA COLI 562
-11536737 163573 meng menaquinone biosynthesis protein meng:hypothetical
protein f161 (db:pir2.dat) S40872 S40872 Escherichia coli 562 -11536737
239728 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library:
lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2 to 89.2
minutes.) (le:80478) (re:80963) (di:complement) ECOUW87 L19201 g305032
Escherichia coli 562 -11536737 7500885497 meng
s-adenosylmethionine:2-demethylmenaquinone (fn:converts demethylmenaquinone
to menaquinone) (sr:escherichia coli strain=k12) (db:genpept-bct1)
(de:escherichia coli 1,4-dihydroxy-2-naphthoate octaprenyltransferase(mena)
and s-adenosylmethionine:2-demethylmenaquinonemethyltransferase (meng)
genes... ECU56082 U56082 g1336002 Escherichia coli 562 -11536737 237146
meng menaquinone biosynthesis:unknown (fn:putative enzyme; biosynthesis of
cofactors,) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 357
of 400 of the completegenome.) (nt:f161; 100 pct identical amino acid
sequence and) (le:5971) (re:6456) (di:complement) AE000467 AE000467 g1790364
Escherichia coli 562 -11536737 5000693819 (de:(ecoli_3827) (pn:menaquinone
biosynthesis protein meng) (gn:meng) (gtcfc:13.7:14.1) (ec:2.1.-.-)
(meng_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli))
ECOLI_3827 ECOLI_3827 Escherichia coli 562 10025667

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874759	13774	35930	1185	394

Description

6500732880 hslu:htpi:b3931 heat shock protein hslu (gtcfc:12.7)
 (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3931 b3931
 Escherichia coli 562 -11536738 77894 hslu:htpi (de:heat shock protein hslu)
 (db:swissprot) HSLU_ECOLI P32168 ESCHERICHIA COLI 562 -11536738 163164 hslu
 heat shock protein hslu (cl:heat shock protein hslu:ftsh/sec18/cdc48-type
 atp-binding domain homology) (db:pir2.dat) JT0761 JT0761 Escherichia coli
 562 -11536738 7500883566 hslu (sr:escherichia coli (sub_strain mg1655,
 strain k-12) (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal
 region from 87.2 to 89.2 minutes.) (nt:matches ps00017: atp_gtp_a; similar
 to pasteurella) (le:82049) (re:83380) (di:complement) ECOUW87 L19201 g305034
 Escherichia coli 562 -11536738 237148 hslu heat shock protein hslvu:atpase
 subunit (fn:factor; adaptations, atypical conditions) (db:genpept-bct2)
 (de:escherichia coli k-12 mg1655 section 357 of 400 of the completegenome.)
 (nt:f443; 100 pct identical to hslu_ecoli sw:) (le:7542) (re:8873)
 (di:complement) AE000467 AE000467 g1790366 Escherichia coli 562 -11536738
 5000693820 (de:(ecoli_3829) (pn:heat shock protein hslu) (gn:hslu)
 (gtcfc:13.7:14.1) (ec:) (hslu_ecoli) (keggfc:11.2) (rileyfc:5.7.0)
 (db:gtc-escherichia coli)) ECOLI_3829 ECOLI_3829 Escherichia coli 562
 10020253

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874760	13775	35931	240	79

Description

6500732881 hslv:htpo:b3932 heat shock protein hslv (gtcfc:12.7)
 (ec:3.4.99.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3932
 b3932 Escherichia coli 562 -11536739 163165 hslv heat shock protein hslv
 (ec:3.4.99.-) (db:pir2.dat) JT0760 JT0760 Escherichia coli 562 -11536739
 7500959760 hslv (sr:escherichia coli (sub_strain mg1655, strain k-12)
 (library: lambda) (db:genpept-bct1) (de:e. coli chromosomal region from 87.2
 to 89.2 minutes.) (nt:similar to s. cerevisiae potential proteasome)
 (le:83390) (re:83920) (di:complement) ECOUW87 L19201 g305035 Escherichia
 coli 562 -11536739 237149 hslv heat shock protein hslvu:proteasome-related
 (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2)
 (ec:3.4.99.-) (de:escherichia coli k-12 mg1655 section 357 of 400 of the
 completegenome.) (nt:f176; 100 pct identical to hslv_ecoli sw:) (le:8883)
 (re:9413) (di:complement) AE000467 AE000467 g1790367 Escherichia coli 562
 -11536739 5000693821 (de:(ecoli_3830) (pn:heat shock protein hslv)
 (gn:hslv) (gtcfc:13.7:14.1) (ec:3.4.99.-) (hslv_ecoli) (keggfc:11.1)
 (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3830 ECOLI_3830 Escherichia
 coli 562 10086797

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874761	13776	35932	1329	442

Description

6500732882 talc:b3946 transaldolase-like protein (gtcfc:14.3) (ec:2.2.1.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3946 b3946
 Escherichia coli 562 -11536740 100448 talc (ec:2.2.1.-) (de:transaldolase-like protein talc,) (db:swissprot) TALC_ECOLI P32669
 ESCHERICHIA COLI 562 -11536740 7000686753 talc transaldolase-like protein (cl:bacillus subtilis 23k phosphoprotein orfu) (ec:2.2.1.-) (db:pir2.dat)
 E65201 E65201 Escherichia coli 562 -11536740 237164 talc putative transaldolase (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:2.2.1.-) (de:escherichia coli k-12 mg1655 section 358 of 400 of the completegenome.) (nt:f220; 100 pct identical amino acid sequence and) (le:10597) (re:11259) (di:complement) AE000468 AE000468 g1790382 Escherichia coli 562 -11536740 7500892742 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to bacillus subtilis hypoth. 20 kda) (le:4288) (re:4950) (di:complement) ECOUW89 U00006 g396293
 Escherichia coli 562 -11536740 5000693825 (de:(ecoli_3844) (pn:transaldolase-like protein) (gn:talc) (gtcfc:13.7:14.1) (ec:2.2.1.-) (talc_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli))
 ECOLI_3844 ECOLI_3844 Escherichia coli 562 10042300

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874793	13777	35933	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874796	13778	35934	276	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874801	13779	35935	705	234

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874812	13780	35936	828	275

Description

6500732883 ptsa:b3947 phosphoenolpyruvate-protein phosphotransferase
 ptsa:phosphotransferase system:enzyme i:enzyme i-ani (gtcfc:1.8:12.2)
 (ec:2.7.3.9) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3947
 b3947 Escherichia coli 562 -11536741 92081 ptsa (ec:2.7.3.9)
 (de:(phosphotransferase system, enzyme i) (enzyme i-ani)) (db:swissprot)
 PT1A_ECOLI P32670 ESCHERICHIA COLI 562 -11536741 7000686204 ptsa
 phosphoenolpyruvate-protein phosphotransferase ptsa (cl:phosphotransferase
 system enzyme i homology) (ec:2.7.3.-) (db:pir2.dat) F65201 F65201
 Escherichia coli 562 -11536741 237165 ptsa pep-protein phosphotransferase
 system enzyme i (fn:enzyme; transport of small molecules:) (db:genpept-bct2)
 (ec:2.7.3.-) (de:escherichia coli k-12 mg1655 section 358 of 400 of the
 completegenome.) (nt:f711; 100 pct identical amino acid sequence and)
 (le:11271) (re:13406) (di:complement) AE000468 AE000468 g1790383 Escherichia
 coli 562 -11536741 7500888901 (sr:escherichia coli (sub_strain mg1655,
 strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal
 region from 89.2 to 92.8 minutes.) (nt:similar to phosphotransferase system
 enzyme i) (le:4962) (re:7097) (di:complement) ECOUW89 U00006 g409787
 Escherichia coli 562 -11536741 5000693826 (de:(ecoli_3845) (pn:pep-protein
 phosphotransferase system enzyme i) (gn:ptsa) (gtcfc:13.7:14.1) (ec:2.7.3.9)
 (pt1a_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli))
 ECOLI_3845 ECOLI_3845 Escherichia coli 562 10034115

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874821	13781	35937	801	266

Description

6500732884 frwc:b3949 phosphotransferase:pts system:fructose-like-2 iic component:phosphotransferase enzyme ii:c component (gtcfc:12.2:1.5) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3949 b3949 Escherichia coli 562 -11536742 92343 frwc (de:ii, c component)) (db:swissprot) PTWC_ECOLI P32672 ESCHERICHIA COLI 562 -11536742 7000686235 frwc pts system:fructose-like-2 iic component (db:pir2.dat) H65201 H65201 Escherichia coli 562 -11536742 237167 frwc pts system:fructose-like enzyme ii component (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 359 of 400 of the completegenome.) (nt:o359; 100 pct identical amino acid sequence and) (le:298) (re:1377) (di:direct) AE000469 AE000469 g1790386 Escherichia coli 562 -11536742 7500889016 (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (nt:similar to phosphotransferase system enzyme ii) (le:7771) (re:8850) (di:direct) ECOUW89 U00006 g396296 Escherichia coli 562 -11536742 5000693828 (de:(ecoli_3847) (pn:pts system, fructose-like-2 iic component:phosphotransferase enzyme ii, c component) (gn:frwc) (gtcfc:13.7:14.1) (ec:) (ptwc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3847 ECOLI_3847 Escherichia coli 562 10034375

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874828	13782	35938	1233	411

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874834	13783	35939	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874840	13784	35940	357	118

Description

6500732885 udha:b3962 unknown dehydrogenase a (gtcfc:14.3) (ec:1.-.-.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3962 b3962 Escherichia coli 562 -11536743 103305 udha (ec:1.-.-.-) (de:unknown dehydrogenase a,) (db:swissprot) UDHA_ECOLI P27306 ESCHERICHIA COLI 562 -11536743 7000686855 udha probable dehydrogenase:udha (ec:1.8.1.-) (db:pir2.dat) E65203 E65203 Escherichia coli 562 -11536743 7500893749 udha putative oxidoreductase (fn:putative enzyme; not classified) (db:genpept-bct2) (ec:1.-.-.-) (de:escherichia coli k-12 mg1655 section 360 of 400 of the completengenome.) (nt:f444; 99 pct identical amino acid sequence and) (le:6276) (re:7610) (di:complement) AE000470 AE000470 g1790400 Escherichia coli 562 -11536743 5000693831 (de:(ecoli_3860) (pn:unknown dehydrogenase a) (gn:udha) (gtcfc:13.7:14.1) (ec:1.-.-.-) (udha_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3860 ECOLI_3860 Escherichia coli 562 10045075

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874841	13785	35941	432	143

Description

6500732886 htrc:b3989 heat shock protein c (gtcfc:12.7) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b3989 b3989 Escherichia coli 562 -11536744 78035 htrc (de:heat shock protein c) (db:swissprot) HTRC_ECOLI P27375 ESCHERICHIA COLI 562 -11536744 7000685569 htrc heat shock protein c (db:pir2.dat) H65205 H65205 Escherichia coli 562 -11536744 237199 htrc heat shock protein htrc (fn:factor; adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 363 of 400 of the completengenome.) (nt:o179; 100 pct identical amino acid sequence and) (le:148) (re:687) (di:direct) AE000473 AE000473 g1790422 Escherichia coli 562 -11536744 7500883608 htrc heat shock protein c (sr:escherichia coli (sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e. coli chromosomal region from 89.2 to 92.8 minutes.) (le:55027) (re:55566) (di:direct) ECOUW89 U00006 g396328 Escherichia coli 562 -11536744 5000693835 (de:(ecoli_3879) (pn:heat shock protein) (gn:htrc) (gtcfc:13.7:14.1) (ec:) (htrc_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3879 ECOLI_3879 Escherichia coli 562 10020374

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874850	13786	35942	582	193

Description

6500732887 dinf:b4044 dna-damage-inducible protein f (gtcfc:13.4)
(keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4044 b4044
Escherichia coli 562 -11536745 68662 dinf (de:dna-damage-inducible protein
f) (db:swissprot) DINF_ECOLI P28303 ESCHERICHIA COLI 562 -11536745
7000685051 dinf dna-damage-inducible protein f (db:pir2.dat) C65212 C65212
Escherichia coli 562 -11536745 237250 dinf dna-damage-inducible protein
(sr:escherichia coli (strain k-12) dna) (db:genpept-bct1) (de:escherichia
coli repressor protein (lexa) gene 3' end;dna-damage-inducible protein
(dinf) gene, complete cds.) (le:48) (re:1427) (di:direct) ECOLEXDIN L02362
g146611 Escherichia coli 562 -11536745 234975 dinf dna-damage-inducible
protein f (fn:factor; dna - replication, repair,) (db:genpept-bct2)
(de:escherichia coli k-12 mg1655 section 367 of 400 of the completegenome.)
(nt:o459; 100 pct identical to dinf_ecoli sw: p28303;) (le:9837) (re:11216)
(di:direct) AE000477 AE000477 g1790477 Escherichia coli 562 -11536745
7500880323 dinf (fn:dna-damage-inducible protein f) (sr:escherichia coli
(sub_strain mg1655, strain k-12) (library: lambda) (db:genpept-bct2) (de:e.
coli chromosomal region from 89.2 to 92.8 minutes.) (nt:cg site no. 854)
(le:122984) (re:124363) (di:direct) ECOUW89 U00006 g396379 Escherichia coli
562 -11536745 5000693854 (de:(ecoli_3930) (pn:dna-damage-inducible protein
f) (gn:dinf) (gtcfc:13.7:14.1) (ec:) (dinf_ecoli) (keggfc:11.2)
(rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3930 ECOLI_3930 Escherichia
coli 562 10011250

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874858	13787	35943	777	258

Description

6500732888 phnb:b4107 protein:phnb protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4107 b4107 Escherichia coli 562 -11536746 89591 phnb (de:phnb protein) (db:swissprot) PHNB_ECOLI P16681 ESCHERICHIA COLI 562 -11536746 164279 phnb phnb protein (db:pir2.dat) C35718 C35718 Escherichia coli 562 -11536746 237315 (sr:e.coli (strain b) dna) (db:genpept-bct1) (de:e.coli psid locus containing alkylphosphonate uptake (phn) genes athrough q, complete cds.) (nt:phnb protein) (le:3767) (re:4210) (di:direct) ECOPHNAQ J05260 g147195 Escherichia coli 562 -11536746 7500888024 phnb (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:16226) (re:16669) (di:complement) ECOUW93 U14003 g536951 Escherichia coli 562 -11536746 235434 phnb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 373 of 400 of the completegenome.) (nt:f147; 100 pct identical amino acid sequence and) (le:97) (re:540) (di:complement) AE000483 AE000483 g1790546 Escherichia coli 562 -11536746 5000693884 (de:(ecoli_3993) (pn:phnb protein) (gn:phnb) (gtcfc:13.7:14.1) (ec:) (phnb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3993 ECOLI_3993 Escherichia coli 562 10031713

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874860	13788	35944	1494	497

Description

6500732889 phna:b4108 phna protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4108 b4108 Escherichia coli 562 -11536747 89587 phna (de:phna protein) (db:swissprot) PHNA_ECOLI P16680 ESCHERICHIA COLI 562 -11536747 164278 phna phna protein (db:pir2.dat) B35718 B35718 Escherichia coli 562 -11536747 237316 (sr:e.coli (strain b) dna) (db:genpept-bct1) (de:e.coli psid locus containing alkylphosphonate uptake (phn) genes athrough q, complete cds.) (nt:phna protein) (le:2874) (re:3209) (di:direct) ECOPHNAQ J05260 g147194 Escherichia coli 562 -11536747 7500888022 phna (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:17228) (re:17563) (di:complement) ECOUW93 U14003 g536952 Escherichia coli 562 -11536747 235433 phna orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 373 of 400 of the completegenome.) (nt:f111; 100 pct identical amino acid sequence and) (le:1198) (re:1533) (di:complement) AE000483 AE000483 g1790547 Escherichia coli 562 -11536747 5000693885 (de:(ecoli_3994) (pn:phna protein) (gn:phna) (gtcfc:13.7:14.1) (ec:) (phna_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_3994 ECOLI_3994 Escherichia coli 562 10031709

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874869	13789	35945	303	100

Description

6500732890 dsbd:b4136 thiol:disulfide interchange protein dsbd:c-type cytochrome (gtcfc:2.7:2.8) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4136 b4136 Escherichia coli 562 -11536748 163915
 dsbd:cycz:cuta2:dipz inner membrane copper tolerance protein
 cycz:thiol:disulfide interchange protein dsbd (db:pir2.dat) S56364 S56364 Escherichia coli 562 -11536748 7500960368 cycz (fn:involved in biogenesis of c-type cytochromes) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:54173) (re:55870) (di:complement) ECOUW93 U14003 g536980 Escherichia coli 562 -11536748 237344 dsbd thiol:disulfide interchange protein:copper (fn:putative enzyme; central intermediary) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 376 of 400 of the completegenome.) (nt:f565; 100 pct identical to 488 amino acids) (le:4718) (re:6415) (di:complement) AE000486 AE000486 g1790578 Escherichia coli 562 -11536748 5000693899 (de:(ecoli_4022) (pn:thiol:disulfide interchange protein dsbd:c-type cytochrome biogenesis protein cycz:inner membrane copper tolerance) (gn:dsbd) (gtcfc:13.7:14.1) (ec:) (dsbd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escher) ECOLI_4022 ECOLI_4022 Escherichia coli 562 10087083

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874870	13790	35946	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874871	13791	35947	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874883	13792	35948	300	100

Description

6500732891 cuta:cycy:cuta1:b4137 c-type cy:periplasmic divalent cation tolerance protein cuta:c-type cytochrome biogenesis protein cycy (gtcfc:11.1:2.8) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4137 b4137 Escherichia coli 562 -11536749 237345 cuta:cycy:cuta1 (de:biogenesis protein cycy)) (db:swissprot) CUTA_ECOLI P36654 ESCHERICHIA COLI 562 -11536749 162938 cuta:cuta1:cycy divalent cation tolerance protein cuta1:cycy protein:hypothetical protein 112 (cl:divalent cation tolerance protein cuta1) (db:pir2.dat) I41027 I41027 Escherichia coli 562 -11536749 232618 cuta1 periplasmic divalent cation tolerance protein (db:genpept-bct1) (de:e.coli cuta1, cuta2, and cuta3 genes.) (le:366) (re:704) (di:direct) ECCUTA123 Z36905 g535291 Escherichia coli 562 -11536749 5000693900 orf112 (db:genpept-bct1) (de:e.coli orf112, dipz and orf191 genes.) (le:180) (re:518) (di:direct) ECCYCYZ X77707 g871028 Escherichia coli 562 -11536749 7500879587 cycy (fn:involved in biogenesis of c-type cytochromes) (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:55846) (re:56184) (di:complement) ECOUW93 U14003 g536981 Escherichia coli 562 -11536749 232599 cuta divalent cation tolerance protein:cytochrome c (fn:phenotype; adaptations, atypical conditions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 376 of 400 of the completegenome.) (nt:f112; 100 pct identical amino acid sequence and) (le:6391) (re:6729) (di:complement) AE000486 AE000486 g1790579 Escherichia coli 562 -11536749 66849 cuta:cycy:cuta1 (de:biogenesis protein cycy)) (db:swissprot) CUTA_ECOLI P36654 ESCHERICHIA COLI 562 -11536749

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874885	13793	35949	753	250

Description

6500732892 efp:b4147 elongation factor p:ef-p (gtcfc:10.7) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4147 b4147 Escherichia coli 562 -11536750 164740 efp translation elongation factor ef-p (cl:translation elongation factor ef-p) (db:pir2.dat) S34443 S34443 Escherichia coli 562 -11536750 237355 elongation factor p (db:genpept-bct1) (de:e.coli gene for elongation factor p (ef-p).) (le:253) (re:819) (di:direct) ECEFPG X61676 g433670 Escherichia coli 562 -11536750 7500960473 efp elongation factor p (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:66527) (re:67093) (di:direct) ECOUW93 U14003 g536991 Escherichia coli 562 -11536750 232757 efp elongation factor p ef-p (fn:factor; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.) (nt:o188; 100 pct identical amino acid sequence and) (le:7189) (re:7755) (di:direct) AE000487 AE000487 g1790590 Escherichia coli 562 -11536750 5000693906 (de:(ecoli_4033) (pn:elongation factor p:ef-p) (gn:efp) (gtcfc:13.7:14.1) (ec:) (efp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4033 ECOLI_4033 Escherichia coli 562 10087448

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874887	13794	35950	354	117

Description

6500732893 suges:b4148 suges:suge protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4148 b4148 Escherichia coli 562 -11536751 164662 suges suges protein (cl:suge protein) (db:pir2.dat) (mp:94 min) S56376 S56376 Escherichia coli 562 -11536751 7500892239 suges suges (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:differences from genbank accession number x69949) (le:67553) (re:68020) (di:direct) ECOUW93 U14003 g536992 Escherichia coli 562 -11536751 237356 suges suppresses groel:may be chaperone (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 377 of 400 of the completegenome.) (nt:o155; 100 pct identical to suges_ecoli sw:) (le:8215) (re:8682) (di:direct) AE000487 AE000487 g1790591 Escherichia coli 562 -11536751 99817 suges (de:suge protein) (db:swissprot) SUGE_ECOLI P30743 ESCHERICHIA COLI 562 -11536751 5000693907 (de:(ecoli_4034) (pn:suge protein, suppresses a groel mutation and mimics the effect of groe overexpression could act as a chaperone) (gn:suge) (gtcfc:13.7:14.1) (ec:) (suge_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherich) ECOLI_4034 ECOLI_4034 Escherichia coli 562 10041672

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874888	13795	35951	189	62
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874889	13796	35952	753	250
<u>Description</u>				

6500732894 vacb:b4179 vacb protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4179 b4179 Escherichia coli 562 -11536752 163339 vacb virulence-associated protein vacb homolog (cl:virulence-associated protein vacb homolog) (db:pir2.dat) (mp:95 min) S56404 S56404 Escherichia coli 562 -11536752 7500955360 vacb (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:97440) (re:99923) (di:direct) ECOUW93 U14003 g537020 Escherichia coli 562 -11536752 237384 vacb putative enzyme (fn:putative enzyme; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 380 of 400 of the completegenome.) (nt:o827; 100 pct identical to 813 amino acids) (le:2296) (re:4779) (di:direct) AE000490 AE000490 g1790622 Escherichia coli 562 -11536752 5000693920 (de:(ecoli_4062) (pn:vacb protein) (gn:vacb) (gtcfc:13.7:14.1) (ec:) (vacb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4062 ECOLI_4062 Escherichia coli 562 10086874

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874894	13797	35953	306	101
<u>Description</u>				

6500732895 fklb:b4207 probable fklb-type 22 kd peptidyl-prolyl cis-trans isomerase (gtcfc:5.10:6.6) (ec:5.2.1.8) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4207 b4207 Escherichia coli 562 -11536753 163786 fklb peptidylprolyl isomerase::fk506-binding protein fklb22 (cl:bklb-type peptidylprolyl isomerase homology) (ec:5.2.1.8) (db:pir2.dat) S56432 S56432 Escherichia coli 562 -11536753 7500960410 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o259a) (le:119608) (re:120387) (di:direct) ECOUW93 U14003 g537048 Escherichia coli 562 -11536753 237412 fklb fklb-type 22kd peptidyl-prolyl cis-trans (fn:enzyme; proteins - translation and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 382 of 400 of the completegenome.) (nt:o259a; 100 pct identical to 205 amino acids) (le:1348) (re:2127) (di:direct) AE000492 AE000492 g1790652 Escherichia coli 562 -11536753 5000693942 (de:(ecoli_4090) (pn:fklb-type 22 kd peptidyl-prolyl cis-trans isomerase:ppiase:rotamase:fklb22) (gn:fklb) (gtcfc:13.7:14.1) (ec:5.2.1.8) (fkbb_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4090 ECOLI_4090 Escherichia coli 562 10087048

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874896	13798	35954	2400	799

Description

6500732896 ytfj:b4216 f18:18.2 kd protein in cysq-msra intergenic region precursor:f184 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4216 b4216 Escherichia coli 562 -11536754 116405 ytfj (de:18.2 kd protein in cysq-msra intergenic region precursor) (db:swissprot) YTFJ_ECOLI P39187 ESCHERICHIA COLI 562 -11536754 163578 ytfj 18.2k protein cysq-msra intergenic region precursor:hypothetical protein f184 (db:pir2.dat) S56441 S56441 Escherichia coli 562 -11536754 7500952761 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f184) (le:129539) (re:130093) (di:complement) ECOUW93 U14003 g537057 Escherichia coli 562 -11536754 237421 ytfj orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 383 of 400 of the completegenome.) (nt:f184; 100 pct identical amino acid sequence and) (le:1156) (re:1710) (di:complement) AE000493 AE000493 g1790662 Escherichia coli 562 -11536754 5000693948 (de:(ecoli_4099) (pn:18) (gn:ytfj) (gtcfc:13.7:14.1) (ec:) (ytfj_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4099 ECOLI_4099 Escherichia coli 562 10058130

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874921	13799	35955	2862	953

Description

6500732897 yjfa:b4223 ile repressor protein:hypothetical 10.6 kd protein in msra-chpbi region (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4223 b4223 Escherichia coli 562 -11536755 113713 (de:very hypothetical 10.6 kd protein in msra-chpbi region) (db:swissprot) YZFA_ECOLI P08339 ESCHERICHIA COLI 562 -11536755 154807 iler:yjfa ile repressor (cl:ile repressor) (db:pir1.dat) (mp:99.5 min) RPECIL S56449 Escherichia coli 562 -11536755 7500953077 iler ile repressor protein (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:cg site no. 15914) (le:138808) (re:139077) (di:complement) ECOUW93 U14003 g537065 Escherichia coli 562 -11536755 237429 yjfa orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 383 of 400 of the completegenome.) (nt:f89; 100 pct identical to yjfa_ecoli sw: p08339; cg) (le:10424) (re:10693) (di:complement) AE000493 AE000493 g1790669 Escherichia coli 562 -11536755 5000693954 (de:(ecoli_4106) (pn:hypothetical 10) (gn:yjfa) (gtcfc:13.7:14.1) (ec:) (yjfa_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4106 ECOLI_4106 Escherichia coli 562 10055441

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874954	13800	35956	2097	698

Description

6500732898 chps:chpbi:b4224 pemi-like protein 2 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4224 b4224 Escherichia coli 562 -11536756 131117 chps cell growth regulatory protein chpbi:pemi-like protein 2 (cl:maze protein) (db:pir1.dat) (mp:99.5 min) QQECR8 S56450 Escherichia coli 562 -11536756 237430 (sr:escherichia coli k12 dna, clone par6-2) (db:genpept-bct1) (de:e.coli k12 iler gene encoding the ile repressor, and orf83 encodinga protein of unknown function, complete cds.) (nt:orf83 protein) (le:84) (re:341) (di:complement) ECOILER M14018 g146448 Escherichia coli 562 -11536756 7500953623 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:o83 of genbank accession number m14018) (le:139273) (re:139530) (di:direct) ECOUW93 U14003 g537066 Escherichia coli 562 -11536756 234842 chps suppressor of inhibitory function of chpb (fn:phenotype; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 384 of 400 of the completegenome.) (nt:o85; 100 pct identical to 83 amino acids) (le:128) (re:385) (di:direct) AE000494 AE000494 g1790671 Escherichia coli 562 -11536756 5000693955 (de:(ecoli_4107) (pn:suppressor of inhibitory function of chpb, pemi-like, autoregulated) (gn:chps) (gtcfc:13.7:14.1) (ec:) (chps_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4107 ECOLI_4107 Escherichia coli 562 10068036

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501874956	13801	35957	738	245

Description

6500732899 chpb:chpbk:b4225 pemk-like protein 2 (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4225 b4225 Escherichia coli 562 -11536757 64413 chpb:chpbk (de:pemk-like protein 2) (db:swissprot) CHPB_ECOLI P33647 ESCHERICHIA COLI 562 -11536757 162811 chpb cell growth regulatory protein chpbk:pemk-like protein 2 (db:pir2.dat) D49339 D49339 Escherichia coli 562 -11536757 237431 chpb chpbk (sr:escherichia coli (strain:k-12) dna) (db:genpept-bct1) (de:e. coli chpb gene for chpbi and chpbk, complete cds.) (le:396) (re:746) (di:direct) ECOCHPB D16451 g506196 Escherichia coli 562 -11536757 7500878697 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o116) (le:139524) (re:139874) (di:direct) ECOUW93 U14003 g537067 Escherichia coli 562 -11536757 233997 chpb probable growth inhibitor:pemk-like (fn:putative factor; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 384 of 400 of the completegenome.) (nt:o116; 100 pct identical amino acid sequence and) (le:379) (re:729) (di:direct) AE000494 AE000494 g1790672 Escherichia coli 562 -11536757 5000693956 (de:(ecoli_4108) (pn:probable growth inhibitor, pemk-like, autoregulated) (gn:chpb) (gtcfc:13.7:14.1) (ec:) (chpb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4108 ECOLI_4108 Escherichia coli 562 10007076

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501874989	13802	35958	1044	347

Description

6500732900 ytfq:b4227 o318:32.1 kd protein in ppa-fbp intergenic region precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4227 b4227 Escherichia coli 562 -11536758 116415 ytfq (de:abc transporter periplasmic binding protein ytfq precursor) (db:swissprot) YTFQ_ECOLI P39325 ESCHERICHIA COLI 562 -11536758 163805 ytfq hypothetical 32.1k protein ppa-fbp intergenic region precursor o318 (db:pir2.dat) S56453 S56453 Escherichia coli 562 -11536758 7500952771 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o318) (le:140794) (re:141750) (di:direct) ECOUW93 U14003 g537069 Escherichia coli 562 -11536758 237433 ytfq putative lacI-type transcriptional regulator (fn:putative regulator; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 384 of 400 of the completegenome.) (nt:o318; 100 pct identical amino acid sequence and) (le:1649) (re:2605) (di:direct) AE000494 AE000494 g1790674 Escherichia coli 562 -11536758 5000693957 (de:(ecoli_4110) (pn:32) (gn:ytfq) (gtcfc:13.7:14.1) (ec:) (ytfq_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4110 ECOLI_4110 Escherichia coli 562 10058140

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875007	13803	35959	1128	375

Description

6500732901 nrdg:b4237 anaerobic ribonucleoside-triphosphate reductase activating pr:anaerobic ribonucleoside-triphosphate reductase activating protein (gtcfc:4.3) (ec:1.97.1.-) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4237 b4237 Escherichia coli 562 -11536759 237443 nrdg (ec:1.97.1.-) (de:(ec 1.97.1.-)) (db:swissprot) NRDG_ECOLI P39329 ESCHERICHIA COLI 562 -11536759 162734 nrdg anaerobic ribonucleotide reductase activase (ec:1.97.1.-) (db:pir2.dat) A55692 A55692 Escherichia coli 562 -11536759 5000693964 nrdg activase for anaerobic ribonucleoside (db:genpept-bct1) (de:e.coli nrdg gene for activase.) (le:193) (re:657) (di:direct) ECNRDGACT Z46865 g619866 Escherichia coli 562 -11536759 7500886576 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f154) (le:150729) (re:151193) (di:complement) ECOUW93 U14003 g537079 Escherichia coli 562 -11536759 233506 nrdg anaerobic ribonucleotide reductase activating (fn:enzyme; central intermediary metabolism:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 385 of 400 of the completegenome.) (nt:f154; 100 pct identical amino acid sequence and) (le:542) (re:1006) (di:complement) AE000495 AE000495 g1790685 Escherichia coli 562 -11536759 86497 nrdg (ec:1.97.1.-) (de:(ec 1.97.1.-)) (db:swissprot) NRDG_ECOLI P39329 ESCHERICHIA COLI 562 -11536759

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875013	13804	35960	429	142

Description

6500732902 yjgf:b4243 13.5 kd protein in mgta-pyri intergenic region (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4243 b4243 Escherichia coli 562 -11536760 163563 yjgf hypothetical 13.5k protein mgta-pyri intergenic region:hypothetical protein f141 (cl:hypothetical protein hi0719) (db:pir2.dat) S56469 S56469 Escherichia coli 562 -11536760 7500955816 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f141) (le:161356) (re:161781) (di:complement) ECOUW93 U14003 g537085 Escherichia coli 562 -11536760 237449 yjgf orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 385 of 400 of the completegenome.) (nt:f141; 100 pct identical to 127 amino acids of) (le:11169) (re:11594) (di:complement) AE000495 AE000495 g1790691 Escherichia coli 562 -11536760 5000693965 (de:(ecoli_4126) (pn:13) (gn:yjgf) (gtcfc:13.7:14.1) (ec:)(yjgf_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4126 ECOLI_4126 Escherichia coli 562 10087003

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875014	13805	35961	456	151

Description

6500732903 intb:b4271 prophage p4 integrase (gtcfc:13.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4271 b4271 Escherichia coli 562 -11536761 79553 intb (de:prophage p4 integrase (int(p4))) (db:swissprot) INTB_ECOLI P39347 ESCHERICHIA COLI 562 -11536761 157211 intb prophage p4 integrase:hypothetical protein o396 (cl:satellite phage p4 integrase) (db:pir2.dat) S56496 S56496 Escherichia coli 562 -11536761 7500884179 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_o396) (le:187585) (re:188775) (di:direct) ECOUW93 U14003 g537112 Escherichia coli 562 -11536761 237476 intb prophage p4 integrase (fn:is, phage, tn; phage-related functions and) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 388 of 400 of the completegenome.) (nt:o396; 100 pct identical intb_ecoli sw: p39347) (le:452) (re:1642) (di:direct) AE000498 AE000498 g1790722 Escherichia coli 562 -11536761 5000693985 (de:(ecoli_4154) (pn:prophage p4 integrase) (gn:intb) (gtcfc:13.7:14.1) (ec:)(intb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4154 ECOLI_4154 Escherichia coli 562 10021870

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875026	13806	35962	816	271

Description

6500732904 insa_7:b4294 insertion element is1f protein insa (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4294 b4294 Escherichia coli 562 -11536762 237499 insa:b4294 (de:insertion element is1f protein insa) (db:swissprot) ISA2_ECOLI P19767 ESCHERICHIA COLI 562 -11536762 157303 insa_7 insa protein (cl:insa protein) (db:pir2.dat) JN0140 JN0140 Escherichia coli 562 -11536762 5000693998 (db:genpept-bct1) (de:escherichia coli dna for insertion sequence is1f.) (nt:insa peptide (aa 1-91)) (le:110) (re:385) (di:direct) ECIS1F X52538 g581117 Escherichia coli 562 -11536762 7500884278 insa insa peptide (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:209361) (re:209636) (di:direct) ECOUW93 U14003 g537135 Escherichia coli 562 -11536762 233244 insa_7 is1 protein insa (fn:is, phage, tn; transposon-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 390 of 400 of the completegenome.) (nt:o91; 100 pct identical amino acid sequence and) (le:1837) (re:2112) (di:direct) AE000500 AE000500 g1790747 Escherichia coli 562 -11536762 7502852318 (db:genpept) (de:escherichia coli dna for insertion sequence is1f.) (nt:insa peptide (aa 1-91)) (le:110) (re:382) (di:direct) ECIS1F X52538 g581117 Escherichia coli 562 -11536762 79955 insa:b4294 (de:insertion element is1f protein insa) (db:swissprot) ISA2_ECOLI P19767 ESCHERICHIA COLI 562 -11536762

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875049	13807	35963	3018	1006

Description

6500732905 gntp:b4321 high-affinity gluconate transporter:gluconate permease 3:gnt-iii system (gtcfc:12.6:11.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4321 b4321 Escherichia coli 562 -11536763 163668 gntp gluconate permease 3 (cl:d-serine permease) (db:pir2.dat) S56546 S56546 Escherichia coli 562 -11536763 7500959746 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f477) (le:240785) (re:242128) (di:complement) ECOUW93 U14003 g537162 Escherichia coli 562 -11536763 237526 gntp gluconate transport system permease 3 (fn:transport; transport of small molecules:) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 392 of 400 of the completegenome.) (nt:f477; 99 pct identical amino acid sequence and) (le:9748) (re:11091) (di:complement) AE000502 AE000502 g1790776 Escherichia coli 562 -11536763 5000694016 (de:(ecoli_4204) (pn:gluconate permease 3) (gn:gntp) (gtcfc:13.7:14.1) (ec:)) (gntp_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4204 ECOLI_4204 Escherichia coli 562 10087017

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875050	13808	35964	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875063	13809	35965	1392	463

Description

6500732906 iada:b4328 isoaspartyl dipeptidase (gtcfc:10.11:5.2) (ec:3.4.19.5) (keggfc:14.1) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4328 b4328 Escherichia coli 562 -11536764 78563 iada (ec:3.4.19.-) (de:isoaspartyl dipeptidase,) (db:swissprot) IADA_ECOLI P39377 ESCHERICHIA COLI 562 -11536764 163938 iada isoaspartyl dipeptidase (ec:3.4.19.-) (db:pir2.dat) B55889 B55889 Escherichia coli 562 -11536764 238678 (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:orf_f390a) (le:249186) (re:250358) (di:complement) ECOUW93 U14003 g537169 Escherichia coli 562 -11536764 237533 iada isoaspartyl dipeptidase (fn:enzyme; degradation of proteins, peptides,) (db:genpept-bct2) (ec:3.4.19.5) (de:escherichia coli k-12 mg1655 section 393 of 400 of the completegenome.) (nt:f390a; 100 pct identical amino acid sequence and) (le:6894) (re:8066) (di:complement) AE000503 AE000503 g1790784 Escherichia coli 562 -11536764 7500883769 iada isoaspartyl dipeptidase (db:genpept-bct2) (de:escherichia coli (orf1) and isoaspartyl dipeptidase (iada) genes,complete cds, and (orf2) gene, partial cds.) (nt:contains putative zinc binding motif -pgfidqhvhl-) (le:1018) (re:2190) (di:direct) ECU15029 U15029 g640031 Escherichia coli 562 -11536764 5000694020 (de:(ecoli_4211) (pn:isoaspartyl dipeptidase) (gn:iada) (gtcfc:13.7:14.1) (ec:3.4.19.5) (iada_ecoli) (keggfc:11.1) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4211 ECOLI_4211 Escherichia coli 562 10020902

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875064	13810	35966	753	250

Description

6500732907 mcrd:b4344 mcrd protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4344 b4344 Escherichia coli 562 -11536765 164047 mcrd mcrd protein (db:pir2.dat) S56570 S56570 Escherichia coli 562 -11536765 237550 mcrd (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:apparent frameshift in genbank accession number) (le:266426) (re:267688) (di:direct) ECOUW93 U14003 g537186 Escherichia coli 562 -11536765 7500960379 mcrd inhibits mcre 5-methylcytosine restriction (fn:regulator; degradation of dna) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 395 of 400 of the completegenome.) (nt:o420; 100 pct identical amino acid sequence and) (le:1604) (re:2866) (di:direct) AE000505 AE000505 g1790803 Escherichia coli 562 -11536765 83252 mcrd_ecoli (de:mcrd protein.) P27301 P27301 Escherichia coli 562 -11536765 5000694037 (de:(ecoli_4228) (pn:inhibits mcre 5-methylcytosine restriction system) (gn:mcrd) (gtcfc:13.7:14.1) (ec:) (mcrd_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4228 ECOLI_4228 Escherichia coli 562 10025471

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875065	13811	35967	450	149

Description

6500732908 yjjb:b4363 p14 protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4363 b4363 Escherichia coli 562 -11536766 154686 yjjb primosomal operon 14k protein:p14 protein (cl:primosomal operon 14k protein) (db:pir1.dat) (mp:99 min) RMEC14 S56590 Escherichia coli 562 -11536766 7500953657 yjjb p14 protein (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:292456) (re:292782) (di:complement) ECOUW93 U14003 g537206 Escherichia coli 562 -11536766 237571 yjjb orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 397 of 400 of the completegenome.) (nt:f108) (le:4573) (re:4899) (di:complement) AE000507 AE000507 g1790825 Escherichia coli 562 -11536766 5000694047 (de:(ecoli_4248) (pn:14) (gn:yjjb) (gtcfc:13.7:14.1) (ec:) (yjjb_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4248 ECOLI_4248 Escherichia coli 562 10081682

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875082	13812	35968	423	141

Description

6500732909 smp:b4387 smp protein precursor:protein precursor (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4387 b4387 Escherichia coli 562 -11536767 7500891762 smp (de:smp protein precursor) (db:swissprot) SMP_ECOLI P18838 ESCHERICHIA COLI 562 -11536767 164631 smp smp protein (db:pir2.dat) (mp:100 min) A26227 A26227 Escherichia coli 562 -11536767 237592 smp (sr:escherichia coli dna) (db:genpept-bct1) (de:escherichia coli smp gene, complete cds.) (nt:orf) (le:141) (re:785) (di:direct) ECOSMP M30784 g436177 Escherichia coli 562 -11536767 238275 smp (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:314977) (re:315621) (di:complement) ECOUW93 U14003 g537227 Escherichia coli 562 -11536767 5000694059 smp smp protein (db:genpept-bct1) (de:e.coli phosphoserine phosphatase (serb) and smp protein genes, complete cds., and orf, 5' end.) (le:1135) (re:1779) (di:direct) ECSMP X03046 g432633 Escherichia coli 562 -11536767 236004 smp orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 398 of 400 of the completegenome.) (nt:f214; 100 pct identical amino acid sequence and) (le:14793) (re:15437) (di:complement) AE000508 AE000508 g1790847 Escherichia coli 562 -11536767 98691 smp (de:smp protein precursor) (db:swissprot) SMP_ECOLI P18838 ESCHERICHIA COLI 562 -11536767

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875105	13813	35969	1197	398

Description

6500732910 yjkk:b4391 abc transporter in nadr-slt intergenic region (gtcfc:12.6) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4391 b4391 Escherichia coli 562 -11536768 7000689374 yjkk abc transporter in nadr-slt intergenic region (cl:unassigned atp-binding cassette proteins:atp-binding cassette homology) (db:pir2.dat) F65254 F65254 Escherichia coli 562 -11536768 7500955267 yjkk putative atp-binding component of a transport (fn:putative transport; not classified) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 399 of 400 of the completegenome.) (nt:f555; sequence change shortens and) (le:4043) (re:5710) (di:complement) AE000509 AE000509 g2367384 Escherichia coli 562 -11536768

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875107	13814	35970	606	201
<u>Description</u>				
6500732911 crea:b4397 crea protein (gtcfc:14.3) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4397 b4397 Escherichia coli 562 -11536769 66383 crea (de:crea protein) (db:swissprot) CREA_ECOLI P08367 ESCHERICHIA COLI 562 -11536769 131473 crea crea protein (cl:crea protein) (db:pir1.dat) (mp:100 min) QQECF1 A25038 Escherichia coli 562 -11536769 237602 (sr:escherichia coli (strain klf125/kl181) dna) (db:genpept-bct1) (de:e.coli (clone pthr34) phom operon, containing phom gene (positveregulation for pho regulon) and three unidentified genes.) (nt:17 kd protein) (le:580) (re:1053) (di:direct) ECOPHOM M13608 g147249 Escherichia coli 562 -11536769 7500879392 crea (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (le:326354) (re:326827) (di:direct) ECOUW93 U14003 g537237 Escherichia coli 562 -11536769 235474 crea orf:hypothetical protein (fn:orf; unknown) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 400 of 400 of the completegenome.) (nt:ol57; 100 pct identical amino acid sequence and) (le:178) (re:651) (di:direct) AE000510 AE000510 g1790859 Escherichia coli 562 -11536769 5000694063 (de:(ecoli_4279) (pn:crea protein) (gn:crea) (gtcfc:13.7:14.1) (ec:) (crea_ecoli) (keggfc:11.2) (rileyfc:5.7.0) (db:gtc-escherichia coli)) ECOLI_4279 ECOLI_4279 Escherichia coli 562 10009005				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875112	13815	35971	471	156
<u>Description</u>				
6500732912 cred:cet:b4400 inner membrane protein cred (gtcfc:14.3:11.1) (keggfc:14.2) (rileyfc:5.8.0) (db:gtc-escherichia coli) b4400 b4400 Escherichia coli 562 -11536770 235477 cred:cet (de:inner membrane protein cred) (db:swissprot) CRED_ECOLI P08369 ESCHERICHIA COLI 562 -11536770 135217 cred:cet inner membrane protein cred:cred protein (cl:cet protein) (db:pir1.dat) (mp:100 min) BVECCT D25038 Escherichia coli 562 -11536770 5000694064 cet protein aa 1-450 (db:genpept-bct1) (de:e. coli cet gene and phom gene 3'-terminal region.) (le:344) (re:1696) (di:direct) ECCET Y00538 g41104 Escherichia coli 562 -11536770 237605 (sr:escherichia coli (strain klf125/kl181) dna) (db:genpept-bct1) (de:e.coli (clone pthr34) phom operon, containing phom gene (positveregulation for pho regulon) and three unidentified genes.) (nt:orf4) (le:3237) (re:4589) (di:direct) ECOPHOM M13608 g147252 Escherichia coli 562 -11536770 7500879396 cred (db:genpept-bct1) (de:escherichia coli k-12 chromosomal region from 92.8 to 00.1 minutes.) (nt:alternate gene name cet; cg site no. 929) (le:329011) (re:330363) (di:direct) ECOUW93 U14003 g537240 Escherichia coli 562 -11536770 232514 cred tolerance to colicin e2 (fn:putative membrane; colicin-related functions) (db:genpept-bct2) (de:escherichia coli k-12 mg1655 section 400 of 400 of the completegenome.) (nt:o450; 100 pct identical to cred_ecoli sw: p08369;) (le:2835) (re:4187) (di:direct) AE000510 AE000510 g1790862 Escherichia coli 562 -11536770 66397 cred:cet (de:inner membrane protein cred) (db:swissprot) CRED_ECOLI P08369 ESCHERICHIA COLI 562 -11536770				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875113	13816	35972	831	277

Description

6500732913 acca:hi0406 acetyl-coenzyme a carboxylase:acetyl-coenzyme a carboxylase carboxyl transferase subunit alpha (gtcfc:1.10:1.8:3.1:3.2) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0406 HI0406 Haemophilus influenzae 727 -11536771 57993 acca:hi0406 (ec:6.4.1.2) (de:(ec 6.4.1.2)) (db:swissprot) ACCA_HAEIN P43872 HAEMOPHILUS INFLUENZAE 727 -11536771 142445 acetyl-coa carboxylase::carboxyltransferase alpha chain (cl:acetyl-coa carboxylase, carboxyltransferase alpha chain) (ec:6.4.1.2) (db:pir2.dat) I64065 I64065 Haemophilus influenzae 727 -11536771 7500876286 hi0406 acetyl-coa carboxylase:carboxyl transferase (db:genpept-bct1) (de:haemophilus influenzae rd section 39 of 163 of the complete genome.) (nt:similar to gb:m96394 sp:p30867 pid:1208956) (le:67) (re:1014) (di:complement) U32724 U32724 g1573379 Haemophilus influenzae Rd 71421 -11536771 5000694087 (de:(hi0406) (pn:acetyl-coenzyme a carboxylase carboxyl transferase subunit alpha:acetyl-coenzyme a carboxylase:acca) (gn:acca) (gtcfc:1.10:1.8:3.1) (ec:6.4.1.2) (acca_haein) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-haemophilu) HI0406 HI0406 Haemophilus influenzae 727 10000773

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875119	13817	35973	618	205

Description

5000694088 thl:thi:hi0771 acetyl coenzyme a acetyltransferase:thiolase:fada:acetyl-coa acetyltransferase:acetoacetyl-coa thiolase (gtcfc:1.10:1.11:1.8:3.1:3.2:3.3:5.14:5.9) (ec:2.3.1.9) (keggfc:1.8:1.10:1.11:3.1:3.2:3.3:5.9:5.14) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0771 HI0771 Haemophilus influenzae 727 -11536772 101349 atob:thl:thi:hi0771 (ec:2.3.1.9) (de:acetyl-coa acetyltransferase, (acetoacetyl-coa thiolase)) (db:swissprot) ATOB_HAEIN P44873 HAEMOPHILUS INFLUENZAE 727 -11536772 7500877342 hi0771 acetyl-coa acetyltransferase atob (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p76461 pid:1736879) (le:78) (re:1259) (di:complement) U32761 U32761 g1573781 Haemophilus influenzae Rd 71421 -11536772 6500732914 thl:thi acetyl coenzyme a acetyltransferase:thiolase:fada:acetyl-coa acetyltransferase:acetoacetyl-coa thiolase (gtcfc:1.10:1.11:1.8:3.1:3.2:3.3:5.14:5.9) (ec:2.3.1.9) (keggfc:1.8:1.10:1.11:3.1:3.2:3.3:5.9:5.14) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0771 HI0771 Haemophilus influenzae 727 -11536772

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875122	13818	35974	1848	615

Description

6500732915 atoa:hi0773 acetyl-coa:acetoacetyl-coa transferase beta subunit (gtcfc:1.10:1.11) (ec:2.8.3.-) (keggfc:1.10:1.11) (db:gtc-haemophilus influenzae) HI0773 HI0773 Haemophilus influenzae 727 -11536773 60603 atoa:hi0773 (ec:2.8.3.8) (de:coa:acetoacetate coa transferase)) (db:swissprot) ATOA_HAEIN P44874 HAEMOPHILUS INFLUENZAE 727 -11536773 139420 butyrate--acetoacetate coa-transferase:large chain:butyrate--acetoacetate coa-transferase beta chain:protein hi0773 (cl:3-oxoadipate coa-transferase beta chain:3-oxoadipate coa-transferase beta chain homology) (ec:2.8.3.9) (db:pir2.dat) G64158 G64158 Haemophilus influenzae 727 -11536773 7500877341 hi0773 acetate coa-transferase:beta subunit atoa (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p76459 pid:1736877) (le:2614) (re:3285) (di:complement) U32761 U32761 g1573783 Haemophilus influenzae Rd 71421 -11536773 5000694098 (de:(hi0773) (pn:acetyl-coa:acetoacetyl-coa transferase beta subunit) (gn:atoa) (gtcfc:1.11) (ec:2.8.3.-) (atoa_haein) (keggfc:1.11) (db:gtc-haemophilus influenzae)) HI0773 HI0773 Haemophilus influenzae 727 10003329

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875123	13819	35975	843	280

Description

6500732916 atod:hi0774 butyrate-acetoacetate coenzyme a transferase subunit a:ctfa:acetyl-coa:acetoacetyl-coa transferase alpha subunit (gtcfc:1.10:1.11:2.2) (ec:2.8.3.-) (keggfc:1.10:1.11) (tigrfc:6.7) (db:gtc-haemophilus influenzae) HI0774 HI0774 Haemophilus influenzae 727 -11536774 60605 atod:hi0774 (ec:2.8.3.8) (de:coa:acetoacetate coa transferase)) (db:swissprot) ATOD_HAEIN P44875 HAEMOPHILUS INFLUENZAE 727 -11536774 139415 butyrate--acetoacetate coa-transferase:small chain (cl:3-oxoadipate coa-transferase alpha chain:3-oxoadipate coa-transferase alpha chain homology) (ec:2.8.3.9) (db:pir2.dat) B64092 B64092 Haemophilus influenzae 727 -11536774 7500877343 hi0774 acetate coa-transferase:alpha subunit (db:genpept-bct1) (de:haemophilus influenzae rd section 76 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p76458 pid:1736876) (le:3296) (re:3949) (di:complement) U32761 U32761 g1573784 Haemophilus influenzae Rd 71421 -11536774 5000694099 (de:(hi0774) (pn:acetyl-coa:acetoacetyl-coa transferase alpha subunit:butyrate-acetoacetate coenzyme a transferase subunit a:ctfa) (gn:atod) (gtcfc:1.11) (ec:2.8.3.-) (atod_haein) (keggfc:1.11) (tigrfc:6.7) (db:gtc-haemophilus i) HI0774 HI0774 Haemophilus influenzae 727 10003331

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875124	13820	35976	363	120

Description

5000694089 accb:fabe:hi0971 biotin carboxyl carrier protein:fabe:biotin carboxyl carrier protein of acetyl-coa carboxylase:bccp (gtcfc:1.10:1.8:3.1:3.2) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0971 HI0971 Haemophilus influenzae 727 -11536775 61449 accb:fabe:hi0971 (ec:6.4.1.2) (de:(ec 6.4.1.2) (bccp)) (db:swissprot) BCCP_HAEIN P43874 HAEMOPHILUS INFLUENZAE 727 -11536775 152979 acetyl-coa carboxylase::biotin carboxyl carrier protein (cl:biotin carboxyl carrier protein:lipoyl/biotin-binding homology) (ec:6.4.1.2) (db:pir2.dat) E64105 E64105 Haemophilus influenzae 727 -11536775 7500877707 hi0971 acetyl-coa carboxylase:biotin carboxyl carrier (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the complete genome.) (nt:similar to gb:m32214 sp:p02905 gb:m83198 gb:x14825) (le:107) (re:574) (di:direct) U32778 U32778 g1573998 Haemophilus influenzae Rd 71421 -11536775 6500732917 accb:fabe biotin carboxyl carrier protein:fabe:biotin carboxyl carrier protein of acetyl-coa carboxylase:bccp (gtcfc:1.10:1.8:3.1:3.2) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0971 HI0971 Haemophilus influenzae 727 -11536775

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875125	13821	35977	327	108

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875133	13822	35978	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875157	13823	35979	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875171	13824	35980	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875172	13825	35981	1017	338

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875174	13826	35982	345	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875189	13827	35983	423	140

Description

6500732918 accc:hi0972 biotin carboxylase:a subunit of acetyl-coa carboxylase:acc (gtcfc:1.10:1.8:3.1:3.2) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0972 HI0972 Haemophilus influenzae 727 -11536776 57999 accc:hi0972 (ec:6.3.4.14:6.4.1.2) (de:carboxylase,) (acc)) (db:swissprot) ACCC_HAEIN P43873 HAEMOPHILUS INFLUENZAE 727 -11536776 142443 biotin carboxylase (cl:biotin carboxylase:biotin carboxylase homology) (ec:6.3.4.14) (db:pir2.dat) F64105 F64105 Haemophilus influenzae 727 -11536776 7500876291 hi0972 acetyl-coa carboxylase:biotin carboxylase (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the complete genome.) (nt:similar to gb:m79446 sp:p24182 gb:m83198 pid:145175) (le:749) (re:2095) (di:direct) U32778 U32778 g1573999 Haemophilus influenzae Rd 71421 -11536776 5000694090 (de:(hi0972) (pn:a subunit of acetyl-coa carboxylase :acc:biotin carboxylase:accc) (gn:accc) (gtcfc:1.10:1.8:3.1) (ec:6.3.4.14) (accc_haein) (keggfc:1.8:1.10:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae)) HI0972 HI0972 Haemophilus influenzae 727 10000779

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875193	13828	35984	297	98

Description

6500732919 succ:hi1196 succinyl-coa synthetase beta-subunit:succinyl-coa synthetase beta chain (gtcfc:1.10:1.12:1.2:2.5) (ec:6.2.1.5) (keggfc:1.2:1.10:1.12:2.4) (tigrfc:6.13) (db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:carbohydrate metabolism-cit... HI1196 HI1196 Haemophilus influenzae 727 -11536777 99801 succ:hi1196 (ec:6.2.1.5) (de:succinyl-coa synthetase beta chain, (scs-beta)) (db:swissprot) SUCC_HAEIN P45101 HAEMOPHILUS INFLUENZAE 727 -11536777 142333 succinate--coa ligase adp-forming:beta chain (cl:succinate--coa ligase (adp-forming) beta chain) (ec:6.2.1.5) (db:pir2.dat) C64189 C64189 Haemophilus influenzae 727 -11536777 7500892230 hi1196 succinyl-coa synthetase:beta subunit succ (db:genpept-bct1) (de:haemophilus influenzae rd section 114 of 163 of the completegenome.) (nt:similar to gb:j01619 sp:p07460 pid:146203 gb:u00096) (le:2286) (re:3455) (di:direct) U32799 U32799 g1574125 Haemophilus influenzae Rd 71421 -11536777 5000694091 (de:(hi1196) (pn:succinyl-coa synthetase beta chain:succinyl-coa synthetase beta-subunit:succ) (gn:succ) (gtcfc:1.10:1.12:1.2:2.5) (ec:6.2.1.5) (succ_haein) (keggfc:1.2:1.10:1.12:2.4) (tigrfc:6.13) (db:gtc-haemophilus influenzae) HI1196 HI1196 Haemophilus influenzae 727 10041656

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875196	13829	35985	2019	672

Description

6500732920 succ:hi1197 succinyl-coa synthetase alpha-subunit:succinyl-coa synthetase alpha chain (gtcfc:1.10:1.12:1.2:2.5) (ec:6.2.1.5) (keggfc:1.2:1.10:1.12:2.4) (tigrfc:6.13) (db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-propanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:carbohydrate metabolism-cit... HI1197 HI1197 Haemophilus influenzae 727 -11536778 99807 succ:hi1197 (ec:6.2.1.5) (de:succinyl-coa synthetase alpha chain, (scs-alpha)) (db:swissprot) SUCD_HAEIN P45102 HAEMOPHILUS INFLUENZAE 727 -11536778 142330 succinate--coa ligase adp-forming:alpha chain (cl:succinate--coa ligase (adp-forming) alpha chain) (ec:6.2.1.5) (db:pir2.dat) D64189 D64189 Haemophilus influenzae 727 -11536778 7500892232 hi1197 succinyl-coa synthetase:alpha subunit succd (db:genpept-bct1) (de:haemophilus influenzae rd section 114 of 163 of the completegenome.) (nt:similar to gb:j01619 sp:p07459 pid:146204) (le:3455) (re:4336) (di:direct) U32799 U32799 g1574126 Haemophilus influenzae Rd 71421 -11536778 5000694092 (de:(hi1197) (pn:succinyl-coa synthetase alpha chain:succinyl-coa synthetase alpha-subunit:succd) (gn:succd) (gtcfc:1.10:1.12:1.2:2.5) (ec:6.2.1.5) (succ_haein) (keggfc:1.2:1.10:1.12:2.4) (tigrfc:6.13) (db:gtc-haemophilus influenz) HI1197 HI1197 Haemophilus influenzae 727 10041662

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875200	13830	35986	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875205	13831	35987	621	206

Description

6500732921 acka:hi1204 acetate kinase:acetokinase (gtcfc:1.10:1.8:5.16) (ec:2.7.2.1) (keggfc:1.8:1.10) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI1204 HI1204 Haemophilus influenzae 727 -11536779 58186 acka:hi1204 (ec:2.7.2.1) (de:acetate kinase, (acetokinase)) (db:swissprot) ACKA_HAEIN P44406 HAEMOPHILUS INFLUENZAE 727 -11536779 138941 acetate kinase (cl:acetate kinase) (ec:2.7.2.1) (db:pir2.dat) G64189 G64189 Haemophilus influenzae 727 -11536779 7500876318 hi1204 acetate kinase acka (db:genpept-bct1) (de:haemophilus influenzae rd section 115 of 163 of the completengenome.) (nt:similar to gb:m22956 sp:p15046 pid:145171 gb:u00096) (le:64) (re:1269) (di:complement) U32800 U32800 g1574134 Haemophilus influenzae Rd 71421 -11536779 5000694093 (de:(hi1204) (pn:acetokinase:acetate kinase:acka) (gn:acka) (gtcfc:1.10:1.8) (ec:2.7.2.1) (acka_haein) (keggfc:1.8:1.10) (tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI1204 HI1204 Haemophilus influenzae 727 10000966

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875219	13832	35988	624	207

Description

6500732922 accd:hi1260 folylpolyglutamate-dihydrofolate synthetase expression regulator:acetyl-coenzyme a carboxylase carboxyl transferase subunit beta (gtcfc:1.10:1.8:3.1:12.13) (ec:6.4.1.2) (keggfc:1.8:1.10:3.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1260 HI1260 Haemophilus influenzae 727 -11536780 58006 accd:hi1260 (ec:6.4.1.2) (de:(ec 6.4.1.2)) (db:swissprot) ACCD_HAEIN P43778 HAEMOPHILUS INFLUENZAE 727 -11536780 126066 acetyl-coa carboxylase:carboxyltransferase beta chain (cl:acetyl-coa carboxylase, carboxyltransferase beta chain) (ec:6.4.1.2) (db:pir1.dat) B64113 B64113 Haemophilus influenzae 727 -11536780 7500876297 hi1260 acetyl-coa carboxylase carboxyl transferase (db:genpept-bct1) (de:haemophilus influenzae rd section 121 of 163 of the completengenome.) (nt:similar to gb:j02808 sp:p08193 gb:m32445 pid:146008) (le:127) (re:1017) (di:direct) U32806 U32806 g1574718 Haemophilus influenzae Rd 71421 -11536780 5000694094 (de:(hi1260) (pn:acetyl-coenzyme a carboxylase carboxyl transferase subunit beta:folylpolyglutamate-dihydrofolate synthetase expression regulator:accd) (gn:accd) (gtcfc:1.10:1.8:3.1) (ec:6.4.1.2) (accd_haein) (keggfc:1.8:1.10:3.1) HI1260 HI1260 Haemophilus influenzae 727 10000786

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875222	13833	35989	789	262

Description

5000694067 gapa:gapdh:hi0001 glyceraldehyde-3-phosphate dehydrogenase:glyceraldehyde 3-phosphate dehydrogenase:gapdh (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (tigrfc:6.9) (db:gtc-haemophilus influenzae) HI0001 HI0001 Haemophilus influenzae 727 -11536781 72718 gapa:gapdh:hi0001 (ec:1.2.1.12) (de:glyceraldehyde 3-phosphate dehydrogenase, (gapdh)) (db:swissprot) G3P_HAEIN P44304 HAEMOPHILUS INFLUENZAE 727 -11536781 136497 glyceraldehyde-3-phosphate dehydrogenase (cl:glyceraldehyde-3-phosphate dehydrogenase) (ec:1.2.1.12) (db:pir2.dat) G64041 G64041 Haemophilus influenzae 727 -11536781 7500881970 hi0001 glyceraldehyde-3-phosphate dehydrogenase (db:genpept-bct1) (de:haemophilus influenzae rd section 1 of 163 of the complete genome.) (nt:similar to gb:x02662 sp:p06977 gb:m66870 gb:m66871) (le:2) (re:1021) (di:direct) U32686 U32686 g3212176 Haemophilus influenzae Rd 71421 -11536781 6500732923 gapa:gapdh glyceraldehyde-3-phosphate dehydrogenase:glyceraldehyde 3-phosphate dehydrogenase:gapdh (gtcfc:1.1:6.14:6.8) (ec:1.2.1.12) (keggfc:1.1:6.7) (tigrfc:6.9) (db:gtc-haemophilus influenzae) HI0001 HI0001 Haemophilus influenzae 727 -11536781

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875230	13834	35990	1881	626

Description

6500732924 adhc:gd-faldh:hi0185 putative alcohol dehydrogenase class iii:glutathione-dependent formaldehyde dehydrogenase:fdh:faldh (gtcfc:1.1:6.16) (keggfc:1.1:1.8:2.2:3.2:3.5:5.12:8.1) (tigrfc:6.7) (db:gtc-haemophilus influenzae) HI0185 HI0185 Haemophilus influenzae 727 -11536782 58687 adhc:hi0185 (ec:1.1.1.1:1.2.1.1) (de:dependent formaldehyde dehydrogenase), (fdh) (faldh)) (db:swissprot) ADH3_HAEIN P44557 HAEMOPHILUS INFLUENZAE 727 -11536782 136043 alcohol dehydrogenase:hi0185:class iii alcohol dehydrogenase (cl:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology) (ec:1.1.1.1) (db:pir1.dat) H64052 H64052 Haemophilus influenzae 727 -11536782 7500876574 hi0185 alcohol dehydrogenase:class iii adhc (db:genpept-bct1) (de:haemophilus influenzae rd section 18 of 163 of the complete genome.) (nt:similar to sp:p25437 pid:887431 gb:u00096) (le:9600) (re:10736) (di:complement) U32703 U32703 g1573141 Haemophilus influenzae Rd 71421 -11536782 5000694068 (de:(hi0185) (pn:putative alcohol dehydrogenase class iii:fdh:faldh:glutathione-dependent formaldehyde dehydrogenase:gd-faldh) (gn:adhc) (gtcfc:1.1:1.8:2.2:3.2:3.5) (ec:1.1.1.1) (adh3_haein) (keggfc:1.1:1.8:2.2:3.2:3.5:5.12) (ti) HI0185 HI0185 Haemophilus influenzae 727 10001433

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875260	13835	35991	735	244

Description

6500732925 frua:hi0446 pts system:fructose-specific iibc
component:eiibc-fru:fructose-permease iibc component:phosphotransferase
enzyme ii:bc component:eii-fru (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2)
(ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1) (tigrfc:13.3) (db:gtc-haemophilus
influenzae) HI0446 HI0446 Haemophilus influenzae 727 -11536783 92154
frua:hi0446 (ec:2.7.1.69) (de:(ec 2.7.1.69) (eii-fru)) (db:swissprot)
PTFB_HAEIN P44714 HAEMOPHILUS INFLUENZAE 727 -11536783 166144
phosphotransferase system enzyme ii::fructose-specific
(cl:phosphotransferase system enzyme ii,
fructose-specific:phosphotransferase system mannitol-specific enzyme ii
factor iii homology) (ec:2.7.1.69) (db:pir2.dat) I64068 I64068 Haemophilus
influenzae 727 -11536783 7500888942 hi0446 pts system:fructose-specific
iibc component (db:genpept-bct1) (de:haemophilus influenzae rd section 42 of
163 of the complete genome.) (nt:similar to sp:p20966 gb:m23196 pid:405893)
(le:7700) (re:9370) (di:complement) U32727 U32727 g1573422 Haemophilus
influenzae Rd 71421 -11536783 5000694069 (de:(hi0446) (pn:pts system,
fructose-specific iibc component:eiibc-fru:phosphotransferase enzyme ii, bc
component:eii-fru:fructose-permease iibc component:frua) (gn:frua)
(gtcfc:1.1:1.5:1.6:7.1:7.2) (ec:2.7.1.69) (ptfb_haein) (k)) HI0446 HI0446
Haemophilus influenzae 727 10034188

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875279	13836	35992	567	188

Description

6500732926 frub:hi0448 fructose-permease iia/fpr component:pts
system:fructose-specific iia/fpr component:eiaa-fru:fructose-permease
iia/hpr component:phosphotransferase enzyme ii:a/hpr
component:phosphotransferase fpr protein:pseudo-hpr:eiii-fru:fructose pts
diphosphoryl transfer protein (gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69)
(keggfc:1.1:1.5:1.6:4.4:7.1) (tigrfc:13.3) (db:gtc-haemophilus influenzae)
HI0448 HI0448 Haemophilus influenzae 727 -11536784 92149 frub:hi0448
(ec:2.7.1.69) (de:hpr) (eiii-fru) (fructose pts diphosphoryl transfer
protein)) (db:swissprot) PTFA HAEIN P44715 HAEMOPHILUS INFLUENZAE 727
-11536784 166143 fructose phosphotransferase multiphosphoryltransfer
protein:fructose-permease iia/fpr component frub homolog (cl:fructose
phosphotransferase multiphosphoryltransfer protein
homolog:phosphotransferase system mannitol-specific enzyme ii factor iii
homology:phosphotransferase system phosphohistidine-containing protein
homology) (db:pir1.dat) B64069 B64069 Haemophilus influenzae 727 -11536784
7500888938 hi0448 pts system:fructose-specific iia/fpr component
(db:genpept-bct1) (de:haemophilus influenzae rd section 42 of 163 of the
complete genome.) (nt:similar to pid:619247 sp:p24217 gb:u00096) (le:10315)
(re:11814) (di:complement) U32727 U32727 g1573424 Haemophilus influenzae Rd
71421 -11536784 5000694070 (de:(hi0448) (pn:pts system, fructose-specific
iia:fructose-permease iia) (gn:frub) (gtcfc:1.1:1.5:1.6:7.1:7.2)
(ec:2.7.1.69) (ptfa_haein) (keggfc:1.1:1.5:1.6:4.4:7.1) (tigrfc:13.3)
(db:gtc-haemophilus influenzae)) HI0448 HI0448 Haemophilus influenzae 727
10034183

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875284	13837	35993	633	210

Description

6500732927 fba:hi0524 fructose-bisphosphate aldolase (gtcfc:1.1:1.3:1.5:2.4) (ec:4.1.2.13) (keggfc:1.1:1.3:1.5:2.3) (tigrfc:6.9) (db:gtc-haemophilus influenzae) HI0524 HI0524 Haemophilus influenzae 727 -11536785 59155 fbba:fba:hi0524 (ec:4.1.2.13) (de:fructose-bisphosphate aldolase,) (db:swissprot) ALF_HAEIN P44429 HAEMOPHILUS INFLUENZAE 727 -11536785 141651 fructose-bisphosphate aldolase:ii (cl:fructose-bisphosphate aldolase ii) (ec:4.1.2.13) (db:pir2.dat) C64074 C64074 Haemophilus influenzae 727 -11536785 7500876746 hi0524 fructose-bisphosphate aldolase fba (db:genpept-bct1) (de:haemophilus influenzae rd section 49 of 163 of the complete genome.) (nt:similar to gb:x14436 sp:p11604 pid:41423 pid:882454) (le:7943) (re:9022) (di:complement) U32734 U32734 g1573507 Haemophilus influenzae Rd 71421 -11536785 5000694071 (de:(hi0524) (pn:fructose-bisphosphate aldolase:fba) (gn:fba) (gtcfc:1.1:1.3:1.5:2.4) (ec:4.1.2.13) (alf_haein) (keggfc:1.1:1.3:1.5:2.3) (tigrfc:6.9) (db:gtc-haemophilus influenzae)) HI0524 HI0524 Haemophilus influenzae 727 10001894

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875288	13838	35994	1140	379

Description

6500732928 pgk:hi0525 phosphoglycerate kinase (gtcfc:1.1:2.4) (ec:2.7.2.3) (keggfc:1.1:2.3) (tigrfc:6.9) (db:gtc-haemophilus influenzae) HI0525 HI0525 Haemophilus influenzae 727 -11536786 138944 phosphoglycerate kinase (cl:phosphoglycerate kinase) (ec:2.7.2.3) (db:pir2.dat) D64074 D64074 Haemophilus influenzae 727 -11536786 7500954141 hi0525 phosphoglycerate kinase pgk (db:genpept-bct1) (de:haemophilus influenzae rd section 49 of 163 of the complete genome.) (nt:similar to sp:p11665 pid:41422 pid:882455 gb:u00096) (le:9133) (re:10293) (di:complement) U32734 U32734 g1573508 Haemophilus influenzae Rd 71421 -11536786 5000694072 (de:(hi0525) (pn:phosphoglycerate kinase:pgk) (gn:pgk) (gtcfc:1.1:2.4) (ec:2.7.2.3) (pgk_haein) (keggfc:1.1:2.3) (tigrfc:6.9) (db:gtc-haemophilus influenzae)) HI0525 HI0525 Haemophilus influenzae 727 10071003

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875310	13839	35995	510	169

Description

5000694073 tpia:tpi:hi0678 tpia:triosephosphate isomerase:tim
 (gtcfc:1.1:1.5:2.4:8.1) (ec:5.3.1.1) (keggfc:1.1:1.5:2.3:8.1) (tigrfc:6.9)
 (db:gtc-haemophilus influenzae) HI0678 HI0678 Haemophilus influenzae 727
 -11536787 101911 tpia:tpi:hi0678 (ec:5.3.1.1) (de:triosephosphate
 isomerase, (tim)) (db:swissprot) TPIS_HAEIN P43727 HAEMOPHILUS INFLUENZAE
 727 -11536787 142124 triose-phosphate isomerase (cl:triose-phosphate
 isomerase) (ec:5.3.1.1) (db:pir2.dat) G64085 G64085 Haemophilus influenzae
 727 -11536787 7500893311 hi0678 triosephosphate isomerase tpia
 (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the
 complete genome.) (nt:similar to gb:l19201 sp:p04790 gb:x00617 pid:305022)
 (le:6722) (re:7513) (di:direct) U32750 U32750 g1573678 Haemophilus
 influenzae Rd 71421 -11536787 6500732929 tpia:tpi tpia:triosephosphate
 isomerase:tim (gtcfc:1.1:1.5:2.4:8.1) (ec:5.3.1.1) (keggfc:1.1:1.5:2.3:8.1)
 (tigrfc:6.9) (db:gtc-haemophilus influenzae) HI0678 HI0678 Haemophilus
 influenzae 727 -11536787

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875314	13840	35996	2199	733

Description

GTC ORF with score 332 to: (fn:required for axial budding pattern of s.)
 (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae tcp1-beta
 gene, partial cds, and axl2p(axl2) and rev7p (rev7) genes, complete cds.)
 (nt:plasma membrane ...)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875318	13841	35997	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875321	13842	35998	264	87

Description

6500732930 gpma:hi0757 phosphoglycerate mutase:phosphoglyceromutase:pgam:bpg-dependent pgam (gtcfc:1.1) (ec:5.4.2.1) (keggfc:1.1) (tigrfc:6.9) (db:gtc-haemophilus influenzae) HI0757 HI0757 Haemophilus influenzae 727 -11536788 90102 gpma:hi0757 (ec:5.4.2.1) (de:(bpg-dependent pgam)) (db:swissprot) PMG_HAEIN P44865 HAEMOPHILUS INFLUENZAE 727 -11536788 142180 phosphoglycerate mutase (cl:phosphoglycerate mutase:phosphoglycerate mutase homology) (ec:5.4.2.1) (db:pir2.dat) A64091 A64091 Haemophilus influenzae 727 -11536788 7500888200 hi0757 phosphoglycerate mutase gpma (db:genpept-bct1) (de:haemophilus influenzae rd section 75 of 163 of the complete genome.) (nt:similar to gb:l09651 sp:p30798 pid:155611 percent) (le:1512) (re:2195) (di:direct) U32760 U32760 g1573766 Haemophilus influenzae Rd 71421 -11536788 5000694074 (de:(hi0757) (pn:phosphoglycerate mutase:pgam:bpg- dependent pgam:phosphoglyceromutase:gpma) (gn:gpma) (gtcfc:1.1) (ec:5.4.2.1) (pmg_haein) (keggfc:1.1) (tigrfc:6.9) (db:gtc-haemophilus influenzae)) HI0757 HI0757 Haemophilus influenzae 727 10032222

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875323	13843	35999	228	75

Description

5000694075 galm:mro:hi0818 aldose 1-epimerase precursor:mro:aldose 1-epimerase:mutarotase (gtcfc:1.1:1.4:7.1) (ec:5.1.3.3) (keggfc:1.1) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI0818 HI0818 Haemophilus influenzae 727 -11536789 73084 galm:mro:hi0818 (ec:5.1.3.3) (de:aldose 1-epimerase, (mutarotase)) (db:swissprot) GALM_HAEIN P31765 HAEMOPHILUS INFLUENZAE 727 -11536789 165993 galm aldose 1-epimerase::mutarotase (cl:aldose 1-epimerase) (ec:5.1.3.3) (db:pir2.dat) C64096 C64096 Haemophilus influenzae 727 -11536789 7500882091 hi0818 aldose 1-epimerase galm (db:genpept-bct1) (de:haemophilus influenzae rd section 79 of 163 of the complete genome.) (nt:similar to sp:p40681 pid:725494 gb:u00096) (le:2674) (re:3696) (di:complement) U32764 U32764 g1573831 Haemophilus influenzae Rd 71421 -11536789 6500732931 galm:mro aldose 1-epimerase precursor:mro:aldose 1-epimerase:mutarotase (gtcfc:1.1:1.4:7.1) (ec:5.1.3.3) (keggfc:1.1) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI0818 HI0818 Haemophilus influenzae 727 -11536789

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875325	13844	36000	714	237

Description

6500732932 eno:hi0932 enolase:lase:2-phosphoglycerate
dehydratase:2-phospho-d-glycerate hydro-lyase (gtcfc:1.1) (ec:4.2.1.11)
(keggfc:1.1) (tigrfc:6.9) (db:gtc-haemophilus influenzae) HI0932 HI0932
Haemophilus influenzae 727 -11536790 141849 phosphopyruvate
hydratase::enolase (cl:enolase) (ec:4.2.1.11) (db:pir2.dat) E64103 E64103
Haemophilus influenzae 727 -11536790 7500954421 hi0932 enolase eno
(db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the
complete genome.) (nt:similar to gb:m12843 sp:p08324 gb:x82400 pid:147479)
(le:2424) (re:3734) (di:complement) U32775 U32775 g1573953 Haemophilus
influenzae Rd 71421 -11536790 5000694076 (de:(hi0932)
(pn:lase:2-phosphoglycerate dehydratase:2-phospho-d-glycerate
hydro-lyase:enolase:eno) (gn:eno) (gtcfc:1.1) (ec:4.2.1.11) (eno_haein)
(keggfc:1.1) (tigrfc:6.9) (db:gtc-haemophilus influenzae)) HI0932 HI0932
Haemophilus influenzae 727 10072634

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875330	13845	36001	765	254

Description

6500732933 pfka:hi0982
6-phosphofructokinase:phosphofructokinase:phosphohexokinase
(gtcfc:1.1:1.3:1.5:1.6) (ec:2.7.1.11) (keggfc:1.1:1.3:1.5:1.6) (tigrfc:6.9)
(db:gtc-haemophilus influenzae) HI0982 HI0982 Haemophilus influenzae 727
-11536791 80270 pfka:hi0982 (ec:2.7.1.11) (de:(phosphohexokinase))
(db:swissprot) K6PF_HAEIN P43863 HAEMOPHILUS INFLUENZAE 727 -11536791
138447 pfka 6-phosphofructokinase
(cl:6-phosphofructokinase:6-phosphofructokinase 1 homology) (ec:2.7.1.11)
(db:pir2.dat) C64106 C64106 Haemophilus influenzae 727 -11536791 7500884438
hi0982 6-phosphofructokinase pfka (db:genpept-bct1) (de:haemophilus
influenzae rd section 94 of 163 of the complete genome.) (nt:similar to
gb:l19201 sp:p06998 gb:x02519 pid:305019) (le:802) (re:1767) (di:complement)
U32779 U32779 g1574011 Haemophilus influenzae Rd 71421 -11536791 5000694077
(de:(hi0982)
(pn:phosphofructokinase:phosphohexokinase:6-phosphofructokinase:pfka)
(gn:pfka) (gtcfc:1.1:1.3:1.5:1.6) (ec:2.7.1.11) (k6pf_haein)
(keggfc:1.1:1.3:1.5:1.6) (tigrfc:6.9) (db:gtc-haemophilus influenzae))
HI0982 HI0982 Haemophilus influenzae 727 10022520

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875342	13846	36002	237	78

Description

6500732934 lpda:hi1231 lipoamide dehydrogenase:dihydrolipoamide dehydrogenase:e3 component of pyruvate and 2-oxoglutarate dehydrogenases complexes (gtcfc:1.1:1.8) (ec:1.8.1.4) (keggfc:1.1:1.2:1.8:5.3) (tigrfc:6.11) (db:gtc-haemophilus influenzae) HI1231 HI1231 Haemophilus influenzae 727 -11536792 122786 dihydrolipoamide dehydrogenase (cl:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology) (ec:1.8.1.4) (db:pir1.dat) H64111 H64111 Haemophilus influenzae 727 -11536792 7500953200 hi1231 dihydrolipoamide dehydrogenase lpda (db:genpept-bct1) (de:haemophilus influenzae rd section 117 of 163 of the completegenome.) (nt:similar to sp:p00391 pid:434012 pid:473785) (le:8634) (re:10070) (di:complement) U32802 U32802 g1574161 Haemophilus influenzae Rd 71421 -11536792 5000694078 (de:(hi1231) (pn:dihydrolipoamide dehydrogenase:e3 component of pyruvate and 2- oxoglutarate dehydrogenases complexes:lipoamide dehydrogenase:lpda) (gn:lpda) (gtcfc:1.1:1.2:5.3) (ec:1.8.1.4) (dldh_haein) (keggfc:1.1:1.2:5.3) (ti) HI1231 HI1231 Haemophilus influenzae 727 10065627

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875344	13847	36003	669	222

Description

6500732935 acef:hi1232 dihydrolipoamide acetyltransferase:dihydrolipoamide acetyltransferase component:e2 of pyruvate dehydrogenase complex (gtcfc:1.1:1.8) (ec:2.3.1.12) (keggfc:1.1:1.8) (tigrfc:6.11) (db:gtc-haemophilus influenzae) HI1232 HI1232 Haemophilus influenzae 727 -11536793 87486 acef:hi1232 (ec:2.3.1.12) (de:complex, (e2)) (db:swissprot) ODP2_HAEIN P45118 HAEMOPHILUS INFLUENZAE 727 -11536793 137894 dihydrolipoamide s-acetyltransferase (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (ec:2.3.1.12) (db:pir2.dat) I64111 I64111 Haemophilus influenzae 727 -11536793 7500887103 hi1232 dihydrolipoamide acetyltransferase acef (db:genpept-bct1) (de:haemophilus influenzae rd section 118 of 163 of the completegenome.) (nt:similar to gb:d26562 sp:p06959 gb:v01498 pid:434011) (le:87) (re:1790) (di:complement) U32803 U32803 g1574163 Haemophilus influenzae Rd 71421 -11536793 5000694079 (de:(hi1232) (pn:dihydrolipoamide acetyltransferase component:e2 of pyruvate dehydrogenase complex:dihydrolipoamide acetyltransferase:acef) (gn:acef) (gtcfc:1.1) (ec:2.3.1.12) (odp2_haein) (keggfc:1.1) (tigrfc:6.11) (db:gtc-haem) HI1232 HI1232 Haemophilus influenzae 727 10029629

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875348	13848	36004	1116	371

Description

6500732936 acee:hi1233 pyruvate dehydrogenase:pyruvate dehydrogenase e1 component (gtcfc:1.1:1.11:1.8:5.7) (ec:1.2.4.1) (keggfc:1.1:1.8:1.11:5.7) (tigrfc:6.11) (db:gtc-haemophilus influenzae) HI1233 HI1233 Haemophilus influenzae 727 -11536794 87477 acee:hi1233 (ec:1.2.4.1) (de:pyruvate dehydrogenase e1 component,) (db:swissprot) ODP1_HAEIN P45119 HAEMOPHILUS INFLUENZAE 727 -11536794 136541 pyruvate dehydrogenase lipoamide (cl:pyruvate dehydrogenase (lipoamide):thiamine pyrophosphate-binding domain homology) (ec:1.2.4.1) (db:pir2.dat) A64112 A64112 Haemophilus influenzae 727 -11536794 7500887102 hi1233 pyruvate dehydrogenase:e1 component acee (db:genpept-bct1) (de:haemophilus influenzae rd section 118 of 163 of the completegenome.) (nt:similar to gb:d26562 sp:p06958 gb:v01498 pid:434010) (le:1853) (re:4513) (di:complement) U32803 U32803 g1574164 Haemophilus influenzae Rd 71421 -11536794 5000694080 (de:(hi1233) (pn:pyruvate dehydrogenase e1 component:pyruvate dehydrogenase:acee) (gn:acee) (gtcfc:1.1:5.7) (ec:1.2.4.1) (odp1_haein) (keggfc:1.1:5.7) (tigrfc:6.11) (db:gtc-haemophilus influenzae)) HI1233 HI1233 Haemophilus influenzae 727 10029620

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875374	13849	36005	453	151

Description

6500732937 pyka:hi1573 pyruvate kinase type ii:pyruvate kinase:pk (gtcfc:1.1:1.8:2.4) (ec:2.7.1.40) (keggfc:1.1:1.8:2.3) (tigrfc:6.9) (db:gtc-haemophilus influenzae) HI1573 HI1573 Haemophilus influenzae 727 -11536795 138880 pyka pyruvate kinase (cl:pyruvate kinase) (ec:2.7.1.40) (db:pir2.dat) C64130 C64130 Haemophilus influenzae 727 -11536795 7500954122 hi1573 pyruvate kinase:type ii pyka (db:genpept-bct1) (de:haemophilus influenzae rd section 146 of 163 of the completegenome.) (nt:similar to gb:m63703 sp:p21599 gb:m87660 pid:147459) (le:8169) (re:9605) (di:direct) U32831 U32831 g1574410 Haemophilus influenzae Rd 71421 -11536795 5000694081 (de:(hi1573) (pn:pyruvate kinase:pk:pyruvate kinase type ii:pyka) (gn:pyka) (gtcfc:1.1:1.8:2.4) (ec:2.7.1.40) (kpyk_haein) (keggfc:1.1:1.8:2.3) (tigrfc:6.9) (db:gtc-haemophilus influenzae)) HI1573 HI1573 Haemophilus influenzae 727 10070966

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875392	13850	36006	255	84

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875393	13851	36007	420	140

Description

5000694082 *pgi:hi1576* glucose-6-phosphate isomerase:*gpi:phosphoglucose isomerase:pgi:phosphohexose isomerase:phi* (gtcfc:1.1:1.3:7.2) (ec:5.3.1.9) (keggfc:1.1:1.3:7.1) (tigrfc:6.9) (db:gtc-haemophilus influenzae) HI1576 HI1576 Haemophilus influenzae 727 -11536796 72804 *pgi:hi1576* (ec:5.3.1.9) (de:isomerase) (*pgi*) (*phosphohexose isomerase*) (*phi*)) (db:swissprot) G6PI_HAEIN P44312 HAEMOPHILUS INFLUENZAE 727 -11536796 142138 glucose-6-phosphate isomerase (cl:glucose-6-phosphate isomerase) (ec:5.3.1.9) (db:pir2.dat) F64130 F64130 Haemophilus influenzae 727 -11536796 7500882018 *hi1576* glucose-6-phosphate isomerase *pgi* (db:genpept-bct1) (de:haemophilus influenzae rd section 146 of 163 of the completegenome.) (nt:similar to sp:p11537 gb:x15196 pid:396360 pid:42377) (le:12300) (re:13991) (di:direct) U32831 U32831 g1574413 Haemophilus influenzae Rd 71421 -11536796 6500732938 *pgi* glucose-6-phosphate isomerase:*gpi:phosphoglucose isomerase:pgi:phosphohexose isomerase:phi* (gtcfc:1.1:1.3:7.2) (ec:5.3.1.9) (keggfc:1.1:1.3:7.1) (tigrfc:6.9) (db:gtc-haemophilus influenzae) HI1576 HI1576 Haemophilus influenzae 727 -11536796

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875395	13852	36008	2115	705

Description

6500732939 *fbp:hi1645* fructose-1:6-bisphosphatase:*d-fructose-1:6-bisphosphate 1-phosphohydrolase:fbpase* (gtcfc:1.1:1.3:1.5:2.4) (ec:3.1.3.11) (keggfc:1.1:1.3:1.5:2.3) (tigrfc:6.8) (db:gtc-haemophilus influenzae) HI1645 HI1645 Haemophilus influenzae 727 -11536797 70896 *fbp:hi1645* (ec:3.1.3.11) (de:1-phosphohydrolase) (*fbpase*)) (db:swissprot) F16P_HAEIN P45292 HAEMOPHILUS INFLUENZAE 727 -11536797 139669 fructose-bisphosphatase (cl:fructose-bisphosphatase) (ec:3.1.3.11) (db:pir2.dat) G64134 G64134 Haemophilus influenzae 727 -11536797 7500881279 *hi1645* fructose-1:6-bisphosphatase *fbp* (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to sp:p09200 gb:x12545 pid:41416 pid:537074) (le:7629) (re:8630) (di:direct) U32837 U32837 g1574493 Haemophilus influenzae Rd 71421 -11536797 5000694083 (de:(*hi1645*) (pn:d-fructose-1,6-bisphosphate 1-phosphohydrolase:fbpase:fructose-1,6-bisphosphatase:fbp) (gn:fbp) (gtcfc:1.1:1.3:1.5:2.4) (ec:3.1.3.11) (f16p_haein) (keggfc:1.1:1.3:1.5:2.3) (tigrfc:6.8) (db:gtc-haemophilus influ) HI1645 HI1645 Haemophilus influenzae 727 10013471

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875405	13853	36009	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875406	13854	36010	417	138

Description

GTC ORF with score 104 to: (or:Boreogadus saida) (db:genpept-vrt)
(de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene,
complete cds.) (nt:cleavage of polyprotein at conserved spacers r or)
(le:209:281) (re:211:1801) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875424	13855	36011	1542	513

Description

6500732940 crr:hi1711 glucose phosphotransferase enzyme iii-glc:pts
system:glucose-specific iia component:eiia-glc:glucose-permease iia
component:phosphotransferase enzyme ii:a component:eiia-glc
(gtcfc:1.1:1.5:1.6:7.1:7.2:12.2) (ec:2.7.1.69) (keggfc:1.1:1.5:1.6:4.4:7.1)
(tigrfc:13.3) (db:gtc-haemophilus influenzae) HI1711 HI1711 Haemophilus
influenzae 727 -11536798 138900 phosphotransferase system enzyme
ii::glucose-specific:factor iii (cl:phosphotransferase system
glucose-specific enzyme ii, factor iii:phosphotransferase system
glucose-specific enzyme ii, factor iii homology) (ec:2.7.1.69) (db:pir2.dat)
G64137 G64137 Haemophilus influenzae 727 -11536798 7500954127 hi1711 pts
system:glucose-specific iia component (db:genpept-bct1) (de:haemophilus
influenzae rd section 159 of 163 of the completegenome.) (nt:similar to
gb:j02796 sp:p08837 gb:m93578 gb:m93579) (le:937) (re:1437) (di:complement)
U32844 U32844 g1574566 Haemophilus influenzae Rd 71421 -11536798 5000694084
(de:(hi1711) (pn:pts system, glucose-specific iia
component:eiia-glc:glucose- permease iia component:phosphotransferase enzyme
ii, a component:eiia-glc:glucose phosphotransferase enzyme iii-glc:crr)
(gn:crr) (gtcfc:1.1:1.5:1.6:7.1:7.2)) HI1711 HI1711 Haemophilus influenzae
727 10070980

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875453	13856	36012	999	332

Description

6500732941 pcka:hi0809 phosphoenolpyruvate carboxykinase:atp
 (gtcfc:1.1:1.2:1.8:2.4) (ec:4.1.1.49) (keggfc:1.2:1.8:2.3) (tigrfc:6.8)
 (db:gtc-haemophilus influenzae) HI0809 HI0809 Haemophilus influenzae 727
 -11536799 90744 pcka:hi0809 (ec:4.1.1.49) (de:phosphoenolpyruvate
 carboxykinase (atp),) (db:swissprot) PPCK_HAEIN P43923 HAEMOPHILUS
 INFLUENZAE 727 -11536799 167092 phosphoenolpyruvate carboxykinase atp
 (cl:phosphoenolpyruvate carboxykinase (atp)) (ec:4.1.1.49) (db:pir2.dat)
 E64095 E64095 Haemophilus influenzae 727 -11536799 7500888351 hi0809
 phosphoenolpyruvate carboxykinase pcka (db:genpept-bct1) (de:haemophilus
 influenzae rd section 78 of 163 of the complete genome.) (nt:similar to
 pid:606337 gb:u00096 pid:1789807 percent) (le:3774) (re:5390)
 (di:complement) U32763 U32763 g1573821 Haemophilus influenzae Rd 71421
 -11536799 5000694108 (de:(hi0809) (pn:atp:phosphoenolpyruvate
 carboxykinase:pcka) (gn:pcka) (gtcfc:1.2:1.8:2.4) (ec:4.1.1.49) (ppck_haein)
 (keggfc:1.2:1.8:2.3) (tigrfc:6.8) (db:gtc-haemophilus influenzae)) HI0809
 HI0809 Haemophilus influenzae 727 10032859

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875464	13857	36013	813	270

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875478	13858	36014	594	197

Description

6500732942 fruk:hi0447 1-phosphofructokinase:fructose 1-phosphate kinase
 (gtcfc:1.1:1.5:1.6) (ec:2.7.1.56) (keggfc:1.5:1.6) (tigrfc:6.9)
 (db:gtc-haemophilus influenzae) HI0447 HI0447 Haemophilus influenzae 727
 -11536800 80222 fruk:hi0447 (ec:2.7.1.56) (de:1-phosphofructokinase,
 (fructose 1-phosphate kinase)) (db:swissprot) K1PF_HAEIN P44330 HAEMOPHILUS
 INFLUENZAE 727 -11536800 165956 1-phosphofructokinase
 (cl:6-phosphofructokinase 2) (ec:2.7.1.56) (db:pir2.dat) A64069 A64069
 Haemophilus influenzae 727 -11536800 7500884415 hi0447
 1-phosphofructokinase fruk (db:genpept-bct1) (de:haemophilus influenzae rd
 section 42 of 163 of the complete genome.) (nt:similar to sp:p23539
 gb:x53948 pid:405894 pid:41487) (le:9372) (re:10313) (di:complement) U32727
 U32727 g1573423 Haemophilus influenzae Rd 71421 -11536800 5000694132
 (de:(hi0447) (pn:fructose 1-phosphate kinase:1-phosphofructokinase:fruk)
 (gn:fruk) (gtcfc:1.5:1.6) (ec:2.7.1.56) (k1pf_haein) (keggfc:1.5:1.6)
 (tigrfc:6.9) (db:gtc-haemophilus influenzae)) HI0447 HI0447 Haemophilus
 influenzae 727 10022472

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875480	13859	36015	759	252

Description

6500732943 ddh:hi0085 2-hydroxyacid dehydrogenase homolog
 (gtcfc:1.11:5.7:13.3) (ec:1.1.1.-)
 (keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3) (tigrfc:14.7)
 (db:gtc-haemophilus influenzae) (keggfc:carbohydrate metabolism-fructose and
 mannose metabolism:carbohydrate metabolism-galactose
 metabolism:carbohydrat... HI0085 HI0085 Haemophilus influenzae 727 -11536801
 68155 ddh:hi0085 (ec:1.1.1.-) (de:2-hydroxyacid dehydrogenase homolog,)
 (db:swissprot) DDH_HAEIN P44501 HAEMOPHILUS INFLUENZAE 727 -11536801 165959
 d-2-hydroxy-acid dehydrogenase (ec:1.1.99.6) (db:pir2.dat) F64047 F64047
 Haemophilus influenzae 727 -11536801 7500880103 hi0085 d-lactate
 dehydrogenase:fermentative ldha (db:genpept-bct1) (de:haemophilus influenzae
 rd section 9 of 163 of the complete genome.) (nt:similar to pid:1049265
 sp:p52643 gb:u00096) (le:90) (re:1085) (di:complement) U32694 U32694
 g1573036 Haemophilus influenzae Rd 71421 -11536801 5000694095 (de:(hi0085)
 (pn:2-hydroxyacid dehydrogenase homolog:2-hydroxyaciddehydrogenase
 homolog:ddh) (gn:ddh) (gtcfc:1.11:1.5:1.6:1.7:3.5:4.3:5.13:5.3:5.9:9.3)
 (ec:1.1.1.-) (ddh_haein) (keggfc:1.5:1.6:1.7:1.11:3.5:4.3:5.3:5.9:5.13:9.3))
 HI0085 HI0085 Haemophilus influenzae 727 10010748

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875484	13860	36016	690	229

Description

5000694096 pflb:pfl:hi0180 pfl:formate acetyltransferase:pyruvate
 formate-lyase (gtcfc:1.11:1.8:2.2) (ec:2.3.1.54) (keggfc:1.8:1.11)
 (tigrfc:6.7) (db:gtc-haemophilus influenzae) HI0180 HI0180 Haemophilus
 influenzae 727 -11536802 167127 formate c-acetyltransferase (cl:formate
 c-acetyltransferase 1:glycyl radical homology) (ec:2.3.1.54) (db:pir2.dat)
 F64052 F64052 Haemophilus influenzae 727 -11536802 7500960653 hi0180
 formate acetyltransferase pfl (db:genpept-bct1) (de:haemophilus influenzae
 rd section 18 of 163 of the complete genome.) (nt:similar to gb:x08035
 sp:p09373 pid:42370 gb:u00096) (le:2337) (re:4655) (di:complement) U32703
 U32703 g1573136 Haemophilus influenzae Rd 71421 -11536802 6500732944
 pflb:pfl pfl:formate acetyltransferase:pyruvate formate-lyase
 (gtcfc:1.11:1.8:2.2) (ec:2.3.1.54) (keggfc:1.8:1.11) (tigrfc:6.7)
 (db:gtc-haemophilus influenzae) HI0180 HI0180 Haemophilus influenzae 727
 -11536802

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875486	13861	36017	735	244

Description

5000694097 lnt:cute:hi0302 cute:apolipoprotein n-acyltransferase:alp
n-acyltransferase:copper homeostasis protein cute
(gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.8:7.1:11.1) (ec:2.3.1.-)
(keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (tigrfc:3.1) (db:gtc-haemophilus
influenzae) HI0302 HI0302 Haemophilus influenzae 727 -11536803 82304
lnt:cute:hi0302 (ec:2.3.1.-) (de:(copper homeostasis protein cute))
(db:swissprot) LNT_HAEIN P44626 HAEMOPHILUS INFLUENZAE 727 -11536803 166005
apolipoprotein n-acyltransferase homolog (cl:apolipoprotein
n-acyltransferase) (db:pir2.dat) H64060 H64060 Haemophilus influenzae 727
-11536803 7500885092 hi0302 apolipoprotein n-acyltransferase cute
(db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the
complete genome.) (nt:similar to sp:p23930 gb:x58070 pid:41173 gb:u00096)
(le:2158) (re:3726) (di:direct) U32716 U32716 g1573271 Haemophilus
influenzae Rd 71421 -11536803 6500732945 lnt:cute cute:apolipoprotein
n-acyltransferase:alp n-acyltransferase:copper homeostasis protein cute
(gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.8:7.1:11.1) (ec:2.3.1.-)
(keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (tigrfc:3.1) (db:gtc-haemophilus
influenzae) HI0302 HI0302 Haemophilus influenzae 727 -11536803

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875488	13862	36018	561	186

Description

6500732946 frdb:hi0834 fumarate reductase:iron-sulfur protein:fumarate
reductase iron-sulfur protein (gtcfc:1.11:1.2:2.1:2.5:2.8) (ec:1.3.99.1)
(keggfc:1.2:1.11:2.1:2.4) (tigrfc:6.3) (db:gtc-haemophilus influenzae)
(gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate
metabolism-citrate cycle (tca cycle):energy metabolism-oxidative phosphor...
HI0834 HI0834 Haemophilus influenzae 727 -11536804 72307 frdb:hi0834
(ec:1.3.99.1) (de:fumarate reductase iron-sulfur protein,) (db:swissprot)
FRDB_HAEIN P44893 HAEMOPHILUS INFLUENZAE 727 -11536804 7500881741 hi0834
fumarate reductase:iron-sulfur protein frdb (db:genpept-bct1)
(de:haemophilus influenzae rd section 80 of 163 of the complete genome.)
(nt:similar to gb:u14003 sp:p00364 gb:j01611 pid:145264) (le:5928) (re:6698)
(di:complement) U32765 U32765 g1573848 Haemophilus influenzae Rd 71421
-11536804 5000694100 (de:(hi0834) (pn:fumarate reductase iron-sulfur
protein:fumarate reductase, iron-sulfur protein:frdb) (gn:frdb)
(gtcfc:1.11:1.2:2.1:2.5) (ec:1.3.99.1) (frdb_haein)
(keggfc:1.2:1.11:2.1:2.4) (tigrfc:6.3) (db:gtc-haemophilus influ) HI0834
HI0834 Haemophilus influenzae 727 10014858

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875494	13863	36019	843	280

Description

6500732947 frda:hi0835 fumarate reductase:flavoprotein subunit:fumarate reductase flavoprotein subunit (gtcfc:2.8:9.5) (ec:1.3.99.1) (keggfc:1.2:1.11:2.1:2.4) (tigrfc:6.3) (db:gtc-haemophilus influenzae) (keggfc:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-butanate metabolism:energy metabolism-oxidative phosphorylation:ener... HI0835 HI0835 Haemophilus influenzae 727 -11536805 72301 frda:hi0835 (ec:1.3.99.1) (de:fumarate reductase flavoprotein subunit,) (db:swissprot) FRDA_HAEIN P44894 HAEMOPHILUS INFLUENZAE 727 -11536805 136569 fumarate reductase:flavoprotein (cl:fumarate reductase flavoprotein:3-oxosteroid 1-dehydrogenase homology:fumarate reductase flavoprotein homology) (ec:1.3.99.1) (db:pir2.dat) H64097 H64097 Haemophilus influenzae 727 -11536805 7500881739 hi0835 fumarate reductase:flavoprotein subunit frda (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p00363 gb:j01611 pid:145263) (le:6691) (re:8490) (di:complement) U32765 U32765 g1573849 Haemophilus influenzae Rd 71421 -11536805 5000694101 (de:(hi0835) (pn:fumarate reductase flavoprotein subunit:fumarate reductase, flavoprotein subunit:frda) (gn:frda) (gtcfc:1.11:1.2:2.1:2.5) (ec:1.3.99.1) (frda_haein) (keggfc:1.2:1.11:2.1:2.4) (tigrfc:6.3) (db:gtc-haemophilus inf) HI0835 HI0835 Haemophilus influenzae 727 10014852

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875510	13864	36020	261	86

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875532	13865	36021	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875539	13866	36022	204	67

Description

6500732948 lpxd:hi0915 r-3-hydroxymyristoyl-glucosamine
n-acyltransferase:lipid biosynthesis protein:fira:udp-3-o-
(gtcfc:1.11:5.12:5.13:5.6:5.8:6.14:6.8:7.1:11.2) (ec:2.3.1.-)
(keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) (tigrfc:3.3) (db:gtc-haemophilus
influenzae) HI0915 HI0915 Haemophilus influenzae 727 -11536806 82463
lpxd:hi0915 (ec:2.3.1.-) (de:(ec 2.3.1.-)) (db:swissprot) LPXD_HAEIN P43888
HAEMOPHILUS INFLUENZAE 727 -11536806 165980 lpxd udp-3-o-3-hydroxymyristoyl
glucosamine n-acyltransferase, :protein hi0915)
(cl:udp-3-o-(3-hydroxymyristoyl) glucosamine n-acyltransferase) (ec:2.3.1.-)
(db:pir2.dat) D64102 D64102 Haemophilus influenzae 727 -11536806 7500885147
hi0915 udp-3-o-3-hydroxymyristoyl -glucosamine (db:genpept-bct1)
(de:haemophilus influenzae rd section 88 of 163 of the complete genome.)
(nt:similar to gb:x54797 sp:p21645 pid:1208950) (le:2909) (re:3934)
(di:complement) U32773 U32773 g1573936 Haemophilus influenzae Rd 71421
-11536806 5000694102 (de:(hi0915)
(pn:udp-3-o-r-3-hydroxymyristoyl-glucosamine n-acyltransferase:lipid
biosynthesis protein:fira) (gn:lpxd)
(gtcfc:1.11:5.13:5.6:6.14:6.16:6.8:7.1:8.1) (ec:2.3.1.-) (lpxd_haein)
(keggfc:1.11:4.4:5.6:5.8:5.12:5.13:6.7) HI0915 HI0915 Haemophilus influenzae
727 10024685

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875552	13867	36023	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875557	13868	36024	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875558	13869	36025	414	137

Description

6500732949 fabz:hi1062 3r-hydroxymyristol acyl carrier protein dehydrase (gtcfc:3.1:1.11:3.5) (ec:4.2.1.-) (keggfc:1.5:1.11:3.5:5.12:5.13:5.15:6.5) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI1062 HI1062 Haemophilus influenzae 727 -11536807 71029 fabz:hi1062 (ec:4.2.1.-) (de:(3r)-hydroxymyristoyl-(acyl carrier protein) dehydratase,) (db:swissprot) FABZ_HAEIN P45012 HAEMOPHILUS INFLUENZAE 727 -11536807 165954 3r -hydroxymyristoyl-acyl carrier protein dehydratase,) (cl:(3r)-hydroxymyristoyl-(acyl carrier protein) dehydratase) (ec:4.2.1.-) (db:pir2.dat) G64180 G64180 Haemophilus influenzae 727 -11536807 7500881316 hi1062 3r -hydroxymyristol acyl carrier protein (db:genpept-bct1) (de:haemophilus influenzae rd section 101 of 163 of the completegenome.) (nt:similar to gb:m19334 sp:p21774 pid:1208951) (le:9385) (re:9831) (di:complement) U32786 U32786 g1574613 Haemophilus influenzae Rd 71421 -11536807 5000694103 (de:(hi1062) (pn:;:3r-hydroxymyristoyl-acyl carrier protein dehydratase:3r-hydroxymyristol acyl carrier protein dehydrase:fabz) (gn:fabz) (gtcfc:1.11:1.5:3.5:5.13:5.15:6.5) (ec:4.2.1.-) (fabz_haein) (keggfc:1.5:1.11:3.5:5.12:5.13) HI1062 HI1062 Haemophilus influenzae 727 10013604

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875561	13870	36026	498	165

Description

6500732950 ilvh:hi1584 acetolactate synthase isozyme iii:small subunit:acetolactate synthase small subunit:ahas:acetohydroxy-acid synthase small subunit:als (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (tigrfc:1.3) (db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:l-amino acid metabolism-vali... HI1584 HI1584 Haemophilus influenzae 727 -11536808 79266 ilvh:hi1584 (ec:4.1.3.18) (de:(acetohydroxy-acid synthase small subunit) (als)) (db:swissprot) ILVH_HAEIN P45260 HAEMOPHILUS INFLUENZAE 727 -11536808 141715 ilvh acetolactate synthase:iii small chain (cl:acetolactate synthase small chain) (ec:4.1.3.18) (db:pir2.dat) B64131 B64131 Haemophilus influenzae 727 -11536808 7500884062 hi1584 acetolactate synthase iii small subunit ilvh (db:genpept-bct1) (de:haemophilus influenzae rd section 147 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p00894 gb:x01609 pid:216495) (le:5262) (re:5753) (di:complement) U32832 U32832 g1574425 Haemophilus influenzae Rd 71421 -11536808 5000694104 (de:(hi1584) (pn:acetolactate synthase small subunit:ahas:acetohydroxy-acid synthase small subunit:als:acetolactate synthase isozyme iii, small subunit:ilvh) (gn:ilvh) (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (ilvh_haein) (keggfc:) HI1584 HI1584 Haemophilus influenzae 727 10021594

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501875580	13871	36027	1314	437

Description

6500732951 ilvi:hi1585 acetolactate synthase iii large chain:acetolactate synthase large subunit:ahas:acetohydroxy-acid synthase large subunit:als (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (keggfc:1.11:1.12:5.7:9.5) (tigrfc:1.3) (db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-butanoate metabolism:carbohydrate metabolism-c5-branched dibasic acid metabolism:l-amino acid metabolism-vali... HI1585 HI1585 Haemophilus influenzae 727 -11536809 79270 ilvi:hi1585 (ec:4.1.3.18) (de:(acetohydroxy-acid synthase large subunit) (als)) (db:swissprot) ILVI_HAEIN P45261 HAEMOPHILUS INFLUENZAE 727 -11536809 141701 acetolactate synthase:iii large chain (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology) (ec:4.1.3.18) (db:pir2.dat) C64131 C64131 Haemophilus influenzae 727 -11536809 7500884063 hi1585 acetolactate synthase iii large subunit ilvi (db:genpept-bct1) (de:haemophilus influenzae rd section 147 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p00893 gb:x01609 pid:216494) (le:5753) (re:7474) (di:complement) U32832 U32832 g1574426 Haemophilus influenzae Rd 71421 -11536809 5000694105 (de:(hi1585) (pn:acetolactate synthase large subunit:ahas:acetohydroxy-acid synthase large subunit:als:acetolactate synthase iii large chain:ilvi) (gn:ilvi) (gtcfc:1.11:1.12:5.7:9.5) (ec:4.1.3.18) (ilvi_haein) (keggfc:1.11:1.12:5) HI1585 HI1585 Haemophilus influenzae 727 10021598

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501875581	13872	36028	450	149

Description

6500732952 citf:hi0022 acyl lyase subunit:citrate lyase alpha chain:citrace (gtcfc:1.2:2.5) (ec:4.1.3.6) (keggfc:1.2:2.4) (tigrfc:6.13) (db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation)) (keggfc:carbohydrate metabolism-citrate c... HI0022 HI0022 Haemophilus influenzae 727 -11536810 64610 citf:hi0022 (ec:4.1.3.6:2.8.3.10) (de:transferase subunit),) (db:swissprot) CILA_HAEIN P44459 HAEMOPHILUS INFLUENZAE 727 -11536810 166055 citrate pro-3s -lyase:alpha chain (ec:4.1.3.6) (db:pir2.dat) C64043 C64043 Haemophilus influenzae 727 -11536810 7500878745 hi0022 citrate lyase:alpha chain citf (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p75726 pid:1778532) (le:194) (re:1696) (di:complement) U32688 U32688 g1572967 Haemophilus influenzae Rd 71421 -11536810 5000694106 (de:(hi0022) (pn:citrace:citrate lyase alpha chain:acyl lyase subunit:citf) (gn:citf) (gtcfc:1.2:2.5) (ec:4.1.3.6) (cila_haein) (keggfc:1.2:2.4) (tigrfc:6.13) (db:gtc-haemophilus influenzae)) HI0022 HI0022 Haemophilus influenzae 727 10007272

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875595	13873	36029	900	299

Description

6500732953 cite:hi0023 citrate lyase beta chain:acyl lyase subunit:citrane (gtcfc:1.2:2.5) (ec:4.1.3.6) (keggfc:1.2:2.4) (tigrfc:6.13) (db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):energy metabolism-reductive carboxylate cycle (co2 fixation)) (keggfc:carbohydrate metabolism-citrate c... HI0023 HI0023 Haemophilus influenzae 727 -11536811 64612 cite:hi0023 (ec:4.1.3.6:4.1.3.34) (de:subunit),) (db:swissprot) CILB_HAEIN P44460 HAEMOPHILUS INFLUENZAE 727 -11536811 166056 citrate pro-3s -lyase:beta chain (ec:4.1.3.6) (db:pir2.dat) D64043 D64043 Haemophilus influenzae 727 -11536811 7500878747 hi0023 citrate lyase:beta chain cite (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77770 pid:1778533) (le:1711) (re:2586) (di:complement) U32688 U32688 g1572968 Haemophilus influenzae Rd 71421 -11536811 5000694107 (de:(hi0023) (pn:citrane:citrate lyase beta chain:acyl lyase subunit:cite) (gn:cite) (gtcfc:1.2:2.5) (ec:4.1.3.6) (cilb_haein) (keggfc:1.2:2.4) (tigrfc:6.13) (db:gtc-haemophilus influenzae)) HI0023 HI0023 Haemophilus influenzae 727 10007274

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875611	13874	36030	864	287

Description

6500732954 mdh:hi1210 malate dehydrogenase (gtcfc:1.2:1.8:1.9:2.4:2.5) (ec:1.1.1.37) (keggfc:1.2:1.8:1.9:2.3:2.4) (tigrfc:6.13) (db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-citrate cycle (tca cycle):carbohydrate metabolism-pyruvate and acetyl-coa metabolism:carbohydrate metabo... HI1210 HI1210 Haemophilus influenzae 727 -11536812 83313 mdh:hi1210 (ec:1.1.1.37) (de:malate dehydrogenase,) (db:swissprot) MDH_HAEIN P44427 HAEMOPHILUS INFLUENZAE 727 -11536812 136226 malate dehydrogenase (cl:l-lactate dehydrogenase) (ec:1.1.1.37) (db:pir2.dat) C64110 C64110 Haemophilus influenzae 727 -11536812 7500885427 hi1210 malate dehydrogenase mdh (db:genpept-bct1) (de:haemophilus influenzae rd section 115 of 163 of the completegenome.) (nt:similar to gb:m24777 sp:p06994 gb:m10417 gb:u04742) (le:5640) (re:6575) (di:direct) U32800 U32800 g1574140 Haemophilus influenzae Rd 71421 -11536812 5000694109 (de:(hi1210) (pn:malate dehydrogenase:mdh) (gn:mdh) (gtcfc:1.2:1.8:1.9:2.4:2.5) (ec:1.1.1.37) (mdh_haein) (keggfc:1.2:1.8:1.9:2.3:2.4) (tigrfc:6.13) (db:gtc-haemophilus influenzae)) HI1210 HI1210 Haemophilus influenzae 727 10025531

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875612	13875	36031	1758	585

Description

6500732955 such:hi1661 dihydrolipoamide succinyltransferase:dihydrolipoamide succinyltransferase component:e2 of 2-oxoglutarate dehydrogenase complex (gtcfc:1.2) (ec:2.3.1.61) (keggfc:1.2) (tigrfc:6.13) (db:gtc-haemophilus influenzae) HI1661 HI1661 Haemophilus influenzae 727 -11536813 87469 such:hi1661 (ec:2.3.1.61) (de:dehydrogenase complex, (e2)) (db:swissprot) ODO2_HAEIN P45302 HAEMOPHILUS INFLUENZAE 727 -11536813 137903 dihydrolipoamide s-succinyltransferase (cl:dihydrolipoamide acetyltransferase:lipoyl/biotin-binding homology) (ec:2.3.1.61) (db:pir2.dat) D64135 D64135 Haemophilus influenzae 727 -11536813 7500887100 hi1661 2-oxoglutarate dehydrogenase e2 component (db:genpept-bct1) (de:haemophilus influenzae rd section 154 of 163 of the completegenome.) (nt:similar to gb:j01619 sp:p07016 gb:x00664 pid:146202) (le:3853) (re:5082) (di:complement) U32839 U32839 g1574511 Haemophilus influenzae Rd 71421 -11536813 5000694110 (de:(hi1661) (pn:dihydrolipoamide succinyltransferase component:e2 of 2- oxoglutarate dehydrogenase complex:dihydrolipoamide succinyltransferase:such) (gn:such) (gtcfc:1.2) (ec:2.3.1.61) (odo2_haein) (keggfc:1.2) (tigrfc:6.13) () HI1661 HI1661 Haemophilus influenzae 727 10029612

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875620	13876	36032	1572	523

Description

6500732956 suca:hi1662 2-oxoglutarate dehydrogenase:2-oxoglutarate dehydrogenase e1 component:alpha-ketoglutarate dehydrogenase (gtcfc:1.2:5.14:5.9) (ec:1.2.4.2) (keggfc:1.2:5.9:5.14) (tigrfc:6.13) (db:gtc-haemophilus influenzae) HI1662 HI1662 Haemophilus influenzae 727 -11536814 136545 oxoglutarate dehydrogenase lipoamide (cl:oxoglutarate dehydrogenase (lipoamide):thiamine pyrophosphate-binding domain homology) (ec:1.2.4.2) (db:pir2.dat) E64135 E64135 Haemophilus influenzae 727 -11536814 7500953839 hi1662 2-oxoglutarate dehydrogenase e1 component (db:genpept-bct1) (de:haemophilus influenzae rd section 154 of 163 of the completegenome.) (nt:similar to gb:j01619 sp:p07015 pid:146201 pid:43019) (le:5185) (re:8037) (di:complement) U32839 U32839 g1574512 Haemophilus influenzae Rd 71421 -11536814 5000694111 (de:(hi1662) (pn:2-oxoglutarate dehydrogenase e1 component:alpha-ketoglutarate dehydrogenase:2-oxoglutarate dehydrogenase:suca) (gn:suca) (gtcfc:1.2:5.9) (ec:1.2.4.2) (odo1_haein) (keggfc:1.2:5.9:5.14) (tigrfc:6.13) (db:gtc-haem) HI1662 HI1662 Haemophilus influenzae 727 10069531

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875629	13877	36033	651	216

Description

6500732957 citd:hi0024 acyl lyase subunit:citrate lyase acyl carrier protein:citrate lyase gamma chain (gtcfc:1.2) (keggfc:14.2) (tigrfc:6.13) (db:gtc-haemophilus influenzae) HI0024 HI0024 Haemophilus influenzae 727 -11536815 64614 citd:hi0024 (de:citrate lyase acyl carrier protein (citrate lyase gamma chain)) (db:swissprot) CILG_HAEIN P44461 HAEMOPHILUS INFLUENZAE 727 -11536815 166057 citrate pro-3s -lyase:gamma chain:citrate lyase acyl carrier protein:citrate lyase:acyl lyase chain citd (cl:citrate lyase acyl carrier protein) (ec:4.1.3.6) (db:pir1.dat) E64043 E64043 Haemophilus influenzae 727 -11536815 7500878749 hi0024 citrate lyase:gamma chain citd (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77618 pid:1778534) (le:2583) (re:2870) (di:complement) U32688 U32688 g1572969 Haemophilus influenzae Rd 71421 -11536815 5000694112 (de:(hi0024) (pn:citrate lyase acyl carrier protein:citrate lyase gamma chain:acyl lyase subunit:citd) (gn:citd) (gtcfc:1.2) (ec:) (cilg_haein) (keggfc:11.2) (tigrfc:6.13) (db:gtc-haemophilus influenzae)) HI0024 HI0024 Haemophilus influenzae 727 10007276

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875632	13878	36034	510	169

Description

6500732958 citc:hi0025 acetate:sh-citrate lyase ligase:amp (gtcfc:1.2) (ec:6.2.1.22) (keggfc:14.1) (tigrfc:6.13) (db:gtc-haemophilus influenzae) HI0025 HI0025 Haemophilus influenzae 727 -11536816 64701 citc:hi0025 (ec:6.2.1.22) (de:synthetase) (acetate:sh-citrate lyase ligase)) (db:swissprot) CITC_HAEIN P44462 HAEMOPHILUS INFLUENZAE 727 -11536816 166054 citrate pro-3s -lyase ligase::citrate lyase ligase (cl:citrate (pro-3s)-lyase ligase) (ec:6.2.1.22) (db:pir2.dat) F64043 F64043 Haemophilus influenzae 727 -11536816 7500878777 hi0025 citrate lyase ligase citc (db:genpept-bct1) (de:haemophilus influenzae rd section 3 of 163 of the complete genome.) (nt:similar to sp:p77390 percent identity: 52.73;) (le:2908) (re:3915) (di:complement) U32688 U32688 g1572970 Haemophilus influenzae Rd 71421 -11536816 5000694113 (de:(hi0025) (pn::acetate:sh-citrate lyase ligase:amp) (gn:citc) (gtcfc:1.2) (ec:6.2.1.22) (citic_haein) (keggfc:11.1) (tigrfc:6.13) (db:gtc-haemophilus influenzae)) HI0025 HI0025 Haemophilus influenzae 727 10007363

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875635	13879	36035	357	118

Description

6500732959 malic acid enzyme:putative malate oxidoreductase:nad:malic enzyme (gtcfc:1.2:1.8) (ec:1.1.1.38) (keggfc:1.8) (tigrfc:6.13) (db:gtc-haemophilus influenzae) HI1245 HI1245 Haemophilus influenzae 727 -11536817 82968 hi1245 (ec:1.1.1.38) (de:putative malate oxidoreductase (nad), (malic enzyme)) (db:swissprot) MAOX_HAEIN P43837 HAEMOPHILUS INFLUENZAE 727 -11536817 166977 malate dehydrogenase oxaloacetate-decarboxylating homolog (db:pir2.dat) F64112 F64112 Haemophilus influenzae 727 -11536817 7500885318 hi1245 malate oxidoreductase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 119 of 163 of the completegenome.) (nt:similar to gb:u00096 pid:1788806 pid:1799885) (le:5741) (re:8011) (di:direct) U32804 U32804 g1574176 Haemophilus influenzae Rd 71421 -11536817 5000694144 (de:(hi1245) (pn:putative malate oxidoreductase:nad:malic enzyme:malic acid enzyme) (gtcfc:1.8) (ec:1.1.1.38) (maox_haein) (keggfc:1.8) (tigrfc:6.13) (db:gtc-haemophilus influenzae)) HI1245 HI1245 Haemophilus influenzae 727 10025188

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875641	13880	36036	2721	907

Description

6500732960 kdgc:hi0049 2-keto-3-deoxy-d-gluconate kinase:2-dehydro-3-deoxygluconokinase:2-keto-3-deoxygluconokinase:3-deoxy-2-oxo-d-gluconate kinase:kdgc kinase (gtcfc:1.3:1.4:2.1) (ec:2.7.1.45) (keggfc:1.3:1.4) (tigrfc:6.6) (db:gtc-haemophilus influenzae) HI0049 HI0049 Haemophilus influenzae 727 -11536818 80578 kdgc:hi0049 (ec:2.7.1.45) (de:deoxygluconokinase) (3-deoxy-2-oxo-d-gluconate kinase) (kdgc kinase) (db:swissprot) KDGK_HAEIN P44482 HAEMOPHILUS INFLUENZAE 727 -11536818 165962 2-dehydro-3-deoxygluconokinase homolog (db:pir2.dat) C64045 C64045 Haemophilus influenzae 727 -11536818 7500884545 hi0049 2-dehydro-3-deoxygluconokinase kdgc (db:genpept-bct1) (de:haemophilus influenzae rd section 5 of 163 of the complete genome.) (nt:similar to gb:x75047 sp:p45416 pid:495249 percent) (le:2817) (re:3761) (di:complement) U32690 U32690 g1572996 Haemophilus influenzae Rd 71421 -11536818 5000694114 (de:(hi0049) (pn:2-dehydro-3-deoxygluconokinase:2-keto-3-deoxygluconokinase:3-deoxy-2-oxo-d-gluconate kinase:kdgc kinase:2-keto-3-deoxy-d-gluconate kinase:kdgc) (gn:kdgc) (gtcfc:1.3:1.4) (ec:2.7.1.45) (kdgc_haein) (keggfc:1.3:1.4)) HI0049 HI0049 Haemophilus influenzae 727 10022820

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875663	13881	36037	330	109

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875673	13882	36038	612	203

Description

6500732961 rpia:hi0464 sp:p27252:ribose 5-phosphate isomerase
a:phosphoriboisomerase a (gtcfc:1.3:2.4) (ec:5.3.1.6) (keggfc:1.3:2.3)
(tigrfc:6.10) (db:gtc-haemophilus influenzae) HI0464 HI0464 Haemophilus
influenzae 727 -11536819 96132 rpia:hi0464 (ec:5.3.1.6) (de:ribose
5-phosphate isomerase a, (phosphoriboisomerase a)) (db:swissprot) RPIA_HAEIN
P44725 HAEMOPHILUS INFLUENZAE 727 -11536819 166420 ribose-5-phosphate
isomerase (cl:haemophilus influenzae ribose-5-phosphate isomerase)
(ec:5.3.1.6) (db:pir2.dat) B64153 B64153 Haemophilus influenzae 727
-11536819 7500890587 hi0464 ribose 5-phosphate isomerase a rpia
(db:genpept-bct1) (de:haemophilus influenzae rd section 44 of 163 of the
complete genome.) (nt:similar to gb:x66836 sp:p27252 gb:x73026 pid:147808)
(le:3938) (re:4597) (di:direct) U32729 U32729 g1573442 Haemophilus
influenzae Rd 71421 -11536819 5000694115 (de:(hi0464)
(pn:phosphoriboisomerase a:ribose 5-phosphate isomerase a:p27252) (gn:rpia)
(gtcfc:1.3:2.4) (ec:5.3.1.6) (rpia_haein) (keggfc:1.3:2.3) (tigrfc:6.10)
(db:gtc-haemophilus influenzae)) HI0464 HI0464 Haemophilus influenzae 727
10038076

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875697	13883	36039	1458	485

Description

6500732962 rbsk:hi0505 ribokinase (gtcfc:1.3:1.4:7.1) (ec:2.7.1.15)
(keggfc:1.3) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI0505 HI0505
Haemophilus influenzae 727 -11536820 93580 rbsk:hi0505 (ec:2.7.1.15)
(de:ribokinase,) (db:swissprot) RBSK_HAEIN P44331 HAEMOPHILUS INFLUENZAE 727
-11536820 138459 ribokinase (cl:ribokinase) (ec:2.7.1.15) (db:pir2.dat)
B64073 B64073 Haemophilus influenzae 727 -11536820 7500889478 hi0505
ribokinase rbsk (db:genpept-bct1) (de:haemophilus influenzae rd section 47
of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p05054 gb:m13169
pid:147516) (le:5416) (re:6336) (di:direct) U32732 U32732 g1573486
Haemophilus influenzae Rd 71421 -11536820 5000694116 (de:(hi0505)
(pn:ribokinase:rbsk) (gn:rbsk) (gtcfc:1.3) (ec:2.7.1.15) (rbsk_haein)
(keggfc:1.3) (tigrfc:6.12) (db:gtc-haemophilus influenzae)) HI0505 HI0505
Haemophilus influenzae 727 10035573

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875702	13884	36040	282	93

Description

6500732963 gnd:hi0553 6-phosphogluconate dehydrogenase:decarboxylating (gtcfc:1.3) (ec:1.1.1.44) (keggfc:1.3) (tigrfc:6.10) (db:gtc-haemophilus influenzae) HI0553 HI0553 Haemophilus influenzae 727 -11536821 57635 gnd:hi0553 (ec:1.1.1.44) (de:6-phosphogluconate dehydrogenase, decarboxylating,) (db:swissprot) 6PGD_HAEIN P43774 HAEMOPHILUS INFLUENZAE 727 -11536821 136293 phosphogluconate dehydrogenase decarboxylating (cl:phosphogluconate dehydrogenase (decarboxylating):3-hydroxyisobutyrate dehydrogenase homology) (ec:1.1.1.44) (db:pir2.dat) C64077 C64077 Haemophilus influenzae 727 -11536821 7500876144 hi0553 6-phosphogluconate dehydrogenase (db:genpept-bct1) (de:haemophilus influenzae rd section 52 of 163 of the complete genome.) (nt:similar to sp:p70718 pid:1651212 percent ident:.) (le:1676) (re:3130) (di:complement) U32737 U32737 g1573539 Haemophilus influenzae Rd 71421 -11536821 5000694117 (de:(hi0553) (pn:6-phosphogluconate dehydrogenase, decarboxylating:gnd) (gn:gnd) (gtcfc:1.3) (ec:1.1.1.44) (6pgd_haein) (keggfc:1.3) (tigrfc:6.10) (db:gtc-haemophilus influenzae)) HI0553 HI0553 Haemophilus influenzae 727 10000418

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875711	13885	36041	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875729	13886	36042	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875733	13887	36043	741	247

Description

5000694118 zwf:g6pd:hi0558 glucose-6-phosphate 1-dehydrogenase:g6pd
 (gtcfc:1.3:6.16) (ec:1.1.1.49) (keggfc:1.3:6.9) (tigrfc:6.10)
 (db:gtc-haemophilus influenzae) HI0558 HI0558 Haemophilus influenzae 727
 -11536822 72784 zwf:g6pd:hi0558 (ec:1.1.1.49) (de:glucose-6-phosphate
 1-dehydrogenase, (g6pd)) (db:swissprot) G6PD_HAEIN P44311 HAEMOPHILUS
 INFLUENZAE 727 -11536822 166158 probable glucose-6-phosphate
 1-dehydrogenase (cl:glucose-6-phosphate dehydrogenase) (ec:1.1.1.49)
 (db:pir2.dat) E64077 E64077 Haemophilus influenzae 727 -11536822 7500882002
 hi0558 glucose-6-phosphate 1-dehydrogenase zwf (db:genpept-bct1)
 (de:haemophilus influenzae rd section 52 of 163 of the complete genome.)
 (nt:similar to sp:p77809 pid:1651208 percent ident:.) (le:5264) (re:6748)
 (di:complement) U32737 U32737 g1573543 Haemophilus influenzae Rd 71421
 -11536822 6500732964 zwf:g6pd glucose-6-phosphate 1-dehydrogenase:g6pd
 (gtcfc:1.3:6.16) (ec:1.1.1.49) (keggfc:1.3:6.9) (tigrfc:6.10)
 (db:gtc-haemophilus influenzae) HI0558 HI0558 Haemophilus influenzae 727
 -11536822

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875741	13888	36044	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875748	13889	36045	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875771	13890	36046	471	156

Description

5000694119 rpe:dod:hi0566 dod protein:dod:ribulose-phosphate
3-epimerase:pentose-5-phosphate 3-epimerase:ppe (gtcfc:1.3:1.4:2.4:10.8)
(ec:5.1.3.1) (keggfc:1.3:1.4:2.3) (tigrfc:10.2) (db:gtc-haemophilus
influenzae) HI0566 HI0566 Haemophilus influenzae 727 -11536823 166113
ribulose-phosphate 3-epimerase (cl:yeast ribulose-5-phosphate-epimerase)
(ec:5.1.3.1) (db:pir2.dat) I64077 I64077 Haemophilus influenzae 727
-11536823 7500960731 hi0566 ribulose-phosphate 3-epimerase dod
(db:genpept-bct1) (de:haemophilus influenzae rd section 53 of 163 of the
complete genome.) (nt:similar to sp:p32661 gb:z19601 pid:41222 gb:u00096)
(le:2991) (re:3695) (di:complement) U32738 U32738 g1573553 Haemophilus
influenzae Rd 71421 -11536823 6500732965 rpe:dod dod
protein:dod:ribulose-phosphate 3-epimerase:pentose-5-phosphate
3-epimerase:ppe (gtcfc:1.3:1.4:2.4:10.8) (ec:5.1.3.1) (keggfc:1.3:1.4:2.3)
(tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0566 HI0566 Haemophilus
influenzae 727 -11536823

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875787	13891	36047	714	237

Description

6500732966 tkta:hi1023 transketolase 1:tk 1:transketolase:tk (gtcfc:1.3:2.4)
(ec:2.2.1.1) (keggfc:1.3:2.3) (tigrfc:6.10) (db:gtc-haemophilus influenzae)
HI1023 HI1023 Haemophilus influenzae 727 -11536824 101622 tkta:hi1023
(ec:2.2.1.1) (de:transketolase, (tk)) (db:swissprot) TKT_HAEIN P43757
HAEMOPHILUS INFLUENZAE 727 -11536824 137857 transketolase
(cl:transketolase:thiamine pyrophosphate-binding domain homology)
(ec:2.2.1.1) (db:pir2.dat) G64108 G64108 Haemophilus influenzae 727
-11536824 7500893209 hi1023 transketolase 1 tkta (db:genpept-bct1)
(de:haemophilus influenzae rd section 98 of 163 of the complete genome.)
(nt:similar to sp:p27302 gb:x68025 pid:312667) (le:1213) (re:3210)
(di:complement) U32783 U32783 g1574055 Haemophilus influenzae Rd 71421
-11536824 5000694120 (de:(hi1023) (pn:transketolase:tk:transketolase 1:tk
1:tkta) (gn:tkta) (gtcfc:1.3:2.4) (ec:2.2.1.1) (tkt_haein) (keggfc:1.3:2.3)
(tigrfc:6.10) (db:gtc-haemophilus influenzae)) HI1023 HI1023 Haemophilus
influenzae 727 10043454

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875790	13892	36048	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875802	13893	36049	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875808	13894	36050	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875814	13895	36051	669	222

Description

6500732967 deoc:hi1116 deoxyribose aldolase:deoxyribose-phosphate
aldolase:phosphodeoxyriboaldolase:deoxyriboaldolase (gtcfc:1.3:1.4:7.1)
(ec:4.1.2.4) (keggfc:1.3) (tigrfc:6.12) (db:gtc-haemophilus influenzae)
HI1116 HI1116 Haemophilus influenzae 727 -11536825 68253 deoc:hi1116
(ec:4.1.2.4) (de:(deoxyriboaldolase)) (db:swissprot) DEOC_HAEIN P44430
HAEMOPHILUS INFLUENZAE 727 -11536825 166087 deoxyribose-phosphate aldolase
(cl:deoxyribose-phosphate aldolase) (ec:4.1.2.4) (db:pir2.dat) H64183 H64183
Haemophilus influenzae 727 -11536825 7500880165 hi1116
deoxyribose-phosphate aldolase deoc (db:genpept-bct1) (de:haemophilus
influenzae rd section 106 of 163 of the completegenome.) (nt:similar to
gb:ae000666 percent ident: 51.58;) (le:8594) (re:9265) (di:direct) U32791
U32791 g1574670 Haemophilus influenzae Rd 71421 -11536825 5000694121
(de:(hi1116) (pn:deoxyribose-phosphate
aldolase:phosphodeoxyriboaldolase:deoxyriboaldolase:deoxyribose
aldolase:deoc) (gn:deoc) (gtcfc:1.3) (ec:4.1.2.4) (deoc_haein) (keggfc:1.3)
(tigrfc:6.12) (db:gtc-haemophilus influenzae)) HI1116 HI1116 Haemophilus
influenzae 727 10010846

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875835	13896	36052	1287	428

Description

6500732968 talb:hi1125 transaldolase b:transaldolase (gtcfc:1.3)
(ec:2.2.1.2) (keggfc:1.3) (tigrfc:6.10) (db:gtc-haemophilus influenzae)
HI1125 HI1125 Haemophilus influenzae 727 -11536826 166651
transaldolase::protein hi1125 (ec:2.2.1.2) (db:pir2.dat) D64167 D64167
Haemophilus influenzae 727 -11536826 7500960740 hi1125 transaldolase b talb
(db:genpept-bct1) (de:haemophilus influenzae rd section 107 of 163 of the
completegenome.) (nt:similar to gb:d10483 sp:p30148 pid:216439 gb:u00096)
(le:7559) (re:8512) (di:direct) U32792 U32792 g1574680 Haemophilus
influenzae Rd 71421 -11536826 5000694122 (de:(hi1125)
(pn:transaldolase:transaldolase b:talb) (gn:talb) (gtcfc:1.3) (ec:2.2.1.2)
(talb_haein) (keggfc:1.3) (tigrfc:6.10) (db:gtc-haemophilus influenzae))
HI1125 HI1125 Haemophilus influenzae 727 10088175

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875846	13897	36053	228	75

Description

6500732969 prsa:hi1609 phosphoribosylpyrophosphate
synthetase:ribose-phosphate pyrophosphokinase:phosphoribosyl pyrophosphate
synthetase (gtcfc:1.3:4.1) (ec:2.7.6.1) (keggfc:1.3:4.1) (tigrfc:8.3)
(db:gtc-haemophilus influenzae) HI1609 HI1609 Haemophilus influenzae 727
-11536827 81015 prsa:hi1609 (ec:2.7.6.1) (de:pyrophosphate synthetase))
(db:swissprot) KPRS_HAEIN P44328 HAEMOPHILUS INFLUENZAE 727 -11536827
139042 prsa ribose-phosphate pyrophosphokinase (cl:ribose-phosphate
pyrophosphokinase catalytic chain) (ec:2.7.6.1) (db:pir2.dat) C64132 C64132
Haemophilus influenzae 727 -11536827 7500884706 hi1609
phosphoribosylpyrophosphate synthetase prsa (db:genpept-bct1)
(de:haemophilus influenzae rd section 149 of 163 of the completegenome.)
(nt:similar to gb:m19488 sp:p15849 pid:154285 percent) (le:8412) (re:9359)
(di:direct) U32834 U32834 g1574451 Haemophilus influenzae Rd 71421 -11536827
5000694123 (de:(hi1609) (pn:ribose-phosphate
pyrophosphokinase:phosphoribosyl pyrophosphate
synthetase:phosphoribosylpyrophosphate synthetase:prsa) (gn:prsa)
(gtcfc:1.3:4.1) (ec:2.7.6.1) (kprs_haein) (keggfc:1.3:4.1) (tigrfc:8.3)
(db:gtc-h) HI1609 HI1609 Haemophilus influenzae 727 10023252

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501875859	13898	36054	459	152

Description

6500732970 eda:hi0047 2-keto-3-deoxy-6-phosphogluconate aldolase:putative
4-hydroxy-2-oxoglutarate aldolase:2-keto-4-hydroxyglutarate
aldolase:khg-aldolase / 2-dehydro-3-deoxyphosphogluconate
aldolase:phospho-2-dehydro-3-deoxygluconate
aldolase:phospho-2-keto-3-deoxygluconate
aldolase:2-keto-3-deoxy-6-phosphogluconate aldolase:kdpg-aldolase
(gtcfc:1.4:1.9:2.1:5.10) (keggfc:1.4:1.9:5.10) (tigrfc:6.6)
(db:gtc-haemophilus influenzae) HI0047 HI0047 Haemophilus influenzae 727
-11536828 59192 eda:hi0047 (ec:4.1.3.16:4.1.2.14)
(de:(2-keto-3-deoxy-6-phosphogluconate aldolase) (kdpg-aldolase))
(db:swissprot) ALKH_HAEIN P44480 HAEMOPHILUS INFLUENZAE 727 -11536828
165961 2-dehydro-3-deoxyphosphogluconate aldolase homolog hi0047
(cl:2-dehydro-3-deoxyphosphogluconate aldolase) (db:pir2.dat) A64045 A64045
Haemophilus influenzae 727 -11536828 7500876760 hi0047
4-hydroxy-2-oxoglutarate (db:genpept-bct1) (de:haemophilus influenzae rd
section 5 of 163 of the complete genome.) (nt:similar to gb:l20897 gb:m87458
gb:x63694 gb:x68871) (le:1303) (re:1941) (di:complement) U32690 U32690
g1572994 Haemophilus influenzae Rd 71421 -11536828 5000694124 (de:(hi0047)
(pn:putative 4-hydroxy-2-oxoglutarate aldolase:2-keto-4- hydroxyglutarate
aldolase:khg-aldolase :2-keto-3-deoxy-6-phosphogluconate aldolase:eda)
(gn:eda) (gtcfc:1.4:1.9:5.10) (ec:4.1.3.16) (alkh_haein) (keggfc:1.4:1.)
HI0047 HI0047 Haemophilus influenzae 727 10001931

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501875860	13899	36055	267	88

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501875868	13900	36056	186	61

Description

Hypothetical protein

ORF Name	NT ID	AA ID	NT LENGTH	AA LENGTH
7501875870	13901	36057	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875907	13902	36058	3354	1117

Description

6500732971 uxua:hi0055 mannonate hydratase:d-mannonate hydrolase
 (gtcfc:1.4:7.1) (ec:4.2.1.8) (keggfc:1.4) (tigrfc:6.12) (db:gtc-haemophilus
 influenzae) HI0055 HI0055 Haemophilus influenzae 727 -11536829 104079
 uxua:hi0055 (ec:4.2.1.8) (de:mannonate dehydratase, (d-mannonate hydrolase))
 (db:swissprot) UXUA_HAEIN P44488 HAEMOPHILUS INFLUENZAE 727 -11536829
 166081 mannonate dehydratase (ec:4.2.1.8) (db:pir2.dat) E64045 E64045
 Haemophilus influenzae 727 -11536829 7500893930 hi0055 mannonate
 dehydratase uxua (db:genpept-bct1) (de:haemophilus influenzae rd section 5
 of 163 of the complete genome.) (nt:similar to sp:p24215 gb:u14003
 pid:1160322) (le:8576) (re:9760) (di:direct) U32690 U32690 g1573002
 Haemophilus influenzae Rd 71421 -11536829 5000694125 (de:(hi0055)
 (pn:mannonate hydratase:d-mannonate hydrolase:uxua) (gn:uxua) (gtcfc:1.4)
 (ec:4.2.1.8) (uxua_haein) (keggfc:1.4) (tigrfc:6.12) (db:gtc-haemophilus
 influenzae)) HI0055 HI0055 Haemophilus influenzae 727 10045849

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875924	13903	36059	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875929	13904	36060	231	76

Description

6500732972 galu:hi0812 glucosephosphate
 uridylyltransferase:utp--glucose-1-phosphate uridylyltransferase:udp-glucose
 pyrophosphorylase:udpgp:alpha-d-glucosyl-1-phosphate
 uridylyltransferase:uridine diphosphoglucose pyrophosphorylase
 (gtcfc:1.4:1.6:4.3:7.2) (ec:2.7.7.9) (keggfc:1.4:1.6:4.3:7.1) (tigrfc:8.6)
 (db:gtc-haemophilus influenzae) HI0812 HI0812 Haemophilus influenzae 727
 -11536830 73094 galu:hi0812 (ec:2.7.7.9) (de:uridylyltransferase) (uridine
 diphosphoglucose pyrophosphorylase)) (db:swissprot) GALU_HAEIN P44878
 HAEMOPHILUS INFLUENZAE 727 -11536830 139259 utp--glucose-1-phosphate
 uridylyltransferase::udp-glucose pyrophosphorylase (cl:escherichia coli
 utp--glucose-1-phosphate uridylyltransferase) (ec:2.7.7.9) (db:pir1.dat)
 G64095 G64095 Haemophilus influenzae 727 -11536830 7500882103 hi0812
 glucosephosphate uridylyltransferase galu (db:genpept-bct1) (de:haemophilus
 influenzae rd section 78 of 163 of the complete genome.) (nt:similar to
 gb:m98830 sp:p25520 gb:x59940 pid:146073) (le:8097) (re:8984)
 (di:complement) U32763 U32763 g1573824 Haemophilus influenzae Rd 71421
 -11536830 5000694126 (de:(hi0812) (pn:utp--glucose-1-phosphate
 uridylyltransferase:udp-glucose
 pyrophosphorylase:udpalpha-d-glucosyl-1-phosphate
 uridylyltransferase:uridine diphosphoglucose
 pyrophosphorylase:glucosephosphate uridylyltransferase:galu) (gn) HI0812
 HI0812 Haemophilus influenzae 727 10015641

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875935	13905	36061	642	213

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875945	13906	36062	504	167

Description

6500732973 arad:hi1025 l-ribulose-phosphate
 4-epimerase:l-ribulose-5-phosphate 4-epimerase (gtcfc:1.4:7.1) (ec:5.1.3.4)
 (keggfc:1.4) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI1025 HI1025
 Haemophilus influenzae 727 -11536831 59964 sgbe:hi1025 (ec:5.1.-.-)
 (de:probable sugar isomerase sgbe,) (db:swissprot) SGBE_HAEIN P44989
 HAEMOPHILUS INFLUENZAE 727 -11536831 7500891592 hi1025
 l-ribulose-5-phosphate 4-epimerase arad (db:genpept-bct1) (de:haemophilus
 influenzae rd section 98 of 163 of the complete genome.) (nt:similar to
 gb:d10483 sp:p08203 gb:m15263 gb:m62646) (le:4066) (re:4761) (di:complement)
 U32783 U32783 g1574057 Haemophilus influenzae Rd 71421 -11536831 5000694127
 (de:(hi1025) (pn:l-ribulose-5-phosphate 4-epimerase:l-ribulose-phosphate
 4-epimerase:arad) (gn:arad) (gtcfc:1.4) (ec:5.1.3.4) (arad_haein)
 (keggfc:1.4) (tigrfc:6.12) (db:gtc-haemophilus influenzae)) HI1025 HI1025
 Haemophilus influenzae 727 10002697

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875947	13907	36063	783	260

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875960	13908	36064	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501875962	13909	36065	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501875973	13910	36066	1374	457

Description

6500732974 lyxk:hi1027 cryptic l-xylulose kinase:probable l-xylulose kinase:l-xylulokinase (gtcfc:1.4:14.1) (ec:2.7.1.53) (keggfc:1.4) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1027 HI1027 Haemophilus influenzae 727 -11536832 82781 lyx:lyxk:sgbk:hi1027 (ec:2.7.1.53) (de:probable l-xylulose kinase, (l-xylulokinase)) (db:swissprot) LYXK_HAEIN P44991 HAEMOPHILUS INFLUENZAE 727 -11536832 166611 hypothetical protein hi1027 (cl:xylulokinase) (db:pir2.dat) H64164 H64164 Haemophilus influenzae 727 -11536832 7500885226 hi1027 l-xylulose kinase lyx (db:genpept-bct1) (de:haemophilus influenzae rd section 98 of 163 of the complete genome.) (nt:similar to sp:p37677 pid:466718 gb:u00096) (le:5629) (re:7086) (di:complement) U32783 U32783 g1574059 Haemophilus influenzae Rd 71421 -11536832 5000694128 (de:(hi1027) (pn:probable l-xylulose kinase:l-xylulokinase:cryptic l-xylulose kinase) (gn:lyxk) (gtcfc:1.4) (ec:2.7.1.53) (lyxk_haein) (keggfc:1.4) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1027 HI1027 Haemophilus influenzae 727 10025001

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876008	13911	36067	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876049	13912	36068	468	155

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876054	13913	36069	432	143

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876055	13914	36070	345	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876064	13915	36071	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876075	13916	36072	399	132

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876076	13917	36073	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876103	13918	36074	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876127	13919	36075	516	172

Description

6500732975 xyla:hi1112 xylose isomerase (gtcfc:1.4:1.5:7.1) (ec:5.3.1.5) (keggfc:1.4:1.5) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI1112 HI1112 Haemophilus influenzae 727 -11536833 108186 xyla:hi1112 (ec:5.3.1.5) (de:xylose isomerase,) (db:swissprot) XYLA_HAEIN P44398 HAEMOPHILUS INFLUENZAE 727 -11536833 125787 xyla xylose isomerase (cl:xylose isomerase) (ec:5.3.1.5) (db:pir1.dat) (mp:for1177317-1178636) ISHIX D64183 Haemophilus influenzae 727 -11536833 7500894485 hi1112 xylose isomerase xyla (db:genpept-bct1) (de:haemophilus influenzae rd section 106 of 163 of the completegenome.) (nt:similar to gb:x04691 sp:p00944 gb:k01996 gb:s68257) (le:4093) (re:5412) (di:direct) U32791 U32791 g1574666 Haemophilus influenzae Rd 71421 -11536833 5000694129 (de:(hi1112) (pn:xylose isomerase:xyla) (gn:xyla) (gtcfc:1.4:1.5) (ec:5.3.1.5) (xyla_haein) (keggfc:1.4:1.5) (tigrfc:6.12) (db:gtc-haemophilus influenzae)) HI1112 HI1112 Haemophilus influenzae 727 10049918

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876133	13920	36076	372	123

Description

6500732976 xylb:hi1113 xylulose kinase (gtcfc:1.4:7.1) (ec:2.7.1.17) (keggfc:1.4) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI1113 HI1113 Haemophilus influenzae 727 -11536834 167272 xylulokinase homolog (cl:xylulokinase) (db:pir2.dat) E64183 E64183 Haemophilus influenzae 727 -11536834 7500960748 hi1113 xylulose kinase (db:genpept-bct1) (de:haemophilus influenzae rd section 106 of 163 of the completegenome.) (nt:similar to pid:2293419 percent ident: 52.56;) (le:5415) (re:6950) (di:direct) U32791 U32791 g1574667 Haemophilus influenzae Rd 71421 -11536834 5000694130 (de:(hi1113) (pn:xylulose kinase:xylulokinase) (gn:xylb) (gtcfc:1.4) (ec:2.7.1.17) (xylb_haein) (keggfc:1.4) (tigrfc:6.12) (db:gtc-haemophilus influenzae)) HI1113 HI1113 Haemophilus influenzae 727 10088329

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876134	13921	36077	639	212

Description

6500732977 nana:hi0142 n-acetylneuraminate lyase:n-acetylneuraminic acid aldolase:n-acetylneuraminate pyruvate lyase:nalase (gtcfc:1.4:7.1) (ec:4.1.3.3) (keggfc:4.4) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI0142 HI0142 Haemophilus influenzae 727 -11536835 86396 nana:hi0142 (ec:4.1.3.3) (de:(nalase)) (db:swissprot) NPL_HAEIN P44539 HAEMOPHILUS INFLUENZAE 727 -11536835 167021 n-acetylneuraminate lyase homolog (db:pir2.dat) G64050 G64050 Haemophilus influenzae 727 -11536835 7500886558 hi0142 n-acetylneuraminate lyase nana (db:genpept-bct1) (de:haemophilus influenzae rd section 15 of 163 of the complete genome.) (nt:similar to pid:1016806 percent identity: 79.05;) (le:2641) (re:3522) (di:complement) U32700 U32700 g1573098 Haemophilus influenzae Rd 71421 -11536835 5000694373 (de:(hi0142) (pn:probable n-acetylneuraminate lyase subunit:n-acetylneuraminic acid aldolase:n-acetylneuraminate pyruvate lyase:nalase:n-acetylneuraminate lyase:nana) (gn:nana) (gtcfc:7.1) (ec:4.1.3.3) (npl_haein) (keggfc:4.4) () HI0142 HI0142 Haemophilus influenzae 727 10028562

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876136	13922	36078	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876148	13923	36079	276	91

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876152	13924	36080	408	135

Description

5000694085 glucose kinase:glk:hypothetical protein (gtcfc:1.4:7.1) (keggfc:14.2) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI0144 HI0144 Haemophilus influenzae 727 -11536836 112683 hi0144 (de:hypothetical protein hi0144) (db:swissprot) YHCI_HAEIN P44541 HAEMOPHILUS INFLUENZAE 727 -11536836 166157 glucose kinase homolog (cl:haemophilus probable glucose kinase:glucose kinase homology) (db:pir2.dat) H64050 H64050 Haemophilus influenzae 727 -11536836 7500936814 hi0144 glucose kinase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 15 of 163 of the complete genome.) (nt:similar to sp:p45425 pid:606161 gb:u00096) (le:4392) (re:5294) (di:complement) U32700 U32700 g1573100 Haemophilus influenzae Rd 71421 -11536836 6500732978 glucose kinase:glk:hypothetical protein (gtcfc:1.4:7.1) (keggfc:14.2) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI0144 HI0144 Haemophilus influenzae 727 -11536836

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876159	13925	36081	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876182	13926	36082	2826	942

Description

6500732979 fuca:hi0611 fucose-1-phosphate aldolase:l-fucose phosphate aldolase (gtcfc:1.4:1.8:7.1) (ec:4.1.2.17) (keggfc:1.8) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI0611 HI0611 Haemophilus influenzae 727 -11536837 72498 fuca:hi0611 (ec:4.1.2.17) (de:l-fucose phosphate aldolase,) (db:swissprot) FUCA_HAEIN P44777 HAEMOPHILUS INFLUENZAE 727 -11536837 142083 l-fucose-phosphate aldolase (cl:l-ribulose-phosphate 4-epimerase) (ec:4.1.2.17) (db:pir2.dat) C64081 C64081 Haemophilus influenzae 727 -11536837 7500881900 hi0611 l-fucose phosphate aldolase fuca (db:genpept-bct1) (de:haemophilus influenzae rd section 58 of 163 of the complete genome.) (nt:similar to gb:m31059 sp:p11550 gb:x15025 pid:146042) (le:7077) (re:7727) (di:complement) U32743 U32743 g1573604 Haemophilus influenzae Rd 71421 -11536837 5000694140 (de:(hi0611) (pn:l-fucose phosphate aldolase:fucose-1-phosphate aldolase:fuca) (gn:fuca) (gtcfc:1.8) (ec:4.1.2.17) (fuca_haein) (keggfc:1.8) (tigrfc:6.12) (db:gtc-haemophilus influenzae)) HI0611 HI0611 Haemophilus influenzae 727 10015049

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876226	13927	36083	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876253	13928	36084	2034	677

Description

6500732980 fuck:hi0613 fucokinase:l-fuculokinase (gtcfc:1.4:1.8:7.1) (ec:2.7.1.51) (keggfc:1.8) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI0613 HI0613 Haemophilus influenzae 727 -11536838 72502 fuck:hi0613 (ec:2.7.1.51) (de:l-fuculokinase,) (db:swissprot) FUCK_HAEIN P44399 HAEMOPHILUS INFLUENZAE 727 -11536838 166145 fucokinase homolog (cl:rhamnulokinase) (db:pir2.dat) E64081 E64081 Haemophilus influenzae 727 -11536838 7500881904 hi0613 fuculokinase fuck (db:genpept-bct1) (de:haemophilus influenzae rd section 58 of 163 of the complete genome.) (nt:similar to sp:p11553 gb:x15025 pid:41506 pid:882698) (le:8195) (re:9607) (di:complement) U32743 U32743 g1573606 Haemophilus influenzae Rd 71421 -11536838 5000694141 (de:(hi0613) (pn:l-fuculokinase:fucokinase:fuck) (gn:fuck) (gtcfc:1.8) (ec:2.7.1.51) (fuck_haein) (keggfc:1.8) (tigrfc:6.12) (db:gtc-haemophilus influenzae)) HI0613 HI0613 Haemophilus influenzae 727 10015053

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876260	13929	36085	579	192

Description

6500732981 fuci:hi0614 l-fucose isomerase (gtcfc:1.4:1.6:7.1) (ec:5.3.1.-) (keggfc:1.6) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI0614 HI0614 Haemophilus influenzae 727 -11536839 72500 fuci:hi0614 (ec:5.3.1.25) (de:l-fucose isomerase,) (db:swissprot) FUCI_HAEIN P44779 HAEMOPHILUS INFLUENZAE 727 -11536839 142243 fuci isomerase fuci (cl:isomerase fuci) (ec:5.-.-.-) (db:pir2.dat) F64081 F64081 Haemophilus influenzae 727 -11536839 7500881902 hi0614 l-fucose isomerase fuci (db:genpept-bct1) (de:haemophilus influenzae rd section 58 of 163 of the complete genome.) (nt:similar to sp:p11552 gb:x15025 pid:41505 pid:882697) (le:9680) (re:11494) (di:complement) U32743 U32743 g1573607 Haemophilus influenzae Rd 71421 -11536839 5000694137 (de:(hi0614) (pn:l-fucose isomerase:fuci) (gn:fuci) (gtcfc:1.6) (ec:5.3.1.-) (fuci_haein) (keggfc:1.6) (tigrfc:6.12) (db:gtc-haemophilus influenzae)) HI0614 HI0614 Haemophilus influenzae 727 10015051

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876276	13930	36086	267	88

Description

6500732982 galk:hi0819 galactokinase (gtcfc:1.4:1.6:7.1) (ec:2.7.1.6) (keggfc:1.6) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI0819 HI0819 Haemophilus influenzae 727 -11536840 138443 galk galactokinase (cl:galactokinase) (ec:2.7.1.6) (db:pir2.dat) D64096 D64096 Haemophilus influenzae 727 -11536840 7500954063 hi0819 galactokinase galk (db:genpept-bct1) (de:haemophilus influenzae rd section 79 of 163 of the complete genome.) (nt:similar to sp:p31767 gb:x65934 pid:1573832 percent) (le:3706) (re:4899) (di:complement) U32764 U32764 g1573832 Haemophilus influenzae Rd 71421 -11536840 5000694138 (de:(hi0819) (pn:galactokinase:galk) (gn:galk) (gtcfc:1.6) (ec:2.7.1.6) (gall_haein) (keggfc:1.6) (tigrfc:6.12) (db:gtc-haemophilus influenzae)) HI0819 HI0819 Haemophilus influenzae 727 10070644

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876278	13931	36087	792	263

Description

6500732983 fuca:hi1012 fucose-1-phosphate aldolase (gtcfc:1.4:7.1) (keggfc:14.2) (tigrfc:6.12) (db:gtc-haemophilus influenzae) HI1012 HI1012 Haemophilus influenzae 727 -11536841 5500686585 hi1012 (de:hypothetical protein hi1012) (db:swissprot) YGBL HAEIN Q57199 HAEMOPHILUS INFLUENZAE 727 -11536841 166146 l-fucose-phosphate aldolase homolog (db:pir2.dat) B64108 B64108 Haemophilus influenzae 727 -11536841 7500924035 hi1012 sugar isomerase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 97 of 163 of the complete genome.) (nt:similar to pid:882631 gb:u00096 sp:q46890) (le:2256) (re:2888) (di:direct) U32782 U32782 g1574044 Haemophilus influenzae Rd 71421 -11536841 5000694086 (de:(hi1012) (pn:fucose-1-phosphate aldolase:fuca) (gn:fuca) (gtcfc:1.1:1.3) (ec:) (keggfc:11.2) (tigrfc:6.12) (db:gtc-haemophilus influenzae)) HI1012 HI1012 Haemophilus influenzae 727 10088086

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876285	13932	36088	870	290

Description

6500732984 kdsb:hi0058 ctp:cmp-3-deoxy-d-manno-octulosonate-cytidylyl-transferase:3-deoxy-manno-octulosonate cytidylyltransferase:cmp-kdo synthetase:cmp-2-keto-3-deoxyoctulosonic acid synthetase:cks (gtcfc:1.5:11.2) (ec:2.7.7.38) (keggfc:1.5) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI0058 HI0058 Haemophilus influenzae 727 -11536842 166066 kdsb 3-deoxy-manno-octulosonate cytidylyltransferase (cl:3-deoxy-manno-octulosonate cytidylyltransferase) (ec:2.7.7.38) (db:pir2.dat) G64045 G64045 Haemophilus influenzae 727 -11536842 7500960644 hi0058 3-deoxy-d-manno-octulosonate (db:genpept-bct1) (de:haemophilus influenzae rd section 6 of 163 of the complete genome.) (nt:similar to gb:j02614 sp:p04951 pid:146554 gb:u00096) (le:1910) (re:2674) (di:complement) U32691 U32691 g1573006 Haemophilus influenzae Rd 71421 -11536842 5000694131 (de:(hi0058) (pn:3-deoxy-manno-octulosonate cytidylyltransferase:cmp-kdo synthetase:cmp-2-keto-3-deoxyoctulosonic acid synthetase:cks:ctp:cmp-3-deoxy-d-manno-octulosonate-cytidylyl-transferase:kd sb) (gn:kdsb) (gtcfc:1.5) (ec:2.7.7.38)) HI0058 HI0058 Haemophilus influenzae 727 10088069

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876289	13933	36089	486	161

Description

6500732985 rffg:hi0873 udp-n-acetylglucosamine epimerase:rffe:dtdp-glucose 4:6-dehydratase (gtcfc:1.5:4.3:11.2) (ec:4.2.1.46) (keggfc:1.5:4.3) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI0873 HI0873 Haemophilus influenzae 727 -11536843 94206 rffg:hi0873 (ec:4.2.1.46) (de:dtdp-glucose 4,6-dehydratase,) (db:swissprot) RFFG_HAEIN P44914 HAEMOPHILUS INFLUENZAE 727 -11536843 167246 dtdpglucose 4:6-dehydratase::dtdp-glucose dehydratase (cl:escherichia coli udpglucose 4-epimerase:udpglucose 4-epimerase homology) (ec:4.2.1.46) (db:pir2.dat) C64099 C64099 Haemophilus influenzae 727 -11536843 7500889703 hi0873 dtdp-glucose 4:6-dehydratase rffg (db:genpept-bct1) (de:haemophilus influenzae rd section 84 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p27830 pid:148191 gb:u00096) (le:3044) (re:4060) (di:direct) U32769 U32769 g1573891 Haemophilus influenzae Rd 71421 -11536843 5000694133 (de:(hi0873) (pn:dtdp-glucose 4,6-dehydratase:udp-n-acetylglucosamine epimerase:rffe) (gn:rffg) (gtcfc:1.5:4.3) (ec:4.2.1.46) (rffg_haein) (keggfc:1.5:4.3) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI0873 HI0873 Haemophilus influenzae 727 10036189

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876290	13934	36090	369	122

Description

6500732986 rfad:hi1114 adp-1-glycero-d-mannoheptose-6-epimerase (gtcfc:1.5:11.2) (ec:5.1.3.-) (keggfc:1.5) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1114 HI1114 Haemophilus influenzae 727 -11536844 94118 rfad:hi1114 (ec:5.1.3.20) (de:glyceromanno-heptose 6-epimerase)) (db:swissprot) RFAD_HAEIN P45048 HAEMOPHILUS INFLUENZAE 727 -11536844 165988 adp-1-glycero-d-mannoheptose-6-epimerase (ec:5.1.3.-) (db:pir2.dat) F64183 F64183 Haemophilus influenzae 727 -11536844 7500889670 hi1114 adp-1-glycero-d-mannoheptose-6-epimerase rfad (db:genpept-bct1) (de:haemophilus influenzae rd section 106 of 163 of the completegenome.) (nt:similar to sp:p17963 gb:m33577 gb:x54492 pid:147576) (le:7001) (re:7927) (di:complement) U32791 U32791 g1574668 Haemophilus influenzae Rd 71421 -11536844 5000694134 (de:(hi1114) (pn:adp-1-glycero-d-mannoheptose-6-epimerase:rfad) (gn:rfad) (gtcfc:1.5) (ec:5.1.3.-) (rfad_haein) (keggfc:1.5) (tigrfc:3.3) (db:gtc-haemophilus influenzae)) HI1114 HI1114 Haemophilus influenzae 727 10036101

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876300	13935	36091	411	136

Description

6500732987 murg:hi1138 transferase:peptidoglycan
synthesis:udp-n-acetylglucosamine--n-acetylmuramyl-pentapeptide
pyrophosphoryl-undecaprenol n-acetylglucosamine transferase
(gtcfc:1.5:7.1:8.5:11.3:11.4) (ec:2.4.1.-) (keggfc:1.5:7.2:7.3:8.5)
(tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1138 HI1138 Haemophilus
influenzae 727 -11536845 84719 murg:hi1138 (ec:2.4.1.-) (de:(ec 2.4.1.-))
(db:swissprot) MURG_HAEIN P45065 HAEMOPHILUS INFLUENZAE 727 -11536845
154441 murg udp-n-acetylglucosamine--n-acetylmuramyl-pentapeptide
pyrophosphoryl-undecaprenol n-acetylglu... (cl:murg protein) (ec:2.4.1.-)
(db:pir2.dat) D64185 D64185 Haemophilus influenzae 727 -11536845 7500886153
hi1138 udp-n-acetylglucosamine--n-acetylmuramyl- (db:genpept-bct1)
(de:haemophilus influenzae rd section 108 of 163 of the completegenome.)
(nt:similar to gb:d10483 sp:p17443 gb:x52540 pid:216504) (le:10346)
(re:11401) (di:direct) U32793 U32793 g1574693 Haemophilus influenzae Rd
71421 -11536845 5000694385 (de:(hi1138)
(pn:udp-n-acetylglucosamine--n-acetylmuramyl-pentapeptide
pyrophosphoryl-undecaprenol n-acetylglucosamine transferase:transferase,
peptidoglycan synthesis:murg) (gn:murg) (gtcfc:7.2:8.5) (ec:2.4.1.-)
(murg_haein) (k)) HI1138 HI1138 Haemophilus influenzae 727 10026910

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876306	13936	36092	414	137

Description

6500732988 kdsa:hi1557 2-dehydro-3-deoxyphosphooctonate
aldolase:phospho-2-dehydro-3-deoxyoctonate
aldolase:3-deoxy-d-manno-octulosonic acid 8-phosphate synthetase:kdo 8-p
synthase (gtcfc:1.5:11.2) (ec:4.1.2.16) (keggfc:1.5) (tigrfc:3.3)
(db:gtc-haemophilus influenzae) HI1557 HI1557 Haemophilus influenzae 727
-11536846 80597 kdsa:hi1557 (ec:4.1.2.16) (de:8-phosphate synthetase) (kdo
8-p synthase)) (db:swissprot) KDSA_HAEIN P45251 HAEMOPHILUS INFLUENZAE 727
-11536846 141671 kdsa 2-dehydro-3-deoxyphosphooctonate aldolase
(cl:phospho-2-dehydro-3-deoxyoctonate aldolase) (ec:4.1.2.16) (db:pir2.dat)
G64129 G64129 Haemophilus influenzae 727 -11536846 7500884573 hi1557
2-dehydro-3-deoxyphosphooctonate aldolase (db:genpept-bct1) (de:haemophilus
influenzae rd section 145 of 163 of the completegenome.) (nt:similar to
sp:p17579 gb:x05552 pid:940498) (le:12179) (re:13033) (di:complement) U32830
U32830 g1574401 Haemophilus influenzae Rd 71421 -11536846 5000694135
(de:(hi1557) (pn:phospho-2-dehydro-3- deoxyoctonate
aldolase:3-deoxy-d-manno-octulosonic acid 8-phosphate synthetase:kdo 8-p
synthase:2-dehydro-3-deoxyphosphooctonate aldolase:kdsa) (gn:kdsa)
(gtcfc:1.5) (ec:4.1.2.16) (kdsa_haein)) HI1557 HI1557 Haemophilus influenzae
727 10022839

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876316	13937	36093	1128	375

Description

5000694386 rfe:hi1716 cgsc no 294 protein:putative undecaprenyl-phosphate alpha-n-acetylglucosaminyltransferase (gtcfc:1.5:7.1:8.5:11.2:11.3:11.4) (ec:2.4.1.-) (keggfc:1.5:7.2:7.3:8.5) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1716 HI1716 Haemophilus influenzae 727 -11536847 94200 rfe:hi1716 (ec:2.4.1.-) (de:(ec 2.4.1.-)) (db:swissprot) RFE_HAEIN P45341 HAEMOPHILUS INFLUENZAE 727 -11536847 167137 rfe rfe protein (db:pir2.dat) A64138 A64138 Haemophilus influenzae 727 -11536847 7500889697 hi1716 undecaprenyl-phosphate (db:genpept-bct1) (de:haemophilus influenzae rd section 159 of 163 of the completegenome.) (nt:similar to gb:m87049 sp:p24235 gb:m76129 pid:147578) (le:5680) (re:6747) (di:complement) U32844 U32844 g1574571 Haemophilus influenzae Rd 71421 -11536847 6500732989 rfe cgsc no 294 protein:putative undecaprenyl-phosphate alpha-n-acetylglucosaminyltransferase (gtcfc:1.5:7.1:8.5:11.2:11.3:11.4) (ec:2.4.1.-) (keggfc:1.5:7.2:7.3:8.5) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1716 HI1716 Haemophilus influenzae 727 -11536847

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876333	13938	36094	537	178

Description

6500732990 gale:hi0351 udp-glucose 4-epimerase:galactowaldenase (gtcfc:1.6:4.3) (ec:5.1.3.2) (keggfc:1.6:4.3) (tigrfc:8.6) (db:gtc-haemophilus influenzae) HI0351 HI0351 Haemophilus influenzae 727 -11536848 73072 gale:hi0351 (ec:5.1.3.2) (de:galactose 4-epimerase)) (db:swissprot) GALE_HAEIN P24325 HAEMOPHILUS INFLUENZAE 727 -11536848 142075 gale udpglucose 4-epimerase::udpgalactose 4-epimerase (cl:escherichia coli udpglucose 4-epimerase:udp-glucose 4-epimerase homology) (ec:5.1.3.2) (db:pir2.dat) A64063 A64063 Haemophilus influenzae 727 -11536848 7500882082 hi0351 udp-glucose 4-epimerase gale (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to sp:p24325 gb:l42023 pid:1003592) (le:9902) (re:10918) (di:complement) U32719 U32719 g1573321 Haemophilus influenzae Rd 71421 -11536848 5000694136 (de:(hi0351) (pn:udp-glucose 4-epimerase:udp-glucose 4-epimerase:galactowaldenase:gale) (gn:gale) (gtcfc:1.6:4.3) (ec:5.1.3.2) (gale_haein) (keggfc:1.6:4.3) (tigrfc:8.6) (db:gtc-haemophilus influenzae)) HI0351 HI0351 Haemophilus influenzae 727 10015619

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876334	13939	36095	639	212

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876337	13940	36096	651	216

Description

6500732991 galt:hi0820 galactose-1-phosphate uridylyltransferase (gtcfc:1.6:4.3) (ec:2.7.7.10) (keggfc:1.6:4.3) (tigrfc:8.6) (db:gtc-haemophilus influenzae) HI0820 HI0820 Haemophilus influenzae 727 -11536849 73042 galt:hi0820 (ec:2.7.7.10) (de:galactose-1-phosphate uridylyltransferase,) (db:swissprot) GAL7_HAEIN P31764 HAEMOPHILUS INFLUENZAE 727 -11536849 139271 galt udpglucose--hexose-1-phosphate uridylyltransferase (cl:udpglucose--hexose-1-phosphate uridylyltransferase) (ec:2.7.7.12) (db:pir2.dat) E64096 E64096 Haemophilus influenzae 727 -11536849 7500882078 hi0820 galactose-1-phosphate uridylyltransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 79 of 163 of the complete genome.) (nt:similar to sp:p31764 gb:x65934 pid:1573833 percent) (le:4937) (re:5986) (di:complement) U32764 U32764 g1573833 Haemophilus influenzae Rd 71421 -11536849 5000694139 (de:(hi0820) (pn:galactose-1-phosphate uridylyltransferase:galt) (gn:galt) (gtcfc:1.6:4.3) (ec:2.7.7.10) (gal7 haein) (keggfc:1.6:4.3) (tigrfc:8.6) (db:gtc-haemophilus influenzae)) HI0820 HI0820 Haemophilus influenzae 727 10015589

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876341	13941	36097	246	81

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876361	13942	36098	2895	965

Description

6500732992 leua:hi0986 isopropylmalate synthase:2-isopropylmalate synthase:alpha-isopropylmalate synthase:alpha-ipm synthetase (gtcfc:1.8:5.7) (ec:4.1.3.12) (keggfc:1.8:5.7) (tigrfc:1.3) (db:gtc-haemophilus influenzae) HI0986 HI0986 Haemophilus influenzae 727 -11536850 166931 2-isopropylmalate synthase::alpha-isopropylmalate synthase (cl:2-isopropylmalate synthase leua) (ec:4.1.3.12) (db:pir2.dat) E64106 E64106 Haemophilus influenzae 727 -11536850 7500960643 hi0986 2-isopropylmalate synthase leua (db:genpept-bct1) (de:haemophilus influenzae rd section 94 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p09151 pid:216492 gb:u00096) (le:4897) (re:6492) (di:direct) U32779 U32779 g1574015 Haemophilus influenzae Rd 71421 -11536850 5000694142 (de:(hi0986) (pn:2-isopropylmalate synthase:alpha-isopropylmalate synthase:alpha-ipm synthetase:isopropylmalate synthase:leua) (gn:leua) (gtcfc:1.8:5.7) (ec:4.1.3.12) (leu1 haein) (keggfc:1.8:5.7) (tigrfc:1.3) (db:gtc-haemophilu) HI0986 HI0986 Haemophilus influenzae 727 10088206

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876367	13943	36099	636	211

Description

GTC ORF with score 112 to: (fn:required for conidial pigmentation)
(db:genpept-pln2) (de:aspergillus fumigatus polyketide synthase (alb1) gene,
completedcds.) (nt:alb1) (le:598:932:1268:4755:5584)
(re:884:1220:4699:5510:7260) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876390	13944	36100	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876397	13945	36101	708	236

Description

6500732993 pta:hi1203 phosphate acetyltransferase:phosphotransacetylase
(gtcfc:1.8) (ec:2.3.1.8) (keggfc:1.8) (db:gtc-haemophilus influenzae) HI1203
HI1203 Haemophilus influenzae 727 -11536851 166678 phosphate
acetyltransferase (cl:phosphate acetyltransferase pta) (ec:2.3.1.8)
(db:pir2.dat) B64169 B64169 Haemophilus influenzae 727 -11536851 7500960724
hi1203 phosphate acetyltransferase pta (db:genpept-bct1) (de:haemophilus
influenzae rd section 114 of 163 of the completegenome.) (nt:similar to
sp:p39184 gb:u00096 pid:1359438) (le:8896) (re:11031) (di:complement) U32799
U32799 g1574131 Haemophilus influenzae Rd 71421 -11536851 5000694143
(de:(hi1203) (pn:phosphate acetyltransferase:phosphotransacetylase) (gn:pta)
(gtcfc:1.8) (ec:2.3.1.8) (pta_haein) (keggfc:1.8) (db:gtc-haemophilus
influenzae)) HI1203 HI1203 Haemophilus influenzae 727 10088180

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876402	13946	36102	456	151

Description

6500732994 ppc:hi1636 phosphoenolpyruvate carboxylase:pepcase:pepc
 (gtcfc:1.8:2.2:2.4:2.5) (ec:4.1.1.31) (keggfc:1.8:2.3:2.4) (tigrfc:6.7)
 (db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-pyruvate and
 acetyl-coa metabolism:energy metabolism-methane metabolism:energy
 metabolism-carbon fixation:energy meta... HI1636 HI1636 Haemophilus
 influenzae 727 -11536852 62746 ppc:hi1636 (ec:4.1.1.31)
 (de:phosphoenolpyruvate carboxylase, (pepcase) (pepc)) (db:swissprot)
 CAPP_HAEIN P43920 HAEMOPHILUS INFLUENZAE 727 -11536852 141508
 phosphoenolpyruvate carboxylase (cl:phosphoenolpyruvate carboxylase)
 (ec:4.1.1.31) (db:pir2.dat) I64133 I64133 Haemophilus influenzae 727
 -11536852 7500878161 hi1636 phosphoenolpyruvate carboxylase ppc
 (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the
 completengenome.) (nt:similar to sp:p00864 gb:j02632 gb:x01700 gb:x05903)
 (le:7782) (re:10421) (di:direct) U32836 U32836 g1574482 Haemophilus
 influenzae Rd 71421 -11536852 5000694145 (de:(hi1636)
 (pn:pepcase:pepc:phosphoenolpyruvate carboxylase:ppc) (gn:ppc)
 (gtcfc:1.8:2.4:2.5) (ec:4.1.1.31) (capp_haein) (keggfc:1.8:2.3:2.4)
 (tigrfc:6.7) (db:gtc-haemophilus influenzae)) HI1636 HI1636 Haemophilus
 influenzae 727 10005420

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876403	13947	36103	630	209

Description

6500732995 dld:hi1649 d-lactate dehydrogenase (gtcfc:1.1:1.8:2.8)
 (ec:1.1.1.28) (keggfc:1.8) (tigrfc:6.1) (db:gtc-haemophilus influenzae)
 HI1649 HI1649 Haemophilus influenzae 727 -11536853 81648 dld:hi1649
 (ec:1.1.1.28) (de:d-lactate dehydrogenase,) (db:swissprot) LDHD_HAEIN P45295
 HAEMOPHILUS INFLUENZAE 727 -11536853 136183 d-lactate dehydrogenase
 (cl:d-lactate dehydrogenase) (ec:1.1.1.28) (db:pir2.dat) I64134 I64134
 Haemophilus influenzae 727 -11536853 7500884840 hi1649 d-lactate
 dehydrogenase dld (db:genpept-bct1) (de:haemophilus influenzae rd section
 153 of 163 of the completengenome.) (nt:similar to gb:m10038 sp:p06149
 gb:x01067 pid:145753) (le:304) (re:1998) (di:complement) U32838 U32838
 g1574498 Haemophilus influenzae Rd 71421 -11536853 5000694146 (de:(hi1649)
 (pn:d-lactate dehydrogenase:dld) (gn:dld) (gtcfc:1.8) (ec:1.1.1.28)
 (ldhd_haein) (keggfc:1.8) (tigrfc:6.1) (db:gtc-haemophilus influenzae))
 HI1649 HI1649 Haemophilus influenzae 727 10023883

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876419	13948	36104	315	104

Description

6500732996 lldd:lctd:hi1739b l-lactate dehydrogenase:cytochrome (gtcfc:1.1:1.8:2.8) (ec:1.1.2.3) (keggfc:1.8) (db:gtc-haemophilus influenzae) HI1739B HI1739B Haemophilus influenzae 727 -11536854 82263 lldd:hi1739.1 (ec:1.1.2.3) (de:l-lactate dehydrogenase (cytochrome),) (db:swissprot) LLDD_HAEIN P46454 HAEMOPHILUS INFLUENZAE 727 -11536854 7500885081 hi1739.1 l-lactate dehydrogenase lctd (db:genpept-bct1) (de:haemophilus influenzae rd section 162 of 163 of the completegenome.) (nt:similar to sp:p33232 gb:l13970 pid:404695) (le:6035) (re:7180) (di:complement) U32847 U32847 g1574598 Haemophilus influenzae Rd 71421 -11536854 5000694147 (de:(hi17391) (pn:l-lactate dehydrogenase:cytochrome) (gn:lldd) (gtcfc:1.8) (ec:1.1.2.3) (lldd_haein) (keggfc:1.8) (db:gtc-haemophilus influenzae)) HI17391 HI17391 Haemophilus influenzae 727 10024493

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876420	13949	36105	1410	470

Description

6500732997 acoc:hi0193 dihydrolipoamide acetyltransferase (gtcfc:1.8) (keggfc:14.2) (tigrfc:6.11) (db:gtc-haemophilus influenzae) HI0193 HI0193 Haemophilus influenzae 727 -11536855 7000687079 hi0193 (ec:3.1.-.-) (de:putative esterase/lipase hi0193,) (db:swissprot) Y193_HAEIN Q57427 HAEMOPHILUS INFLUENZAE 727 -11536855 166094 hypothetical protein hi0193 (cl:tropinesterase) (db:pir2.dat) E64053 E64053 Haemophilus influenzae 727 -11536855 7500894852 hi0193 esterase/lipase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 19 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1786902 percent identity:) (le:5197) (re:6060) (di:complement) U32704 U32704 g1573150 Haemophilus influenzae Rd 71421 -11536855 5000694150 (de:(hi0193) (pn:dihydrolipoamide acetyltransferase:acoc) (gn:acoc) (gtcfc:1.8) (ec:) (keggfc:11.2) (tigrfc:6.11) (db:gtc-haemophilus influenzae)) HI0193 HI0193 Haemophilus influenzae 727 10088073

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876424	13950	36106	186	61

Description

6500732998 gph:hi0565 phosphoglycolate phosphatase (gtcfc:1.9) (ec:3.1.3.18) (keggfc:1.9) (db:gtc-haemophilus influenzae) HI0565 HI0565 Haemophilus influenzae 727 -11536856 74360 gph:hi0565 (ec:3.1.3.18) (de:phosphoglycolate phosphatase, (pgp)) (db:swissprot) GPH_HAEIN P44755 HAEMOPHILUS INFLUENZAE 727 -11536856 166449 hypothetical protein hi0565 (db:pir2.dat) G64154 G64154 Haemophilus influenzae 727 -11536856 7500882663 hi0565 phosphoglycolate phosphatase gph (db:genpept-bct1) (de:haemophilus influenzae rd section 53 of 163 of the complete genome.) (nt:similar to sp:p32662 gb:z19601 pid:41223 pid:606319) (le:2271) (re:2945) (di:complement) U32738 U32738 g1573552 Haemophilus influenzae Rd 71421 -11536856 5000694151 (de:(hi0565) (pn:phosphoglycolate phosphatase) (gn:gph) (gtcfc:1.9) (ec:3.1.3.18) (gph_haein) (keggfc:1.9) (db:gtc-haemophilus influenzae)) HI0565 HI0565 Haemophilus influenzae 727 10016877

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876449	13951	36107	1071	356

Description

6500732999 fold:hi0609 5:10-methylene-tetrahydrofolate dehydrogenase:methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase (gtcfc:1.9:9.6) (keggfc:1.9:9.8) (tigrfc:2.2) (db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-glyoxylate and dicarboxylate metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) HI0609 HI0609 Haemophilus influenzae 727 -11536857 136632 methylenetetrahydrofolate dehydrogenase nadp+:methenyltetrahydrofolate cyclohydrolase (cl:methylenetetrahydrofolate dehydrogenase (nad+):methylenetetrahydrofolate dehydrogenase (nad+) homology) (ec:1.5.1.5:3.5.4.9) (db:pir2.dat) A64081 A64081 Haemophilus influenzae 727 -11536857 7500953856 hi0609 methylenetetrahydrofolate (db:genpept-bct1) (de:haemophilus influenzae rd section 58 of 163 of the complete genome.) (nt:similar to gb:d10588 sp:p24186 gb:m74789 pid:146011) (le:4376) (re:5224) (di:complement) U32743 U32743 g1573602 Haemophilus influenzae Rd 71421 -11536857 5000694153 (de:(hi0609) (pn:methylenetetrahydrofolate dehydrogenase :5,10-methylene-tetrahydrofolate dehydrogenase:fold) (gn:fold) (gtcfc:1.9:9.8) (ec:1.5.1.5) (fold_haein) (keggfc:1.9:9.8) (tigrfc:2.2) (db:gtc-haemophilus influenzae)) HI0609 HI0609 Haemophilus influenzae 727 10069586

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876456	13952	36108	1062	353
<u>Description</u>				

GTC ORF with score 144 to: (sr:thale cress) (db:genpept-pln2)
 (de:arabidopsis thaliana dna chromosome 4, bac clone f4b14 (essaiiproject).)
 (nt:contains eukaryotic rna polymerase ii heptapeptide)
 (le:24678:24953:25138) (re:24846:25024:28199) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876458	13953	36109	1095	364
<u>Description</u>				

GTC ORF with score 352 to: (sr:human) (db:genpept) (de:homo sapiens s164
 gene, partial cds; ps1 and hypothetical proteingenes, complete cds; and s171
 gene, partial cds.) (nt:unknown; intron-exon boundaries defined by ests)
 (le:<1465:5979:14890:17363) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876459	13954	36110	630	209
<u>Description</u>				

6500733000 def:hi0622 polypeptide deformylase:formylmethionine
 deformylase:polypeptide ormylase:pdf:formylmethionine ormylase
 (gtcfc:1.9:5.4:10.6:10.7) (ec:3.5.1.31) (keggfc:1.9:5.4:10.1) (tigrfc:12.4)
 (db:gtc-haemophilus influenzae) HI0622 HI0622 Haemophilus influenzae 727
 -11536858 68224 def:hi0622 (ec:3.5.1.31) (de:deformylase) (db:swissprot)
 DEF_HAEIN P44786 HAEMOPHILUS INFLUENZAE 727 -11536858 167096
 n-formylmethionylaminoacyl-trna deformylase (cl:polypeptide deformylase)
 (ec:3.5.1.27) (db:pir2.dat) D64082 D64082 Haemophilus influenzae 727
 -11536858 7500880140 hi0622 polypeptide deformylase def (db:genpept-bct1)
 (de:haemophilus influenzae rd section 60 of 163 of the complete genome.)
 (nt:similar to sp:p27251 gb:x77800 pid:41474 pid:443989) (le:3927) (re:4436)
 (di:direct) U32745 U32745 g1573618 Haemophilus influenzae Rd 71421 -11536858
 5000694154 (de:(hi0622) (pn:polypeptide ormylase:pdf:formylmethionine
 ormylase:polypeptide deformylase:formylmethionine deformylase:def) (gn:def)
 (gtcfc:1.9:5.4:10.5) (ec:3.5.1.31) (def_haein) (keggfc:1.9:5.4:10.1)
 (tigrfc:12.4) (db:gtc-ha) HI0622 HI0622 Haemophilus influenzae 727 10010817

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876470	13955	36111	609	202

Description

6500733001 puru:hi1588 formyltetrahydrofolate
hydrolase:formyltetrahydrofolate deformylase:formyl-fh:4 hydrolase
(gtcfc:1.9:4.1:9.6) (ec:3.5.1.10) (keggfc:1.9:9.8) (tigrfc:8.3)
(db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-glyoxylate
and dicarboxylate metabolism:nucleotide metabolism-purine
metabolism:metabolism of cofactors and vitamins-biotin m... HI1588 HI1588
Haemophilus influenzae 727 -11536859 92483 puru:hi1588 (ec:3.5.1.10)
(de:hydrolase)) (db:swissprot) PURU_HAEIN Q03432 HAEMOPHILUS INFLUENZAE 727
-11536859 137833 purn formyltetrahydrofolate deformylase
(cl:phosphoribosylglycinamide formyltransferase:phosphoribosylglycinamide
formyltransferase homology) (ec:3.5.1.10) (db:pir2.dat) E64131 E64131
Haemophilus influenzae 727 -11536859 7500889094 hi1588
formyltetrahydrofolate deformylase puru (db:genpept-bct1) (de:haemophilus
influenzae rd section 148 of 163 of the completegenome.) (nt:similar to
gb:120251 sp:p37051 gb:m64675 pid:402694) (le:65) (re:901) (di:direct)
U32833 U32833 g1574433 Haemophilus influenzae Rd 71421 -11536859 5000694155
(de:(hi1588) (pn:formyltetrahydrofolate deformylase:formyl-fh:4
hydrolase:formyltetrahydrofolate hydrolase:puru) (gn:puru) (gtcfc:1.9:9.8)
(ec:3.5.1.10) (puru_haein) (keggfc:1.9:9.8) (tigrfc:8.3) (db:gtc-haemophilus
influenzae)) HI1588 HI1588 Haemophilus influenzae 727 10034515

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876484	13956	36112	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876489	13957	36113	1110	369

Description

6500733002 ppa:hi0124 inorganic pyrophosphatase:probable inorganic pyrophosphatase:pyrophosphate phospho-hydrolase:ppase (gtcfc:2.1:13.10) (ec:3.6.1.1) (keggfc:2.1) (tigrfc:5.3) (db:gtc-haemophilus influenzae) HI0124 HI0124 Haemophilus influenzae 727 -11536860 79864 ppa:hi0124 (ec:3.6.1.1) (de:phospho-hydrolase) (ppase)) (db:swissprot) IPYR_HAEIN P44529 HAEMOPHILUS INFLUENZAE 727 -11536860 166920 inorganic pyrophosphatase homolog (cl:inorganic pyrophosphatase) (db:pir2.dat) G64049 G64049 Haemophilus influenzae 727 -11536860 7500884232 hi0124 inorganic pyrophosphatase ppa (db:genpept-bct1) (de:haemophilus influenzae rd section 13 of 163 of the complete genome.) (nt:similar to pid:886704 sp:p50308 percent identity:) (le:8185) (re:8715) (di:complement) U32698 U32698 g1573079 Haemophilus influenzae Rd 71421 -11536860 5000694156 (de:(hi0124) (pn:probable inorganic pyrophosphatase:pyrophosphate phospho-hydrolase:ppase:inorganic pyrophosphatase:ppa) (gn:ppa) (gtcfc:2.1) (ec:3.6.1.1) (ipyr_haein) (keggfc:2.1) (tigrfc:5.3) (db:gtc-haemophilus influenzae)) HI0124 HI0124 Haemophilus influenzae 727 10022118

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876499	13958	36114	258	85

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876504	13959	36115	348	115

Description

6500733003 atpc:hi0478 atp synthase f1 epsilon subunit:atp synthase epsilon chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae) HI0478 HI0478 Haemophilus influenzae 727 -11536861 60981 atpc:hi0478 (ec:3.6.1.34) (de:atp synthase epsilon chain,) (db:swissprot) ATPE_HAEIN P43718 HAEMOPHILUS INFLUENZAE 727 -11536861 141133 h+-transporting atp synthase:epsilon chain (cl:h+-transporting atp synthase epsilon chain) (ec:3.6.1.34) (db:pir2.dat) C64071 C64071 Haemophilus influenzae 727 -11536861 7500877524 hi0478 atp synthase f1:subunit epsilon atpc (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p00832 gb:m25464 gb:v00267) (le:6893) (re:7321) (di:complement) U32730 U32730 g1573456 Haemophilus influenzae Rd 71421 -11536861 5000694157 (de:(hi0478) (pn:atp synthase epsilon chain:atp synthase f1 epsilon subunit:atpc) (gn:atpc) (gtcfc:2.1) (ec:3.6.1.34) (atpe_haein) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae)) HI0478 HI0478 Haemophilus influenzae 727 10003699

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876510	13960	36116	354	117

Description

GTC ORF with score 267 to: (fn:involved in rhamnolipids synthesis)
(db:genpept-bct2) (de:pseudomonas aeruginosa ctra, beta-ketoacyl reductase
(rhlg), andregulator protein (rscsf) genes, complete cds.) (nt:rhlg)
(le:1723) (re:2757) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876518	13961	36117	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876523	13962	36118	897	298

Description

6500733004 atpd:hi0479 atp synthase f1 beta subunit:atp synthase f1 beta chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4)
(db:gtc-haemophilus influenzae) HI0479 HI0479 Haemophilus influenzae 727 -11536862 60871 atpd:hi0479 (ec:3.6.1.34) (de:atp synthase beta chain,)
(db:swissprot) ATPB_HAEIN P43715 HAEMOPHILUS INFLUENZAE 727 -11536862
7500877486 hi0479 atp synthase f1:subunit beta atpd (db:genpept-bct1)
(de:haemophilus influenzae rd section 45 of 163 of the complete genome.)
(nt:similar to gb:l10328 sp:p00824 gb:m25464 gb:v00267) (le:7351) (re:8724)
(di:complement) U32730 U32730 g1573457 Haemophilus influenzae Rd 71421 -11536862 5000694158 (de:(hi0479) (pn:atp synthase f1 beta chain:atp synthase f1 beta subunit:atpd) (gn:atpd) (gtcfc:2.1) (ec:3.6.1.34) (atpb_haein) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae))
HI0479 HI0479 Haemophilus influenzae 727 10126687

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876538	13963	36119	732	243

Description

GTC ORF with score 152 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln1) (de:schizosaccharomyces pombe 38 kb genomic dna, clone 1750.) (le:12253:13516:13613) (re:13407:13548:13624) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876542	13964	36120	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876548	13965	36121	987	328

Description

6500733005 atpg:hi0480 atp synthase f1 gamma subunit:atp synthase gamma chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae) HI0480 HI0480 Haemophilus influenzae 727 -11536863 61063 atpg:hi0480 (ec:3.6.1.34) (de:atp synthase gamma chain,) (db:swissprot) ATPG_HAEIN P43716 HAEMOPHILUS INFLUENZAE 727 -11536863 141152 h+-transporting atp synthase:gamma chain (cl:h+-transporting atp synthase gamma chain) (ec:3.6.1.34) (db:pir2.dat) E64071 E64071 Haemophilus influenzae 727 -11536863 7500877551 hi0480 atp synthase f1:subunit gamma atpg (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p00837 gb:m25464 gb:v00267) (le:8741) (re:9610) (di:complement) U32730 U32730 g1573458 Haemophilus influenzae Rd 71421 -11536863 5000694159 (de:(hi0480) (pn:atp synthase gamma chain:atp synthase f1 gamma subunit:atpg) (gn:atpg) (gtcfc:2.1) (ec:3.6.1.34) (atpg_haein) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae)) HI0480 HI0480 Haemophilus influenzae 727 10003778

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876550	13966	36122	213	70

Description

6500733006 atpa:hi0481 atp synthase f1 alpha subunit:atp synthase alpha chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae) HI0481 HI0481 Haemophilus influenzae 727 -11536864 60804 atpa:hi0481 (ec:3.6.1.34) (de:atp synthase alpha chain,) (db:swissprot) ATPA_HAEIN P43714 HAEMOPHILUS INFLUENZAE 727 -11536864 141099 h+-transporting atp synthase:alpha chain (cl:h+-transporting atp synthase alpha chain:h+-transporting atp synthase alpha chain homology) (ec:3.6.1.34) (db:pir2.dat) F64071 F64071 Haemophilus influenzae 727 -11536864 7500877460 hi0481 atp synthase f1:subunit alpha atpa (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p00822 gb:m25464 gb:v00265) (le:9626) (re:11167) (di:complement) U32730 U32730 g1573459 Haemophilus influenzae Rd 71421 -11536864 5000694160 (de:(hi0481) (pn:atp synthase alpha chain:atp synthase f1 alpha subunit:atpa) (gn:atpa) (gtcfc:2.1) (ec:3.6.1.34) (atpa_haein) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae)) HI0481 HI0481 Haemophilus influenzae 727 10003524

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876553	13967	36123	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876559	13968	36124	279	92

Description

6500733007 atph:hi0482 atp synthase f1 delta subunit:atp synthase delta chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae) HI0482 HI0482 Haemophilus influenzae 727 -11536865 60936 atph:hi0482 (ec:3.6.1.34) (de:atp synthase delta chain,) (db:swissprot) ATPD_HAEIN P43717 HAEMOPHILUS INFLUENZAE 727 -11536865 141118 h+-transporting atp synthase:delta chain (cl:h+-transporting atp synthase delta chain) (ec:3.6.1.34) (db:pir2.dat) G64071 G64071 Haemophilus influenzae 727 -11536865 7500877514 hi0482 atp synthase f1:subunit delta atph (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p00831 gb:m25464 gb:v00264) (le:11180) (re:11713) (di:complement) U32730 U32730 g1573460 Haemophilus influenzae Rd 71421 -11536865 5000694161 (de:(hi0482) (pn:atp synthase delta chain:atp synthase f1 delta subunit:atph) (gn:atph) (gtcfc:2.1) (ec:3.6.1.34) (atpd_haein) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae)) HI0482 HI0482 Haemophilus influenzae 727 10003654

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876595	13969	36125	1167	388

Description

6500733008 atpf:hi0483 atp synthase f0 subunit b:atp synthase b chain (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae) HI0483 HI0483 Haemophilus influenzae 727 -11536866 61027 atpf:hi0483 (ec:3.6.1.34) (de:atp synthase b chain,) (db:swissprot) ATPF_HAEIN P43720 HAEMOPHILUS INFLUENZAE 727 -11536866 141296 h+-transporting atp synthase:chain b (cl:h+-transporting atp synthase chain i) (ec:3.6.1.34) (db:pir2.dat) H64071 H64071 Haemophilus influenzae 727 -11536866 7500877541 hi0483 atp synthase f0:subunit b atpf (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p00859 gb:m10422 gb:m25464) (le:11726) (re:12196) (di:complement) U32730 U32730 g1573461 Haemophilus influenzae Rd 71421 -11536866 5000694162 (de:(hi0483) (pn:atp synthase b chain:atp synthase f0 subunit b:atpf) (gn:atpf) (gtcfc:2.1) (ec:3.6.1.34) (atpf_haein) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae)) HI0483 HI0483 Haemophilus influenzae 727 10003742

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876607	13970	36126	573	190

Description

6500733009 atpe:hi0484 atp synthase c chain:lipid-binding protein:dicyclohexylcarbodiimide-binding protein (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae) HI0484 HI0484 Haemophilus influenzae 727 -11536867 61131 atpe:hi0484 (ec:3.6.1.34) (de:(dicyclohexylcarbodiimide-binding protein)) (db:swissprot) ATPL_HAEIN P43721 HAEMOPHILUS INFLUENZAE 727 -11536867 141195 h+-transporting atp synthase:lipid-binding protein (cl:h+-transporting atp synthase lipid-binding protein) (ec:3.6.1.34) (db:pir2.dat) I64071 I64071 Haemophilus influenzae 727 -11536867 7500877574 hi0484 atp synthase f0:subunit c atpe (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:similar to sp:p12991 pid:48334 percent ident:.) (le:12246) (re:12500) (di:complement) U32730 U32730 g1573462 Haemophilus influenzae Rd 71421 -11536867 5000694163 (de:(hi0484) (pn:lipid-binding protein:dicyclohexylcarbodiimide-binding protein:atp synthase c chain:atpe) (gn:atpe) (gtcfc:2.1) (ec:3.6.1.34) (atpl_haein) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae)) HI0484 HI0484 Haemophilus influenzae 727 10003843

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876610	13971	36127	423	140

Description

6500733010 atpb:hi0485 atp synthase f0 subunit a:atp synthase a chain:protein 6 (gtcfc:2.1:2.8) (ec:3.6.1.34) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae) HI0485 HI0485 Haemophilus influenzae 727 -11536868 60674 atpb:hi0485 (ec:3.6.1.34) (de:atp synthase a chain, (protein 6)) (db:swissprot) ATP6_HAEIN P43719 HAEMOPHILUS INFLUENZAE 727 -11536868 141257 h+-transporting atp synthase:protein 6 (cl:h+-transporting atp synthase protein 6) (ec:3.6.1.34) (db:pir2.dat) A64072 A64072 Haemophilus influenzae 727 -11536868 7500877363 hi0485 atp synthase f0:subunit a atpb (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p00855 gb:m14019 gb:m25464) (le:12556) (re:13344) (di:complement) U32730 U32730 g1573463 Haemophilus influenzae Rd 71421 -11536868 5000694164 (de:(hi0485) (pn:atp synthase a chain:protein 6:atp synthase f0 subunit a:atpb) (gn:atpb) (gtcfc:2.1) (ec:3.6.1.34) (atp6_haein) (keggfc:2.1) (tigrfc:6.4) (db:gtc-haemophilus influenzae)) HI0485 HI0485 Haemophilus influenzae 727 10003400

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876615	13972	36128	360	119

Description

6500733011 gpsa:hi0605 glycerol-3-phosphate dehydrogenase:nad+ (gtcfc:2.1:8.1) (ec:1.1.1.8) (keggfc:8.1) (tigrfc:6.1) (db:gtc-haemophilus influenzae) HI0605 HI0605 Haemophilus influenzae 727 -11536869 74347
gpsa:hi0605 (ec:1.1.1.8) (de:glycerol-3-phosphate dehydrogenase (nad+),) (db:swissprot) GPDA_HAEIN P43798 HAEMOPHILUS INFLUENZAE 727 -11536869
166163 glycerol-3-phosphate dehydrogenase nad+ (cl:glycerol-3-phosphate dehydrogenase) (ec:1.1.1.8) (db:pir2.dat) F64080 F64080 Haemophilus influenzae 727 -11536869 7500882658 hi0605 glycerol-3-phosphate dehydrogenase nad+ (db:genpept-bct1) (de:haemophilus influenzae rd section 58 of 163 of the complete genome.) (nt:similar to sp:p37606 pid:466746 gb:u00096) (le:67) (re:1074) (di:direct) U32743 U32743 g1573598 Haemophilus influenzae Rd 71421 -11536869 5000694396 (de:(hi0605) (pn:nad:glycerol-3-phosphate dehydrogenase:gpsa) (gn:gpsa) (gtcfc:8.1) (ec:1.1.1.8) (gpda_haein) (keggfc:8.1) (tigrfc:6.1) (db:gtc-haemophilus influenzae)) HI0605 HI0605 Haemophilus influenzae 727 10016864

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876616	13973	36129	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876626	13974	36130	690	229

Description

6500733012 ndh:hi0747 nadh dehydrogenase (gtcfc:9.12) (ec:1.6.99.3) (keggfc:14.1) (tigrfc:6.1) (db:gtc-haemophilus influenzae) HI0747 HI0747 Haemophilus influenzae 727 -11536870 68555 ndh:hi0747 (ec:1.6.99.3) (de:nadh dehydrogenase,) (db:swissprot) DHNA_HAEIN P44856 HAEMOPHILUS INFLUENZAE 727 -11536870 136963 ndh nadh dehydrogenase (cl:nadh dehydrogenase) (ec:1.6.99.3) (db:pir2.dat) C64090 C64090 Haemophilus influenzae 727 -11536870 7500880262 hi0747 nadh dehydrogenase ndh (db:genpept-bct1) (de:haemophilus influenzae rd section 73 of 163 of the complete genome.) (nt:similar to sp:p00393 pid:581140 gb:u00096) (le:6175) (re:7509) (di:direct) U32758 U32758 g1573754 Haemophilus influenzae Rd 71421 -11536870 5000694148 (de:(hi0747) (pn:nadh dehydrogenase:ndh) (gn:ndh) (gtcfc:1.8:8.1) (ec:1.6.99.3) (dhna_haein) (keggfc:11.1) (tigrfc:6.1) (db:gtc-haemophilus influenzae)) HI0747 HI0747 Haemophilus influenzae 727 10011147

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876631	13975	36131	693	230

Description

6500733013 dld:hi1163 d-lactate dehydrogenase (gtcfc:1.1:1.8:2.8) (keggfc:14.2) (tigrfc:6.1) (db:gtc-haemophilus influenzae) HI1163 HI1163 Haemophilus influenzae 727 -11536871 5500686545 hi1163 (de:hypothetical protein hi1163) (db:swissprot) YDIJ_HAEIN Q57252 HAEMOPHILUS INFLUENZAE 727 -11536871 166080 conserved hypothetical protein hi1163 (db:pir2.dat) B64187 B64187 Haemophilus influenzae 727 -11536871 7500922354 hi1163 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 111 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p77748 pid:1742760) (le:2483) (re:5566) (di:complement) U32796 U32796 g1574090 Haemophilus influenzae Rd 71421 -11536871 5000694149 (de:(hi1163) (pn:d-lactate dehydrogenase:dld) (gn:dld) (gtcfc:1.8:8.1) (ec:)) (keggfc:11.2) (tigrfc:6.1) (db:gtc-haemophilus influenzae)) HI1163 HI1163 Haemophilus influenzae 727 10088072

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876653	13976	36132	1080	359

Description

6500733014 gly:hi0889 serine hydroxymethyltransferase:serine methylase:shmt (gtcfc:2.2:5.3:5.9:6.5:9.3:9.6) (ec:2.1.2.1) (keggfc:2.2:5.3:5.9:6.5:9.3:9.8) (tigrfc:1.6) (db:gtc-haemophilus influenzae) (gtcfc:energy metabolism-methane metabolism:l-amino acid metabolism-glycine--serine and threonine metabolism:l-amino acid metabol... HI0889 HI0889 Haemophilus influenzae 727 -11536872 74196 gly:hi0889 (ec:2.1.2.1) (de:(shmt)) (db:swissprot) GLYA_HAEIN P43844 HAEMOPHILUS INFLUENZAE 727 -11536872 137816 glycine hydroxymethyltransferase::serine methylase (cl:glycine hydroxymethyltransferase) (ec:2.1.2.1) (db:pir2.dat) D64100 D64100 Haemophilus influenzae 727 -11536872 7500882596 hi0889 serine hydroxymethyltransferase serine (db:genpept-bct1) (de:haemophilus influenzae rd section 86 of 163 of the complete genome.) (nt:similar to sp:p34894 gb:z23269 pid:313832 percent) (le:92) (re:1357) (di:direct) U32771 U32771 g1573908 Haemophilus influenzae Rd 71421 -11536872 5000694165 (de:(hi0889) (pn:shmt:serine hydroxymethyltransferase:serine methylase:glya) (gn:glya) (gtcfc:2.2:5.3:6.5:9.3:9.8) (ec:2.1.2.1) (glya_haein) (keggfc:2.2:5.3:6.5:9.3:9.8) (tigrfc:1.6) (db:gtc-haemophilus influenzae)) HI0889 HI0889 Haemophilus influenzae 727 10016718

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876656	13977	36133	336	111

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876658	13978	36134	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876666	13979	36135	726	241

Description

6500733015 hkte:hi0928 kw20 catalase:catalase (gtcfc:2.2:5.14:12.12) (ec:1.11.1.6) (keggfc:2.2:5.14) (tigrfc:4.4) (db:gtc-haemophilus influenzae) HI0928 HI0928 Haemophilus influenzae 727 -11536873 62936 hkte:hi0928 (ec:1.11.1.6) (de:catalase,) (db:swissprot) CATA_HAEIN P44390 HAEMOPHILUS INFLUENZAE 727 -11536873 137279 catalase (cl:catalase) (ec:1.11.1.6) (db:pir2.dat) D64103 D64103 Haemophilus influenzae 727 -11536873 7500878202 hi0928 catalase hkte (db:genpept-bct1) (de:haemophilus influenzae rd section 89 of 163 of the complete genome.) (nt:similar to gb:u02682 pid:1573949 percent ident:.) (le:8898) (re:10424) (di:direct) U32774 U32774 g1573949 Haemophilus influenzae Rd 71421 -11536873 5000694166 (de:(hi0928) (pn:catalase:kw20 catalase:hkte) (gn:hkte) (gtcfc:2.2) (ec:1.11.1.6) (cata_haein) (keggfc:2.2:5.14) (tigrfc:4.4) (db:gtc-haemophilus influenzae)) HI0928 HI0928 Haemophilus influenzae 727 10005610

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876674	13980	36136	867	288

Description

6500733016 metf:hi1444 5:10 methylenetetrahydrofolate reductase:5:10-methylenetetrahydrofolate reductase (gtcfc:1.9:4.1:9.6) (ec:1.7.99.5) (keggfc:2.2:9.8) (tigrfc:2.2) (db:gtc-haemophilus influenzae) (gtcfc:carbohydrate metabolism-glyoxylate and dicarboxylate metabolism:nucleotide metabolism-purine metabolism:metabolism of cofactors and vitamins-biotin m... HI1444 HI1444 Haemophilus influenzae 727 -11536874 83550 metf:hi1444 (ec:1.7.99.5) (de:5,10-methylenetetrahydrofolate reductase,) (db:swissprot) METF_HAEIN P45208 HAEMOPHILUS INFLUENZAE 727 -11536874 137000 5:10-methylenetetrahydrofolate reductase fadh2 (cl:5,10-methylenetetrahydrofolate reductase (fadh2)) (ec:1.7.99.5) (db:pir2.dat) H64123 H64123 Haemophilus influenzae 727 -11536874 7500885534 hi1444 5:10 methylenetetrahydrofolate reductase metf (db:genpept-bct1) (de:haemophilus influenzae rd section 138 of 163 of the completegenome.) (nt:similar to gb:l19201 sp:p00394 gb:v01502 pid:305044) (le:1422) (re:2300) (di:direct) U32823 U32823 g1574284 Haemophilus influenzae Rd 71421 -11536874 5000694461 (de:(hi1444) (pn:5,10-methylenetetrahydrofolate reductase:5,10 methylenetetrahydrofolate reductase:metf) (gn:metf) (gtcfc:9.8) (ec:1.7.99.5) (metf_haein) (keggfc:9.8) (tigrfc:2.2) (db:gtc-haemophilus influenzae)) HI1444 HI1444 Haemophilus influenzae 727 10025764

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876682	13981	36137	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876686	13982	36138	234	77

Description

5000695770 pfla:act:hi0179 pyruvate formate-lyase activating enzyme:act:pyruvate formate-lyase 1 activating enzyme (gtcfc:2.2) (ec:1.97.1.4) (keggfc:14.1) (tigrfc:6.7) (db:gtc-haemophilus influenzae) HI0179 HI0179 Haemophilus influenzae 727 -11536875 167128 pfla:act pyruvate formate-lyase 1-activating enzyme (cl:pyruvate formate-lyase activating enzyme) (ec:1.97.1.-) (db:pir2.dat) E64052 E64052 Haemophilus influenzae 727 -11536875 7500960727 hi0179 pyruvate formate-lyase activating enzyme act (db:genpept-bct1) (de:haemophilus influenzae rd section 18 of 163 of the complete genome.) (nt:similar to gb:x08035 sp:p09374 pid:42371 gb:u00096) (le:1466) (re:2206) (di:complement) U32703 U32703 g1573135 Haemophilus influenzae Rd 71421 -11536875 6500733017 pfla:act pyruvate formate-lyase activating enzyme:act:pyruvate formate-lyase 1 activating enzyme (gtcfc:2.2) (ec:1.97.1.4) (keggfc:14.1) (tigrfc:6.7) (db:gtc-haemophilus influenzae) HI0179 HI0179 Haemophilus influenzae 727 -11536875

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876690	13983	36139	990	329

Description

6500733018 ordl:hi0499 aldehyde dehydrogenase:aldh:probable oxidoreductase (gtcfc:1.1:1.8) (ec:1.-.-.-) (keggfc:14.1) (tigrfc:6.7) (db:gtc-haemophilus influenzae) HI0499 HI0499 Haemophilus influenzae 727 -11536876 87867 ordl:hi0499 (ec:1.-.-.-) (de:probable oxidoreductase ordl,) (db:swissprot) ORDL_HAEIN P44732 HAEMOPHILUS INFLUENZAE 727 -11536876 165991 probable oxidoreductase:hi0499 (cl:hypothetical protein hi0499) (ec:1.-.-.-) (db:pir2.dat) F64072 F64072 Haemophilus influenzae 727 -11536876 7500887362 hi0499 oxidoreductase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 46 of 163 of the complete genome.) (nt:similar to gb:m38433 sp:p37906 pid:1054921) (le:8274) (re:9569) (di:direct) U32731 U32731 g1573476 Haemophilus influenzae Rd 71421 -11536876 5000695771 (de:(hi0499) (pn:probable oxidoreductase :aldehyde dehydrogenase:aldh) (gn:ordl) (gtcfc:13.7) (ec:1.-.-.-) (ordl_haein) (keggfc:11.1) (tigrfc:6.7) (db:gtc-haemophilus influenzae)) HI0499 HI0499 Haemophilus influenzae 727 10030008

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876691	13984	36140	621	206

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876707	13985	36141	324	107

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876713	13986	36142	1413	470

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876731	13987	36143	540	179

Description

6500733019 hype:hi1305 hydrogenase gene region (gtcfc:2.2) (keggfc:14.2) (tigrfc:6.7) (db:gtc-haemophilus influenzae) HI1305 HI1305 Haemophilus influenzae 727 -11536877 1500687058 thil:hi1305 (ec:2.7.4.16) (de:thiamin-monophosphate kinase, (thiamin-phosphate kinase)) (db:swissprot) THIL_HAEIN Q57190 HAEMOPHILUS INFLUENZAE 727 -11536877 166208 thil thiamin-phosphate kinase (ec:2.7.4.16) (db:pir2.dat) E64115 E64115 Haemophilus influenzae 727 -11536877 7500893073 hi1305 thiamin-monophosphate kinase thil (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p77785 pid:1773101) (le:2625) (re:3662) (di:direct) U32810 U32810 g1574764 Haemophilus influenzae Rd 71421 -11536877 5000695772 (de:(hi1305) (pn:hydrogenase gene region:hype) (gn:hype) (gtcfc:13.7) (ec:) (keggfc:11.2) (tigrfc:6.7) (db:gtc-haemophilus influenzae)) HI1305 HI1305 Haemophilus influenzae 727 10063512

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876746	13988	36144	1623	540

Description

6500733020 short chain alcohol dehydrogenase:hypothetical oxidoreductase
 hil430 (gtcfc:1.1) (ec:1.-.-.-) (keggfc:14.1) (tigrfc:6.7)
 (db:gtc-haemophilus influenzae) HI1430 HI1430 Haemophilus influenzae 727
 -11536878 111325 hil430 (ec:1.-.-.-) (de:hypothetical oxidoreductase
 hil430,) (db:swissprot) YDFG_HAEIN P45200 HAEMOPHILUS INFLUENZAE 727
 -11536878 167159 ydfg protein (cl:short-chain alcohol dehydrogenase
 homology) (db:pir2.dat) H64122 H64122 Haemophilus influenzae 727 -11536878
 7500922273 hil430 short chain dehydrogenase/reductase (db:genpept-bct1)
 (de:haemophilus influenzae rd section 137 of 163 of the completegenome.)
 (nt:similar to gb:u00096 pid:1787820 percent ident:.) (le:1980) (re:2738)
 (di:direct) U32822 U32822 g1574268 Haemophilus influenzae Rd 71421 -11536878
 5000695773 (de:(hil430) (pn:hypothetical oxidoreductase hil430:short chain
 alcohol dehydrogenase) (gtcfc:13.7) (ec:1.-.-.-) (ydfg_haein) (keggfc:11.1)
 (tigrfc:6.7) (db:gtc-haemophilus influenzae)) HI1430 HI1430 Haemophilus
 influenzae 727 10053055

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876747	13989	36145	594	198

Description

6500733021 aspc:hi1617 aspartate aminotransferase:transaminase a:aspat
 (gtcfc:2.4:5.1:5.10:5.15:5.2:5.5) (ec:2.6.1.1)
 (keggfc:2.3:5.1:5.2:5.5:5.10:5.15) (tigrfc:1.2) (db:gtc-haemophilus
 influenzae) HI1617 HI1617 Haemophilus influenzae 727 -11536879 57894
 aspc:hi1617 (ec:2.6.1.1) (de:aspartate aminotransferase, (transaminase a)
 (aspat)) (db:swissprot) AAT_HAEIN P44425 HAEMOPHILUS INFLUENZAE 727
 -11536879 138368 aspartate transaminase (cl:aspartate aminotransferase)
 (ec:2.6.1.1) (db:pir2.dat) I64132 I64132 Haemophilus influenzae 727
 -11536879 7500876247 hi1617 aspartate aminotransferase aspc
 (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the
 completegenome.) (nt:similar to sp:p00509 gb:x03629 gb:x05904 pid:41011)
 (le:4627) (re:5817) (di:direct) U32835 U32835 g1574463 Haemophilus
 influenzae Rd 71421 -11536879 5000694167 (de:(hi1617) (pn:transaminase
 a:aspat:aspartate aminotransferase:aspc) (gn:aspc) (gtcfc:2.4:5.1:5.10:5.2)
 (ec:2.6.1.1) (aat_haein) (keggfc:2.3:5.1:5.2:5.5:5.10) (tigrfc:1.2)
 (db:gtc-haemophilus influenzae)) HI1617 HI1617 Haemophilus influenzae 727
 10000674

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876765	13990	36146	840	279

Description

6500733022 metc:hi0122 cystathionine
 beta-lyase:cb1:beta-cystathionase:cysteine lyase
 (gtcfc:2.6:2.7:5.2:5.4:5.5:6.4) (ec:4.4.1.8) (keggfc:2.5:2.6:5.4:5.5:6.4)
 (tigrfc:1.2) (db:gtc-haemophilus influenzae) HI0122 HI0122 Haemophilus
 influenzae 727 -11536880 83543 metc:hi0122 (ec:4.4.1.8) (de:(cysteine
 lyase)) (db:swissprot) METC_HAEIN P44527 HAEMOPHILUS INFLUENZAE 727
 -11536880 141954 cystathionine beta-lyase (cl:o-succinylhomoserine
 (thiol)-lyase) (ec:4.4.1.8) (db:pir2.dat) E64049 E64049 Haemophilus
 influenzae 727 -11536880 7500885519 hi0122 cystathionine beta-lyase metc
 (db:genpept-bct1) (de:haemophilus influenzae rd section 13 of 163 of the
 complete genome.) (nt:similar to gb:m12858 sp:p06721 pid:146824) (le:5596)
 (re:6786) (di:complement) U32698 U32698 g1573077 Haemophilus influenzae Rd
 71421 -11536880 5000694168 (de:(hi0122) (pn:cystathionine
 beta-lyase:cb1:cysteine lyase:beta-cystathionase:metc) (gn:metc)
 (gtcfc:2.6:5.4:6.4) (ec:4.4.1.8) (metc_haein) (keggfc:2.5:5.4:5.5:6.4)
 (tigrfc:1.2) (db:gtc-haemophilus influenzae)) HI0122 HI0122 Haemophilus
 influenzae 727 10025757

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876770	13991	36147	525	174

Description

6500733023 gdha:hi0189 glutamate dehydrogenase:nadp-specific glutamate
 dehydrogenase:nadp-gdh (gtcfc:2.6:5.1) (ec:1.4.1.4) (keggfc:2.5:5.1)
 (tigrfc:1.4) (db:gtc-haemophilus influenzae) HI0189 HI0189 Haemophilus
 influenzae 727 -11536881 68486 gdha:hi0189 (ec:1.4.1.4) (de:nadp-specific
 glutamate dehydrogenase, (nadp-gdh)) (db:swissprot) DHE4_HAEIN P43793
 HAEMOPHILUS INFLUENZAE 727 -11536881 136597 glutamate dehydrogenase nadp+
 (cl:glutamate dehydrogenase (nad(p)+)) (ec:1.4.1.4) (db:pir2.dat) A64053
 A64053 Haemophilus influenzae 727 -11536881 7500880252 hi0189 glutamate
 dehydrogenase gdha (db:genpept-bct1) (de:haemophilus influenzae rd section
 19 of 163 of the complete genome.) (nt:similar to sp:p00370 pid:146124
 pid:146126) (le:2650) (re:3999) (di:direct) U32704 U32704 g1573147
 Haemophilus influenzae Rd 71421 -11536881 5000694169 (de:(hi0189)
 (pn:nadp-specific glutamate dehydrogenase:nadp-gdh:glutamate
 dehydrogenase:gdha) (gn:gdha) (gtcfc:2.6:5.1) (ec:1.4.1.4) (dhe4_haein)
 (keggfc:2.5:5.1:5.14) (tigrfc:1.4) (db:gtc-haemophilus influenzae)) HI0189
 HI0189 Haemophilus influenzae 727 10011078

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876786	13992	36148	723	240

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876789	13993	36149	867	288

Description

GTC ORF with score 164 to: (de:(pn:glyceraldehyde-3-phosphate dehydrogenase) (gn:gapdh) (db:genpept-bct) (de:mycobacterium avium glyceraldehyde-3-phosphate dehydrogenasehomolog (gapdh) gene, complete cds; and phosphoglycerate kinasegene, partial cds.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876794	13994	36150	252	83

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876797	13995	36151	1275	425

Description

6500733024 aspa:hi0534 aspartate ammonia-lyase:aspartase (gtcfc:2.6:5.2:6.6) (ec:4.3.1.1) (keggfc:2.5:5.2) (tigrfc:6.2) (db:gtc-haemophilus influenzae) HI0534 HI0534 Haemophilus influenzae 727 -11536882 60393 aspa:hi0534 (ec:4.3.1.1) (de:aspartate ammonia-lyase, (aspartase)) (db:swissprot) ASPA_HAEIN P44324 HAEMOPHILUS INFLUENZAE 727 -11536882 141807 aspartate ammonia-lyase (cl:fumarate hydratase) (ec:4.3.1.1) (db:pir2.dat) C64075 C64075 Haemophilus influenzae 727 -11536882 7500877256 hi0534 aspartate ammonia-lyase aspa (db:genpept-bct1) (de:haemophilus influenzae rd section 50 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p04422 gb:l20944 gb:x02307) (le:8879) (re:10306) (di:complement) U32735 U32735 g1573518 Haemophilus influenzae Rd 71421 -11536882 5000694170 (de:(hi0534) (pn:aspartate ammonia-lyase:aspartase:aspa) (gn:aspa) (gtcfc:2.6:5.2) (ec:4.3.1.1) (aspa_haein) (keggfc:2.5:5.2) (tigrfc:6.2) (db:gtc-haemophilus influenzae)) HI0534 HI0534 Haemophilus influenzae 727 10003119

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876801	13996	36152	543	180

Description

6500733025 asna:hi0564 aspartate--ammonia ligase:asparagine synthetase a (gtcfc:2.6:5.2:6.5) (ec:6.3.1.1) (keggfc:2.5:5.2:6.5) (tigrfc:1.2) (db:gtc-haemophilus influenzae) HI0564 HI0564 Haemophilus influenzae 727 -11536883 60369 asna:hi0564 (ec:6.3.1.1) (de:aspartate--ammonia ligase, (asparagine synthetase a)) (db:swissprot) ASNA_HAEIN P44338 HAEMOPHILUS INFLUENZAE 727 -11536883 142336 aspartate--ammonia ligase (cl:aspartate--ammonia ligase) (ec:6.3.1.1) (db:pir2.dat) H64077 H64077 Haemophilus influenzae 727 -11536883 7500877249 hi0564 aspartate--ammonia ligase asna (db:genpept-bct1) (de:haemophilus influenzae rd section 53 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p00963 gb:j01657 gb:k00826) (le:1214) (re:2206) (di:direct) U32738 U32738 g1573551 Haemophilus influenzae Rd 71421 -11536883 5000694171 (de:(hi0564) (pn:aspartate--ammonia ligase:asparagine synthetase a:asna) (gn:asna) (gtcfc:2.6:5.2:6.5) (ec:6.3.1.1) (asna_haein) (keggfc:2.5:5.2:6.5) (tigrfc:1.2) (db:gtc-haemophilus influenzae)) HI0564 HI0564 Haemophilus influenzae 727 10003095

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876803	13997	36153	384	127

Description

GTC ORF with score 96 to: (fn:helicase, helicase-primase complex) (db:genpept-vrl) (de:human herpesvirus 6 serotype b putative major immediate-earlygenes.) (nt:similar to hhv6a u86, region ie-b) (le:16386) (re:19235) (di:complement)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876816	13998	36154	834	277

Description

GTC ORF with score 419 to: (db:genpept-bct1) (de:methanobacterium thermoautotrophicum from bases 739092 to 749403(section 65 of 148) of the complete genome.) (nt:function code:4.04 - nucleotide metabolism, salvage) (le:4625) (re:5299) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876833	13999	36155	582	193

Description

6500733026 arcc:hi0595 carbamate kinase (gtcfc:2.6:5.1:5.10:6.6) (ec:2.7.2.2) (keggfc:2.5:5.1:5.10) (tigrfc:6.2) (db:gtc-haemophilus influenzae) HI0595 HI0595 Haemophilus influenzae 727 -11536884 59993 arcc:hi0595 (ec:2.7.2.2) (de:carbamate kinase,) (db:swissprot) ARCC_HAEIN P44769 HAEMOPHILUS INFLUENZAE 727 -11536884 166038 carbamate kinase (cl:carbamate kinase) (ec:2.7.2.2) (db:pir2.dat) G64079 G64079 Haemophilus influenzae 727 -11536884 7500877079 hi0595 carbamate kinase arcc (db:genpept-bct1) (de:haemophilus influenzae rd section 56 of 163 of the complete genome.) (nt:similar to sp:p13982 gb:x14693 pid:45290 percent) (le:2525) (re:3457) (di:complement) U32741 U32741 g1573584 Haemophilus influenzae Rd 71421 -11536884 5000694172 (de:(hi0595) (pn:carbamate kinase:arcc) (gn:arcc) (gtcfc:2.6:5.1:5.10) (ec:2.7.2.2) (arcc_haein) (keggfc:2.5:5.1:5.10) (tigrfc:6.2) (db:gtc-haemophilus influenzae)) HI0595 HI0595 Haemophilus influenzae 727 10002726

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876836	14000	36156	480	159

Description

6500733027 ansb:hi0745 l-asparaginase ii:probable l-asparaginase periplasmic precursor (gtcfc:2.6:5.2:6.5:6.6) (ec:3.5.1.1) (keggfc:2.5:5.2:6.5) (tigrfc:6.2) (db:gtc-haemophilus influenzae) HI0745 HI0745 Haemophilus influenzae 727 -11536885 60348 ansb:hi0745 (ec:3.5.1.1) (de:probable l-asparaginase periplasmic precursor,) (db:swissprot) ASG2_HAEIN P43843 HAEMOPHILUS INFLUENZAE 727 -11536885 140855 asparaginase:ii precursor (cl:asparaginase) (ec:3.5.1.1) (db:pir2.dat) A64090 A64090 Haemophilus influenzae 727 -11536885 7500877239 hi0745 l-asparaginase ii ansb (db:genpept-bct1) (de:haemophilus influenzae rd section 73 of 163 of the complete genome.) (nt:similar to gb:m34234 sp:p00805 gb:m34277 pid:145277) (le:3444) (re:4493) (di:direct) U32758 U32758 g1573752 Haemophilus influenzae Rd 71421 -11536885 5000694173 (de:(hi0745) (pn:probable l-asparaginase periplasmic precursor:l-asparaginase ii:ansb) (gn:ansb) (gtcfc:2.6:5.2:6.5) (ec:3.5.1.1) (asg2_haein) (keggfc:2.5:5.2:6.5) (tigrfc:6.2) (db:gtc-haemophilus influenzae)) HI0745 HI0745 Haemophilus influenzae 727 10003074

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876837	14001	36157	474	157

Description

6500733028 glna:hi0865 glutamine synthetase:glutamate--ammonia ligase
(gtcfc:2.6:5.1:11.4) (ec:6.3.1.2) (keggfc:2.5:5.1:7.3) (tigrfc:1.4)
(db:gtc-haemophilus influenzae) HI0865 HI0865 Haemophilus influenzae 727
-11536886 73933 glna:hi0865 (ec:6.3.1.2) (de:glutamine synthetase,
(glutamate--ammonia ligase)) (db:swissprot) GLNA_HAEIN P43794 HAEMOPHILUS
INFLUENZAE 727 -11536886 142345 glutamate--ammonia ligase::glutamine
synthetase (cl:glutamate--ammonia ligase) (ec:6.3.1.2) (db:pir2.dat) I64098
I64098 Haemophilus influenzae 727 -11536886 7500882464 hi0865 glutamine
synthetase glna (db:genpept-bct1) (de:haemophilus influenzae rd section 83
of 163 of the complete genome.) (nt:similar to sp:p28786 gb:x68129 pid:45900
percent) (le:3827) (re:5245) (di:direct) U32768 U32768 g1573882 Haemophilus
influenzae Rd 71421 -11536886 5000694174 (de:(hi0865)
(pn:glutamate--ammonia ligase:glutamine synthetase:glna) (gn:glna)
(gtcfc:2.6:5.1:7.2) (ec:6.3.1.2) (glna_haein) (keggfc:2.5:5.1:7.3)
(tigrfc:1.4) (db:gtc-haemophilus influenzae)) HI0865 HI0865 Haemophilus
influenzae 727 10016463

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876838	14002	36158	528	175

Description

6500733029 metb:hi0086 cystathionine
gamma-synthase:cgs:o-succinylhomoserine:thiol-lyase
(gtcfc:2.7:5.2:5.3:5.4:5.5:6.4) (ec:4.2.99.9) (keggfc:2.6:5.3:5.4:5.5:6.4)
(tigrfc:1.2) (db:gtc-haemophilus influenzae) HI0086 HI0086 Haemophilus
influenzae 727 -11536887 166068 cystathionine gamma-lyase homolog
(cl:o-succinylhomoserine (thiol)-lyase) (db:pir2.dat) G64047 G64047
Haemophilus influenzae 727 -11536887 7500960650 hi0086 cystathionine
gamma-synthase metb (db:genpept-bct1) (de:haemophilus influenzae rd section
9 of 163 of the complete genome.) (nt:similar to gb:al009126 percent
identity: 64.19;) (le:1098) (re:2243) (di:complement) U32694 U32694 g1573037
Haemophilus influenzae Rd 71421 -11536887 5000694175 (de:(hi0086)
(pn:cgs:o-succinylhomoserine:thiol-lyase:cystathionine gamma-synthase:metb)
(gn:metb) (gtcfc:2.7:5.3:5.4:6.4) (ec:4.2.99.9) (metb_haein)
(keggfc:2.6:5.3:5.4:5.5:6.4) (tigrfc:1.2) (db:gtc-haemophilus influenzae))
HI0086 HI0086 Haemophilus influenzae 727 10088070

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876844	14003	36159	1404	467

Description

6500733030 cyse:hi0606 serine acetyltransferase:sat (gtcfc:2.7:5.3:5.5) (ec:2.3.1.30) (keggfc:2.6:5.5) (tigrfc:1.6) (db:gtc-haemophilus influenzae) HI0606 HI0606 Haemophilus influenzae 727 -11536888 67652 cyse:hi0606 (ec:2.3.1.30) (de:serine acetyltransferase, (sat)) (db:swissprot) CYSE_HAEIN P43886 HAEMOPHILUS INFLUENZAE 727 -11536888 137927 serine o-acetyltransferase (cl:serine acetyltransferase:serine acetyltransferase homology) (ec:2.3.1.30) (db:pir2.dat) G64080 G64080 Haemophilus influenzae 727 -11536888 7500879905 hi0606 serine acetyltransferase cyse (db:genpept-bct1) (de:haemophilus influenzae rd section 58 of 163 of the complete genome.) (nt:similar to sp:p05796 gb:m15745 gb:m34333 pid:145676) (le:1086) (re:1889) (di:direct) U32743 U32743 g1573599 Haemophilus influenzae Rd 71421 -11536888 5000694176 (de:(hi0606) (pn:sat:serine acetyltransferase:cyse) (gn:cyse) (gtcfc:2.7) (ec:2.3.1.30) (cyse_haein) (keggfc:2.6:5.5) (tigrfc:1.6) (db:gtc-haemophilus influenzae)) HI0606 HI0606 Haemophilus influenzae 727 10010250

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876860	14004	36160	294	97

Description

6500733031 cysk:hi1103 cysteine synthetase:cysteine synthase:o-acetylserine sulfhydrylase:o-acetylserine:thiol-lyase:csase (gtcfc:2.7:5.3:5.5:6.4) (ec:4.2.99.8) (keggfc:2.6:5.5:6.4) (tigrfc:1.6) (db:gtc-haemophilus influenzae) HI1103 HI1103 Haemophilus influenzae 727 -11536889 67669 cysk:hi1103 (ec:4.2.99.8) (de:(o-acetylserine (thiol)-lyase) (csase)) (db:swissprot) CYSK_HAEIN P45040 HAEMOPHILUS INFLUENZAE 727 -11536889 141886 cysteine synthase (cl:threonine dehydratase) (ec:4.2.99.8) (db:pir2.dat) F64182 F64182 Haemophilus influenzae 727 -11536889 7500879911 hi1103 cysteine synthetase cysk (db:genpept-bct1) (de:haemophilus influenzae rd section 105 of 163 of the completegenome.) (nt:similar to gb:m21451 sp:pl1096 gb:x12615 pid:145686) (le:2129) (re:3079) (di:direct) U32790 U32790 g1574657 Haemophilus influenzae Rd 71421 -11536889 5000694177 (de:(hi1103) (pn:cysteine synthase:o-acetylserine sulfhydrylase:o-acetylserine:thiol-lyase:csase:cysteine synthetase:cysk) (gn:cysk) (gtcfc:2.7:6.4) (ec:4.2.99.8) (cysk_haein) (keggfc:2.6:5.5:6.4) (tigrfc:1.6) (db:gtc-haemophil) HI1103 HI1103 Haemophilus influenzae 727 10010267

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876862	14005	36161	507	168

Description

6500733032 homoserine acetyltransferase:met2:putative homoserine
o-acetyltransferase:homoserine o-trans-acetylase (gtcfc:2.7:5.2:5.4)
(ec:2.3.1.31) (keggfc:2.6:5.4) (tigrfc:1.2) (db:gtc-haemophilus influenzae)
HI1263 HI1263 Haemophilus influenzae 727 -11536890 83525 hi1263
(ec:2.3.1.31) (de:trans-acetylase) (db:swissprot) MET2_HAEIN P45131
HAEMOPHILUS INFLUENZAE 727 -11536890 166203 homoserine o-acetyltransferase
homolog (db:pir2.dat) D64113 D64113 Haemophilus influenzae 727 -11536890
7500885510 hi1263 homoserine acetyltransferase met2 (db:genpept-bct1)
(de:haemophilus influenzae rd section 121 of 163 of the completegenome.)
(nt:similar to pid:1835114 percent ident: 43.68;) (le:3449) (re:4525)
(di:direct) U32806 U32806 g1574721 Haemophilus influenzae Rd 71421 -11536890
5000694178 (de:(hi1263) (pn:putative homoserine
o-acetyltransferase:homoserine o-trans- acetylase:homoserine
acetyltransferase:met2) (gtcfc:2.7:5.4) (ec:2.3.1.31) (met2_haein)
(keggfc:2.6:5.4) (tigrfc:1.2) (db:gtc-haemophilus influenzae)) HI1263 HI1263
Haemophilus influenzae 727 10025739

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876867	14006	36162	396	131

Description

6500733033 cysq:hi0559 sulfite synthesis pathway protein:protein homolog
(gtcfc:2.7) (keggfc:14.2) (tigrfc:5.6) (db:gtc-haemophilus influenzae)
HI0559 HI0559 Haemophilus influenzae 727 -11536891 67702 cysq:hi0559
(de:cysq protein homolog) (db:swissprot) CYSQ_HAEIN P44332 HAEMOPHILUS
INFLUENZAE 727 -11536891 167180 cysq protein homolog (db:pir2.dat) F64077
F64077 Haemophilus influenzae 727 -11536891 7500879923 hi0559 sulfite
synthesis pathway protein cysq (db:genpept-bct1) (de:haemophilus influenzae
rd section 52 of 163 of the complete genome.) (nt:similar to sp:p22255
gb:m55170 gb:m80795 pid:145275) (le:6824) (re:7510) (di:complement) U32737
U32737 g1573544 Haemophilus influenzae Rd 71421 -11536891 5000695742
(de:(hi0559) (pn:protein homolog:sulfite synthesis pathway protein:cysq)
(gn:cysq) (gtcfc:13.7) (ec:) (cysq_haein) (keggfc:11.2) (tigrfc:5.6)
(db:gtc-haemophilus influenzae)) HI0559 HI0559 Haemophilus influenzae 727
10010300

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876874	14007	36163	849	282

Description

5000695743 desulfovirodin gamma subunit:dsvc:hypothetical protein (gtcfc:2.7) (keggfc:14.2) (tigrfc:5.6) (db:gtc-haemophilus influenzae) HI1371 HI1371 Haemophilus influenzae 727 -11536892 110633 hi1371 (de:hypothetical protein hi1371) (db:swissprot) YCKK_HAEIN P45184 HAEMOPHILUS INFLUENZAE 727 -11536892 166088 probable sulfite reductase gamma chain (cl:sulfite reductase gamma chain) (db:pir2.dat) A64120 A64120 Haemophilus influenzae 727 -11536892 7500921626 hi1371 desulfovirodin gamma subunit:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 132 of 163 of the complete genome.) (nt:similar to gb:l05610 sp:p45573 pid:145087 percent) (le:2962) (re:3291) (di:complement) U32817 U32817 g1574204 Haemophilus influenzae Rd 71421 -11536892 6500733034 desulfovirodin gamma subunit:dsvc:hypothetical protein (gtcfc:2.7) (keggfc:14.2) (tigrfc:5.6) (db:gtc-haemophilus influenzae) HI1371 HI1371 Haemophilus influenzae 727 -11536892

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876879	14008	36164	687	228

Description

6500733035 fdhd:hi0005 formate dehydrogenase-n effector:protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0005 HI0005 Haemophilus influenzae 727 -11536893 71252 fdhd:hi0005 (de:fdhd protein) (db:swissprot) FDHD_HAEIN P44449 HAEMOPHILUS INFLUENZAE 727 -11536893 166139 fdhd fdhd protein (db:pir2.dat) I64041 I64041 Haemophilus influenzae 727 -11536893 7500881377 hi0005 fdhd protein fdhd (db:genpept-bct1) (de:haemophilus influenzae rd section 1 of 163 of the complete genome.) (nt:similar to gb:l19201 sp:p32177 pid:304999 gb:u00096) (le:4579) (re:5391) (di:complement) U32686 U32686 g1572949 Haemophilus influenzae Rd 71421 -11536893 5000695750 (de:(hi0005) (pn:protein:formate dehydrogenase-n effector:fdhd) (gn:fdhd) (gtcfc:13.7) (ec:)) (fdhd_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0005 HI0005 Haemophilus influenzae 727 10013825

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501876915	14009	36165	2130	709

Description

GTC ORF with score 616 to: (sr:thale cress) (db:genpept) (de:arabidopsis thaliana chromosome i bac f21m11 genomic sequence,complete sequence.) (nt:hypothetical protein; similar to dna helicases and) (le:115812:116202) (re:116107:116427) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876918	14010	36166	669	222

Description

6500733036 fdxh:hi0007 formate dehydrogenase-o:beta subunit:fdoh:formate dehydrogenase:iron-sulfur subunit:formate dehydrogenase beta subunit (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0007 HI0007 Haemophilus influenzae 727 -11536894 71270 fdxh:hi0007 (de:subunit) (fdh beta subunit)) (db:swissprot) FDXH_HAEIN P44450 HAEMOPHILUS INFLUENZAE 727 -11536894 166141 formate dehydrogenase::nitrate-inducible:beta chain (cl:ferredoxin 2(4fe-4s) homology) (ec:1.2.1.2) (db:pir2.dat) A64042 A64042 Haemophilus influenzae 727 -11536894 7500881385 hi0007 formate dehydrogenase:beta subunit fdxh (db:genpept-bct1) (de:haemophilus influenzae rd section 1 of 163 of the complete genome.) (nt:similar to sp:p24184 gb:u00096 pid:1742408) (le:8750) (re:9688) (di:direct) U32686 U32686 g1572950 Haemophilus influenzae Rd 71421 -11536894 5000695751 (de:(hi0007) (pn:formate dehydrogenase, iron-sulfur subunit:formate dehydrogenase beta subunit:formate dehydrogenase-o, beta subunit:fdoh) (gn:fdxh) (gtcfc:13.7) (ec:) (fdxh haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus) HI0007 HI0007 Haemophilus influenzae 727 10013843

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876919	14011	36167	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876950	14012	36168	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876962	14013	36169	309	102

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876963	14014	36170	1275	424

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876964	14015	36171	840	279

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876967	14016	36172	600	199

Description

6500733037 fdxi:hi0008 formate dehydrogenase-o gamma subunit:fdxi:formate dehydrogenase:cytochrome b556 subunit:formate dehydrogenase gamma subunit (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0008 HI0008 Haemophilus influenzae 727 -11536895 71271 fdxi:hi0008 (de:gamma subunit) (fdh gamma subunit)) (db:swissprot) FDXI_HAEIN P44451 HAEMOPHILUS INFLUENZAE 727 -11536895 7500881386 hi0008 formate dehydrogenase:gamma subunit fdxi (db:genpept-bct1) (de:haemophilus influenzae rd section 1 of 163 of the complete genome.) (nt:similar to gb:119201 sp:p32174 pid:304996 gb:u00096) (le:9681) (re:10397) (di:direct) U32686 U32686 g1572951 Haemophilus influenzae Rd 71421 -11536895 5000695752 (de:(hi0008) (pn:formate dehydrogenase, cytochrome b556 subunit:formate dehydrogenase gamma subunit:formate dehydrogenase-o gamma subunit:fdxi) (gn:fdxi) (gtcfc:13.7) (ec:) (fdxi_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemoph) HI0008 HI0008 Haemophilus influenzae 727 10126670

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876974	14017	36173	1404	467

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501876976	14018	36174	465	154

Description

6500733038 fdhe:hi0009 fdhe protein:protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0009 HI0009 Haemophilus influenzae 727 -11536896 71256 fdhe:hi0009 (de:fdhe protein) (db:swissprot) FDHE_HAEIN P44452 HAEMOPHILUS INFLUENZAE 727 -11536896 166128 fdhe fdhe protein (db:pir2.dat) C64042 C64042 Haemophilus influenzae 727 -11536896 7500881379 hi0009 fdhe protein fdhe (db:genpept-bct1) (de:haemophilus influenzae rd section 1 of 163 of the complete genome.) (nt:similar to sp:p13024 pid:304995 gb:u00096) (le:10467) (re:11375) (di:direct) U32686 U32686 g1572952 Haemophilus influenzae Rd 71421 -11536896 5000695753 (de:(hi0009) (pn:protein:fdhe protein:fdhe) (gn:fdhe) (gtcfc:13.7) (ec:) (fdhe_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae)) HI0009 HI0009 Haemophilus influenzae 727 10013829

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877033	14019	36175	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877039	14020	36176	633	210

Description

6500733039 napc:hi0348 denitrification system component:nirt:cytochrome c-type protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0348 HI0348 Haemophilus influenzae 727 -11536897 85224 napc:hi0348 (de:cytochrome c-type protein napc) (db:swissprot) NAPC_HAEIN P44655 HAEMOPHILUS INFLUENZAE 727 -11536897 135349 nirt denitrification system component nirt (cl:denitrification system component nirt:nirt homology) (db:pir2.dat) H64062 H64062 Haemophilus influenzae 727 -11536897 7500886291 hi0348 cytochrome c-type protein napc (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to sp:p33932 pid:405927 gb:u00096) (le:6992) (re:7594) (di:direct) U32719 U32719 g1573318 Haemophilus influenzae Rd 71421 -11536897 5000695754 (de:(hi0348) (pn:cytochrome c-type protein :denitrification system component:nirt) (gn:napc) (gtcfc:13.7) (ec:) (napc_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae)) HI0348 HI0348 Haemophilus influenzae 727 10027405

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877042	14021	36177	330	110

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877043	14022	36178	993	330

Description

6500733040 glpg:hi0618 glp regulon protein:protein homolog (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0618 HI0618 Haemophilus influenzae 727 -11536898 74035 glpg:hi0618 (de:glpg protein homolog) (db:swissprot) GLPG_HAEIN P44783 HAEMOPHILUS INFLUENZAE 727 -11536898 166152 glpg protein homolog (db:pir2.dat) I64081 I64081 Haemophilus influenzae 727 -11536898 7500882500 hi0618 glp protein:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 59 of 163 of the complete genome.) (nt:similar to gb:m54940 sp:p09391 gb:m96795 pid:146185) (le:4528) (re:5106) (di:direct) U32744 U32744 g1573612 Haemophilus influenzae Rd 71421 -11536898 5000695755 (de:(hi0618) (pn:protein homolog:glp regulon protein:glpg) (gn:glpg) (gtcfc:13.7) (ec:) (glpg_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae)) HI0618 HI0618 Haemophilus influenzae 727 10016565

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877045	14023	36179	297	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877080	14024	36180	186	61

Description

6500733041 yeck:hi0644 cytochrome c-type protein:torc:probable cytochrome c-type protein hi0644 (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0644 HI0644 Haemophilus influenzae 727 -11536899 111515 hi0644 (de:probable cytochrome c-type protein hi0644) (db:swissprot) YECK_HAEIN P44799 HAEMOPHILUS INFLUENZAE 727 -11536899 122005 torc membrane-bound cytochrome torc (cl:membrane-bound cytochrome torc:nirt homology) (db:pir1.dat) I64083 I64083 Haemophilus influenzae 727 -11536899 7500922941 hi0644 cytochrome c-type protein yeck (db:genpept-bct1) (de:haemophilus influenzae rd section 62 of 163 of the complete genome.) (nt:similar to sp:p52005 gb:u00096 pid:1736519) (le:8387) (re:9493) (di:complement) U32747 U32747 g1573642 Haemophilus influenzae Rd 71421 -11536899 5000695756 (de:(hi0644) (pn:probable cytochrome c-type protein hi0644:cytochrome c-type protein:torc) (gn:yeck) (gtcfc:13.7) (ec:) (yeck_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae)) HI0644 HI0644 Haemophilus influenzae 727 10053244

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877081	14025	36181	417	138

Description

6500733042 glpe:hi0679 glpe protein:protein homolog (gtcfc:2.8)
 (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0679 HI0679
 Haemophilus influenzae 727 -11536900 74025 glpe:hi0679 (de:glpe protein
 homolog) (db:swissprot) GLPE_HAEIN P44819 HAEMOPHILUS INFLUENZAE 727
 -11536900 166154 glpe protein homolog (cl:glpe protein) (db:pir2.dat)
 H64085 H64085 Haemophilus influenzae 727 -11536900 7500882495 hi0679 glpe
 protein glpe (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of
 163 of the complete genome.) (nt:similar to gb:x07520 sp:p09390 gb:m96795
 pid:146184) (le:7596) (re:7913) (di:complement) U32750 U32750 g1573679
 Haemophilus influenzae Rd 71421 -11536900 5000695757 (de:(hi0679)
 (pn:protein homolog:glpe protein:glpe) (gn:glpe) (gtcfc:13.7) (ec:)
 (glpe_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae))
 HI0679 HI0679 Haemophilus influenzae 727 10016555

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877085	14026	36182	417	138

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877087	14027	36183	645	214

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877088	14028	36184	1500	499

Description

6500733043 glpc:hi0683 glycerol-3-phosphate dehydrogenase:subunit
c:anaerobic glycerol-3-phosphate dehydrogenase subunit c:g-3-p dehydrogenase
(gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae)
HI0683 HI0683 Haemophilus influenzae 727 -11536901 74016 glpc:hi0683
(de:dehydrogenase)) (db:swissprot) GLPC_HAEIN P43801 HAEMOPHILUS INFLUENZAE
727 -11536901 136392 glycerol-3-phosphate dehydrogenase:chain c:anaerobic
(cl:glycerol-3-phosphate dehydrogenase (anaerobic) chain c:ferredoxin
2(4fe-4s) homology) (ec:1.1.99.5) (db:pir2.dat) C64086 C64086 Haemophilus
influenzae 727 -11536901 7500882490 hi0683 anaerobic glycerol-3-phosphate
dehydrogenase (db:genpept-bct1) (de:haemophilus influenzae rd section 66 of
163 of the complete genome.) (nt:similar to gb:m20938 sp:p13034 pid:146179
gb:u00096) (le:1958) (re:3238) (di:complement) U32751 U32751 g1573685
Haemophilus influenzae Rd 71421 -11536901 5000695758 (de:(hi0683)
(pn:anaerobic glycerol-3-phosphate dehydrogenase subunit c:g-3-p
dehydrogenase:glycerol-3-phosphate dehydrogenase, subunit c:glpc) (gn:glpc)
(gtcfc:13.7) (ec:) (glpc_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemoph)
HI0683 HI0683 Haemophilus influenzae 727 10016546

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877105	14029	36185	357	118

Description

6500733044 glpb:hi0684 glycerol-3-phosphate dehydrogenase:subunit
b:anaerobic glycerol-3-phosphate dehydrogenase subunit b:g-3-p dehydrogenase
(gtcfc:2.8:8.1) (ec:1.1.99.5) (keggfc:8.1) (tigrfc:6.3) (db:gtc-haemophilus
influenzae) HI0684 HI0684 Haemophilus influenzae 727 -11536902 74013
glpb:hi0684 (ec:1.1.99.5) (de:(g-3-p dehydrogenase)) (db:swissprot)
GLPB_HAEIN P43800 HAEMOPHILUS INFLUENZAE 727 -11536902 7500882488 hi0684
anaerobic glycerol-3-phosphate dehydrogenase (db:genpept-bct1)
(de:haemophilus influenzae rd section 66 of the complete genome.)
(nt:similar to gb:m20938 sp:p13033 pid:146178 gb:u00096) (le:3250) (re:4548)
(di:complement) U32751 U32751 g1573686 Haemophilus influenzae Rd 71421
-11536902 5000694397 (de:(hi0684) (pn:anaerobic glycerol-3-phosphate
dehydrogenase subunit b:g-3-p dehydrogenase:glycerol-3-phosphate
dehydrogenase, subunit b:glpb) (gn:glpb) (gtcfc:8.1) (ec:1.1.99.5)
(glpb_haein) (keggfc:8.1) (tigrfc:6.3) (db:gtc-h) HI0684 HI0684 Haemophilus
influenzae 727 10016543

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877106	14030	36186	465	154

Description

6500733045 glpa:hi0685 glycerol-3-phosphate dehydrogenase:subunit
a:anaerobic glycerol-3-phosphate dehydrogenase subunit a:g-3-p dehydrogenase
(gtcfc:2.8:8.1) (ec:1.1.99.5) (keggfc:8.1) (tigrfc:6.3) (db:gtc-haemophilus
influenzae) HI0685 HI0685 Haemophilus influenzae 727 -11536903 74010
glpa:hi0685 (ec:1.1.99.5) (de:(g-3-p dehydrogenase)) (db:swissprot)
GLPA_HAEIN P43799 HAEMOPHILUS INFLUENZAE 727 -11536903 136390 glpa
glycerol-3-phosphate dehydrogenase:chain a:anaerobic
(cl:glycerol-3-phosphate dehydrogenase (aerobic)) (ec:1.1.99.5)
(db:pir2.dat) E64086 E64086 Haemophilus influenzae 727 -11536903 7500882486
hi0685 anaerobic glycerol-3-phosphate dehydrogenase (db:genpept-bct1)
(de:haemophilus influenzae rd section 66 of 163 of the complete genome.)
(nt:similar to gb:m20938 sp:p13032 pid:146177 gb:u00096) (le:4538) (re:6229)
(di:complement) U32751 U32751 g1573687 Haemophilus influenzae Rd 71421
-11536903 5000694398 (de:(hi0685) (pn:anaerobic glycerol-3-phosphate
dehydrogenase subunit a:g-3-p dehydrogenase:glycerol-3-phosphate
dehydrogenase, subunit a:glpa) (gn:glpa) (gtcfc:8.1) (ec:1.1.99.5)
(glpa_haein) (keggfc:8.1) (tigrfc:6.3) (db:gtc-h) HI0685 HI0685 Haemophilus
influenzae 727 10016540

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877115	14031	36187	195	64

Description

6500733046 frdd:hi0832 fumarate reductase 13 kda hydrophobic
protein:fumarate reductase 13 kd hydrophobic protein (gtcfc:2.8)
(keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0832 HI0832
Haemophilus influenzae 727 -11536904 72317 frdd:hi0832 (de:fumarate
reductase 13 kd hydrophobic protein) (db:swissprot) FRDD_HAEIN P44891
HAEMOPHILUS INFLUENZAE 727 -11536904 136582 fumarate reductase:13k protein
(cl:fumarate reductase 13k protein) (ec:1.3.99.1) (db:pir2.dat) E64097
E64097 Haemophilus influenzae 727 -11536904 7500881747 hi0832 fumarate
reductase:13 kda hydrophobic protein (db:genpept-bct1) (de:haemophilus
influenzae rd section 80 of 163 of the complete genome.) (nt:similar to
sp:p03806 gb:j01611 pid:145266 pid:41484) (le:5150) (re:5494)
(di:complement) U32765 U32765 g1573846 Haemophilus influenzae Rd 71421
-11536904 5000695759 (de:(hi0832) (pn:fumarate reductase 13 kd hydrophobic
protein:fumarate reductase 13 kda hydrophobic protein:frdd) (gn:frdd)
(gtcfc:13.7) (ec:) (frdd_haein) (keggfc:11.2) (tigrfc:6.3)
(db:gtc-haemophilus influenzae)) HI0832 HI0832 Haemophilus influenzae 727
10014868

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877117	14032	36188	660	219

Description

6500733047 frdc:hi0833 fumarate reductase:fumarate reductase 15 kd hydrophobic protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0833 HI0833 Haemophilus influenzae 727 -11536905 72312 frdc:hi0833 (de:fumarate reductase 15 kd hydrophobic protein) (db:swissprot) FRDC_HAEIN P44892 HAEMOPHILUS INFLUENZAE 727 -11536905 166147 fumarate reductase 15k protein homolog (db:pir2.dat) F64097 F64097 Haemophilus influenzae 727 -11536905 7500881744 hi0833 fumarate reductase:15 kda hydrophobic protein (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to sp:p03805 gb:j01611 pid:145265 pid:41483) (le:5507) (re:5905) (di:complement) U32765 U32765 g1573847 Haemophilus influenzae Rd 71421 -11536905 5000695760 (de:(hi0833) (pn:fumarate reductase 15 kd hydrophobic protein:fumarate reductase:frdc) (gn:frdc) (gtcfc:13.7) (ec:) (frdc_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae)) HI0833 HI0833 Haemophilus influenzae 727 10014863

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877127	14033	36189	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877145	14034	36190	681	226

Description

5000695761 nrff:hi0934 nrff protein:cytochrome c biogenesis:sp:p32711:cytochrome c-type biogenesis protein precursor (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0934 HI0934 Haemophilus influenzae 727 -11536906 166570 hypothetical protein hi0934 (db:pir2.dat) H64161 H64161 Haemophilus influenzae 727 -11536906 7500960674 hi0934 cytochrome c-type biogenesis protein nrff (db:genpept-bct1) (de:haemophilus influenzae rd section 90 of 163 of the complete genome.) (nt:similar to sp:p32711 gb:x72298 pid:396410) (le:5057) (re:6211) (di:complement) U32775 U32775 g1573955 Haemophilus influenzae Rd 71421 -11536906 6500733048 nrff nrff protein:cytochrome c biogenesis:sp:p32711:cytochrome c-type biogenesis protein precursor (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI0934 HI0934 Haemophilus influenzae 727 -11536906

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877148	14035	36191	1167	388

Description

6500733049 dmhc:hi1045 anaerobic dimethyl sulfoxide reductase c:anaerobic dimethyl sulfoxide reductase chain c:dmsc reductase anchor subunit (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI1045 HI1045 Haemophilus influenzae 727 -11536907 68816 dmhc:hi1045 (de:subunit)) (db:swissprot) DMSC_HAEIN P45002 HAEMOPHILUS INFLUENZAE 727 -11536907 166000 dimethylsulfoxide reductase chain c homolog (cl:probable dimethylsulfoxide reductase chain c) (db:pir2.dat) E64109 E64109 Haemophilus influenzae 727 -11536907 7500880386 hi1045 anaerobic dimethyl sulfoxide reductase:chain c (db:genpept-bct1) (de:haemophilus influenzae rd section 100 of 163 of the complete genome.) (nt:similar to gb:j03412 sp:p18777 pid:145757 gb:u00096) (le:1305) (re:2144) (di:complement) U32785 U32785 g1574079 Haemophilus influenzae Rd 71421 -11536907 5000695762 (de:(hi1045) (pn:anaerobic dimethyl sulfoxide reductase chain c:dmsc reductase anchor subunit:anaerobic dimethyl sulfoxide reductase c:dmsc) (gn:dmsc) (gtcfc:13.7) (ec:) (dmsc_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilu) HI1045 HI1045 Haemophilus influenzae 727 10011401

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877158	14036	36192	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877161	14037	36193	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877167	14038	36194	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877183	14039	36195	1191	396

Description

6500733050 dmsb:hi1046 anaerobic dimethyl sulfoxide reductase b:anaerobic dimethyl sulfoxide reductase chain b:dmsb iron-sulfur subunit (gtcfc:2.8) (ec:1.-.-.) (keggfc:14.1) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI1046 HI1046 Haemophilus influenzae 727 -11536908 68814 dmsb:hi1046 (ec:1.-.-.) (de:reductase iron-sulfur subunit)) (db:swissprot) DMSB_HAEIN P45003 HAEMOPHILUS INFLUENZAE 727 -11536908 165999 dmsb dimethylsulfoxide reductase:chain b:anaerobic (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (ec:1.8.-.-) (db:pir2.dat) F64109 F64109 Haemophilus influenzae 727 -11536908 7500880384 hi1046 anaerobic dimethyl sulfoxide reductase:chain b (db:genpept-bct1) (de:haemophilus influenzae rd section 100 of 163 of the completegenome.) (nt:similar to gb:j03412 sp:p18776 pid:145756 gb:u00096) (le:2146) (re:2763) (di:complement) U32785 U32785 g1574080 Haemophilus influenzae Rd 71421 -11536908 5000695763 (de:(hi1046) (pn:anaerobic dimethyl sulfoxide reductase chain b:dmsb iron-sulfur subunit:anaerobic dimethyl sulfoxide reductase b:dmsb) (gn:dmsb) (gtcfc:13.7) (ec:1.-.-.) (dmsb_haein) (keggfc:11.1) (tigrfc:6.3) (db:gt) HI1046 HI1046 Haemophilus influenzae 727 10011399

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877191	14040	36196	636	211

Description

6500733051 dmsa:hi1047 anaerobic dimethyl sulfoxide reductase a:anaerobic dimethyl sulfoxide reductase chain a precursor:dmsb iron-sulfur subunit (gtcfc:2.8) (ec:1.-.-.) (keggfc:14.1) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI1047 HI1047 Haemophilus influenzae 727 -11536909 68812 dmsa:hi1047 (ec:1.-.-.) (de:(dmsb reductase)) (db:swissprot) DMSA_HAEIN P45004 HAEMOPHILUS INFLUENZAE 727 -11536909 165998 dmsa dimethylsulfoxide reductase:chain a precursor:anaerobic (ec:1.8.-.-) (db:pir2.dat) G64109 G64109 Haemophilus influenzae 727 -11536909 7500880381 hi1047 anaerobic dimethyl sulfoxide reductase:chain a (db:genpept-bct1) (de:haemophilus influenzae rd section 100 of 163 of the completegenome.) (nt:similar to gb:j03412 sp:p18775 pid:145755 gb:u00096) (le:2774) (re:5194) (di:complement) U32785 U32785 g1574081 Haemophilus influenzae Rd 71421 -11536909 5000695764 (de:(hi1047) (pn:anaerobic dimethyl sulfoxide reductase chain a precursor:dmsb iron-sulfur subunit:anaerobic dimethyl sulfoxide reductase a:dmsa) (gn:dmsa) (gtcfc:13.7) (ec:1.-.-.) (dmsa_haein) (keggfc:11.1) (tigrfc:6.3) (db:gtc-haemophi) HI1047 HI1047 Haemophilus influenzae 727 10011397

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877237	14041	36197	297	98

Description

6500733052 nrfd:hi1066 formate-dependent nitrite reductase transmembrane protein (gtcfc:2.8:2.6) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI1066 HI1066 Haemophilus influenzae 727 -11536910 86506 nrfd:hi1066 (de:nrfd protein homolog) (db:swissprot) NRFD_HAEIN P45014 HAEMOPHILUS INFLUENZAE 727 -11536910 122907 nrfd nrfd protein (cl:nrfd protein) (db:pir1.dat) I64180 I64180 Haemophilus influenzae 727 -11536910 7500886588 hi1066 nitrite reductase:transmembrane protein nrfd (db:genpept-bct1) (de:haemophilus influenzae rd section 102 of 163 of the completegenome.) (nt:similar to sp:p32709 gb:x72298 pid:396408) (le:150) (re:1115) (di:complement) U32787 U32787 g1574620 Haemophilus influenzae Rd 71421 -11536910 5000695765 (de:(hi1066) (pn:protein homolog:formate-dependent nitrite reductase transmembrane protein:nrfd) (gn:nrfd) (gtcfc:13.7) (ec:) (nrfd_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae)) HI1066 HI1066 Haemophilus influenzae 727 10028671

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877238	14042	36198	1413	470

Description

6500733053 nrfc:hi1067 formate-dependent nitrite reductase protein fe-s centers:protein homolog (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI1067 HI1067 Haemophilus influenzae 727 -11536911 86504 nrfc:hi1067 (de:nrfc protein homolog) (db:swissprot) NRFC_HAEIN P45015 HAEMOPHILUS INFLUENZAE 727 -11536911 122905 nrfc nrfc protein (cl:nrfc protein:ferredoxin 2(4fe-4s) homology) (db:pir1.dat) A64181 A64181 Haemophilus influenzae 727 -11536911 7500886586 hi1067 nitrite reductase:fe-s protein nrfc (db:genpept-bct1) (de:haemophilus influenzae rd section 102 of 163 of the completegenome.) (nt:similar to sp:p32708 gb:x72298 pid:396407) (le:1112) (re:1789) (di:complement) U32787 U32787 g1574621 Haemophilus influenzae Rd 71421 -11536911 5000695766 (de:(hi1067) (pn:protein homolog:formate-dependent nitrite reductase protein fe-s centers:nrfc) (gn:nrfc) (gtcfc:13.7) (ec:) (nrfc_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae)) HI1067 HI1067 Haemophilus influenzae 727 10028669

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877239	14043	36199	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877256	14044	36200	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877258	14045	36201	306	101

Description

6500733054 nrfb:hi1068 formate-dependent nitrite reductase:cytochrome c-type protein precursor (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI1068 HI1068 Haemophilus influenzae 727 -11536912 86502 nrfb:hi1068 (de:cytochrome c-type protein nrfb precursor) (db:swissprot) NRFB_HAEIN P45016 HAEMOPHILUS INFLUENZAE 727 -11536912 122903 nrfb nrfb protein (cl:nrfb protein) (db:pir1.dat) B64181 B64181 Haemophilus influenzae 727 -11536912 7500886584 hi1068 nitrite reductase:cytochrome c-type protein (db:genpept-bct1) (de:haemophilus influenzae rd section 102 of 163 of the completegenome.) (nt:similar to gb:u00006 sp:p32707 gb:x72298 pid:404303) (le:1786) (re:2466) (di:complement) U32787 U32787 g1574622 Haemophilus influenzae Rd 71421 -11536912 5000695767 (de:(hi1068) (pn:cytochrome c-type protein precursor:formate-dependent nitrite reductase:nrfb) (gn:nrfb) (gtcfc:13.7) (ec:) (nrfb_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae)) HI1068 HI1068 Haemophilus influenzae 727 10028667

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877265	14046	36202	330	109

Description

6500733055 nrfa:hi1069 formate-dependent nitrite reductase:cytochrome c552:cytochrome c552 precursor (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI1069 HI1069 Haemophilus influenzae 727 -11536913 86500 nrfa:hi1069 (de:cytochrome c552 precursor) (db:swissprot) NRFA_HAEIN P45017 HAEMOPHILUS INFLUENZAE 727 -11536913 122901 formate-dependent nitrite reductase:cytochrome c552 (cl:formate-dependent nitrite reductase cytochrome c552) (ec:1.7.-.-) (db:pir1.dat) C64181 C64181 Haemophilus influenzae 727 -11536913 7500886582 hi1069 nitrite reductase:cytochrome c552 nrfa (db:genpept-bct1) (de:haemophilus influenzae rd section 102 of 163 of the completegenome.) (nt:similar to sp:p32050 gb:x72298 pid:396405) (le:2510) (re:4126) (di:complement) U32787 U32787 g1574623 Haemophilus influenzae Rd 71421 -11536913 5000695768 (de:(hi1069) (pn:cytochrome c552 precursor:formate-dependent nitrite reductase:cytochrome c552:nrfa) (gn:nrfa) (gtcfc:13.7) (ec:) (nrfa_haein) (keggfc:11.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae)) HI1069 HI1069 Haemophilus influenzae 727 10028665

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877272	14047	36203	411	136

Description

5000695769 hydrogenase isoenzymes formation protein:hypc:hypothetical protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI1390 HI1390 Haemophilus influenzae 727 -11536914 111185 hi1390 (de:hypothetical protein hi1390) (db:swissprot) YD90_HAEIN P45194 HAEMOPHILUS INFLUENZAE 727 -11536914 166209 hypothetical protein hi1390 (db:pir2.dat) F64121 F64121 Haemophilus influenzae 727 -11536914 7500922128 hi1390 hydrogenase formation protein hypg (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the completegenome.) (nt:similar to sp:p37185 gb:u09177 pid:544489) (le:7528) (re:7593) (di:direct) U32819 U32819 g1574229 Haemophilus influenzae Rd 71421 -11536914 6500733056 hydrogenase isoenzymes formation protein:hypc:hypothetical protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.3) (db:gtc-haemophilus influenzae) HI1390 HI1390 Haemophilus influenzae 727 -11536914

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877273	14048	36204	1986	661

Description

6500733057 atp:hi1274 atp synthase subunit 3 region protein (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.4) (db:gtc-haemophilus influenzae) HI1274 HI1274 Haemophilus influenzae 727 -11536915 500684912 glob:hi1274 (ec:3.1.2.6) (de:ii) (glx ii) (db:swissprot) GLO2_HAEIN P71374 HAEMOPHILUS INFLUENZAE 727 -11536915 166016 hypothetical protein hi1274 (cl:glyoxalase) (db:pir2.dat) G64113 G64113 Haemophilus influenzae 727 -11536915 7500882478 hi1274 hydroxyacylglutathione hydrolase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 122 of 163 of the completegenome.) (nt:similar to pid:1208973 gb:u00096 sp:q47677) (le:2848) (re:3564) (di:direct) U32807 U32807 g1574729 Haemophilus influenzae Rd 71421 -11536915 5000694188 (de:(hi1274) (pn:atp synthase subunit 3 region protein:atp) (gn:atp) (gtcfc:2.8) (ec:) (keggfc:11.2) (tigrfc:6.4) (db:gtc-haemophilus influenzae)) HI1274 HI1274 Haemophilus influenzae 727 10060538

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877274	14049	36205	294	97

Description

6500733058 flda:hi0191 flavodoxin (gtcfc:2.8:9.5) (keggfc:14.2) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI0191 HI0191 Haemophilus influenzae 727 -11536916 135961 flavodoxin a (cl:flavodoxin:flavodoxin homology) (db:pir2.dat) C64053 C64053 Haemophilus influenzae 727 -11536916 7500953769 hi0191 flavodoxin flda (db:genpept-bct1) (de:haemophilus influenzae rd section 19 of 163 of the complete genome.) (nt:similar to gb:m59426 sp:p23243 pid:145986 gb:u00096) (le:4576) (re:5100) (di:complement) U32704 U32704 g1573149 Haemophilus influenzae Rd 71421 -11536916 5000694179 (de:(hi0191) (pn:flavodoxin:flda) (gn:flda) (gtcfc:2.8) (ec:) (flav_haein) (keggfc:11.2) (tigrfc:6.5) (db:gtc-haemophilus influenzae)) HI0191 HI0191 Haemophilus influenzae 727 10069197

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877299	14050	36206	336	111

Description

6500733059 fdx:hi0372 ferredoxin:2fe-2s (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI0372 HI0372 Haemophilus influenzae 727 -11536917 135751 ferredoxin 2fe-2s) (cl:ferredoxin (2fe-2s):ferredoxin (2fe-2s) homology) (db:pir2.dat) A64064 A64064 Haemophilus influenzae 727 -11536917 7500953747 hi0372 ferredoxin fdx-1 (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to gb:m88654 sp:p25528 pid:145915 gb:u00096) (le:4876) (re:5217) (di:complement) U32721 U32721 g1573341 Haemophilus influenzae Rd 71421 -11536917 5000694180 (de:(hi0372) (pn:2fe-2s:ferredoxin:fdx) (gn:fdx) (gtcfc:2.8) (ec:) (fer_haein) (keggfc:11.2) (tigrfc:6.5) (db:gtc-haemophilus influenzae)) HI0372 HI0372 Haemophilus influenzae 727 10069093

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877308	14051	36207	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877310	14052	36208	273	90

Description

GTC ORF with score 215 to: (sr:fission yeast) (db:genpept-pln1) (de:s.pombe chromosome i cosmid c23c4.) (nt:spac23c4.08, rho protein, len:208aa, similar eg. to) (le:10487:10643:10773:11170) (re:10503:10698:10845:11650) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877313	14053	36209	789	263

Description

5000694181 ferredoxin:fdx:putative ferredoxin-like protein hi0527 (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI0527 HI0527 Haemophilus influenzae 727 -11536918 111918 hi0527 (de:putative ferredoxin-like protein hi0527) (db:swissprot) YFHL_HAEIN P44746 HAEMOPHILUS INFLUENZAE 727 -11536918 135802 ferredoxin 2 4fe-4s) (cl:ferredoxin 2(4fe-4s):ferredoxin 2(4fe-4s) homology) (db:pir2.dat) E64074 E64074 Haemophilus influenzae 727 -11536918 7500923490 hi0527 ferredoxin fdx-2 (db:genpept-bct1) (de:haemophilus influenzae rd section 50 of 163 of the complete genome.) (nt:similar to sp:p00208 percent ident: 59.49;) (le:977) (re:1237) (di:direct) U32735 U32735 g1573511 Haemophilus influenzae Rd 71421 -11536918 6500733060 ferredoxin:fdx:putative ferredoxin-like protein hi0527 (gtcfc:2.8:9.5:6.4) (keggfc:14.2) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI0527 HI0527 Haemophilus influenzae 727 -11536918

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877319	14054	36210	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877325	14055	36211	417	138

Description

GTC ORF with score 118 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f47d12.) (nt:coded for by c. elegans cdna ceess77r) (le:15:345:607:833) (re:251:424:781:949) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877330	14056	36212	474	157

Description

5000694182 dsbd:cy cz:hi0885 c-type cytochrome biogenesis protein:copper tolerance:cy cz:thiol:disulfide interchange protein dsbd:c-type cytochrome biogenesis protein cy cz (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI0885 HI0885 Haemophilus influenzae 727 -11536919 69313 dsbd:cy cz:hi0885 (de:biogenesis protein cy cz)) (db:swissprot) DSB_D_HAEIN P44919 HAEMOPHILUS INFLUENZAE 727 -11536919 166035 inner membrane copper tolerance protein cy cz homolog (db:pir2.dat) A64100 A64100 Haemophilus influenzae 727 -11536919 7500880672 hi0885 th:disulfide interchange protein dsbd (db:genpept-bct1) (de:haemophilus influenzae rd section 85 of 163 of the complete genome.) (nt:similar to sp:p36655 gb:x77707 gb:z36905 pid:536980) (le:4643) (re:6382) (di:direct) U32770 U32770 g1573902 Haemophilus influenzae Rd 71421 -11536919 6500733061 dsbd:cy cz c-type cytochrome biogenesis protein:copper tolerance:cy cz:thiol:disulfide interchange protein dsbd:c-type cytochrome biogenesis protein cy cz (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI0885 HI0885 Haemophilus influenzae 727 -11536919

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877331	14057	36213	756	251

Description

GTC ORF with score 512 to: (fn:catalyst for urea hydrolysis; plays a pivotal) (db:genpept-pln2) (ec:3.5.1.5) (de:coccidioides immitis urease (ure) gene, complete cds.) (nt:believed to be expressed during sporulation in) (le:864:1092:1253:1395:1878) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877340	14058	36214	1116	371

Description

GTC ORF with score 1335 to: (fn:catalyst for urea hydrolysis; plays a pivotal) (db:genpept-pln2) (ec:3.5.1.5) (de:coccidioides immitis urease (ure) gene, complete cds.) (nt:believed to be expressed during sporulation in) (le:864:1092:1253:1395:1878) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877349	14059	36215	1101	366

Description

6500733062 cytochrome oxidase d subunit ii:cydb:probable cytochrome oxidase subunit ii (gtcfc:2.8) (ec:1.10.3.-) (keggfc:14.1) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI1075 HI1075 Haemophilus influenzae 727 -11536920 67531 hi1075 (ec:1.10.3.-) (de:probable cytochrome oxidase subunit ii,) (db:swissprot) CYOB_HAEIN P45020 HAEMOPHILUS INFLUENZAE 727 -11536920 166075 cytochrome d complex terminal oxidase:chain ii (cl:cytochrome d ubiquinol oxidase) (ec:1.10.3.-) (db:pir2.dat) D64181 D64181 Haemophilus influenzae 727 -11536920 7500879865 hi1075 cytochrome d ubiquinol oxidase:subunit ii (db:genpept-bct1) (de:haemophilus influenzae rd section 102 of 163 of the completegenome.) (nt:similar to gb:j03939 sp:p11027 pid:145640 gb:u00096) (le:9291) (re:10427) (di:complement) U32787 U32787 g1574626 Haemophilus influenzae Rd 71421 -11536920 5000694183 (de:(hi1075) (pn:probable cytochrome oxidase subunit ii:cytochrome oxidase d subunit ii:cydb) (gtcfc:2.8) (ec:1.10.3.-) (cyob_haein) (keggfc:11.1) (tigrfc:6.5) (db:gtc-haemophilus influenzae)) HI1075 HI1075 Haemophilus influenzae 727 10010130

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877362	14060	36216	582	193

Description

6500733063 cytochrome oxidase d subunit i:cyda:probable cytochrome oxidase subunit i (gtcfc:2.8) (ec:1.10.3.-) (keggfc:14.1) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI1076 HI1076 Haemophilus influenzae 727 -11536921 67529 hi1076 (ec:1.10.3.-) (de:probable cytochrome oxidase subunit i,) (db:swissprot) CYOA_HAEIN P45021 HAEMOPHILUS INFLUENZAE 727 -11536921 166074 cytochrome d complex terminal oxidase:chain i (cl:cytochrome d complex terminal oxidase chain i) (ec:1.10.3.-) (db:pir2.dat) E64181 E64181 Haemophilus influenzae 727 -11536921 7500879863 hi1076 cytochrome d ubiquinol oxidase:subunit i (db:genpept-bct1) (de:haemophilus influenzae rd section 102 of 163 of the completegenome.) (nt:similar to gb:j03939 sp:p11026 pid:497637 gb:u00096) (le:10442) (re:12007) (di:complement) U32787 U32787 g1574627 Haemophilus influenzae Rd 71421 -11536921 5000694184 (de:(hi1076) (pn:probable cytochrome oxidase subunit i:cytochrome oxidase d subunit i:cyda) (gtcfc:2.8) (ec:1.10.3.-) (cyoa_haein) (keggfc:11.1) (tigrfc:6.5) (db:gtc-haemophilus influenzae)) HI1076 HI1076 Haemophilus influenzae 727 10010128

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877368	14061	36217	312	103

Description

5000694185 nad:ph-flavin oxidoreductase (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI1278 HI1278 Haemophilus influenzae 727 -11536922 5500686489 hi1278 (ec:1.-.-.-) (de:putative nad(p)h nitroreductase,) (db:swissprot) YC78_HAEIN Q57431 HAEMOPHILUS INFLUENZAE 727 -11536922 167028 probable nad p h-flavin oxidoreductase (cl:nitroreductase) (ec:1.6.6.-) (db:pir2.dat) B64114 B64114 Haemophilus influenzae 727 -11536922 7500921510 hi1278 nad p h-flavin oxidoreductase (db:genpept-bct1) (de:haemophilus influenzae rd section 122 of 163 of the completegenome.) (nt:similar to gb:d17743 sp:p46072 pid:517169 percent) (le:7951) (re:8613) (di:complement) U32807 U32807 g1574733 Haemophilus influenzae Rd 71421 -11536922 6500733064 nad:ph-flavin oxidoreductase (gtcfc:2.8) (keggfc:14.2) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI1278 HI1278 Haemophilus influenzae 727 -11536922

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877369	14062	36218	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877371	14063	36219	549	182

Description

6500733065 pnta:hi1362 nad:p transhydrogenase subunit alpha:pyridine nucleotide transhydrogenase subunit alpha:nicotinamide nucleotide transhydrogenase subunit alpha (gtcfc:2.8:9.4) (ec:1.6.1.1) (keggfc:9.4) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI1362 HI1362 Haemophilus influenzae 727 -11536923 90184 pnta:hi1362 (ec:1.6.1.1) (de:transhydrogenase subunit alpha)) (db:swissprot) PNTA_HAEIN P43842 HAEMOPHILUS INFLUENZAE 727 -11536923 136636 nad p + transhydrogenase b-specific:alpha chain (cl:nad(p)+ transhydrogenase (b-specific) alpha chain:alanine dehydrogenase homology:nad(p)+ transhydrogenase (b-specific) alpha chain homology) (ec:1.6.1.1) (db:pir2.dat) E64119 E64119 Haemophilus influenzae 727 -11536923 7500888237 hi1362 nad p transhydrogenase:subunit alpha pnta (db:genpept-bct1) (de:haemophilus influenzae rd section 131 of 163 of the completegenome.) (nt:similar to sp:p07001 gb:x04195 gb:x66086 pid:42456) (le:161) (re:1699) (di:direct) U32816 U32816 g1574194 Haemophilus influenzae Rd 71421 -11536923 5000694186 (de:(hi1362) (pn:pyridine nucleotide transhydrogenase subunit alpha:nicotinamide nucleotide transhydrogenase subunit alpha:nad:p transhydrogenase subunit alpha:pnta) (gn:pnta) (gtcfc:2.8) (ec:1.6.1.1) (pnta_haein) (keggfc:11.1)) HI1362 HI1362 Haemophilus influenzae 727 10032304

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877373	14064	36220	465	154

Description

6500733066 pntb:hi1363 nad:p transhydrogenase subunit beta:pyridine nucleotide transhydrogenase subunit beta:nicotinamide nucleotide transhydrogenase subunit beta (gtcfc:2.8:9.4) (ec:1.6.1.1) (keggfc:9.4) (tigrfc:6.5) (db:gtc-haemophilus influenzae) HI1363 HI1363 Haemophilus influenzae 727 -11536924 90186 pntb:hi1363 (ec:1.6.1.1) (de:transhydrogenase subunit beta)) (db:swissprot) PNTB_HAEIN P43010 HAEMOPHILUS INFLUENZAE 727 -11536924 136637 nad p + transhydrogenase b-specific:beta chain (cl:nad(p)+ transhydrogenase (b-specific) beta chain:nad(p)+ transhydrogenase (b-specific) beta chain homology) (ec:1.6.1.1) (db:pir2.dat) F64119 F64119 Haemophilus influenzae 727 -11536924 7500888238 hi1363 nad p transhydrogenase:subunit beta pntb (db:genpept-bct1) (de:haemophilus influenzae rd section 131 of 163 of the completegenome.) (nt:similar to sp:p07002 gb:x66086 pid:42457 gb:u00096) (le:1710) (re:3134) (di:direct) U32816 U32816 g1574195 Haemophilus influenzae Rd 71421 -11536924 5000694187 (de:(hi1363) (pn:pyridine nucleotide transhydrogenase subunit beta:nicotinamide nucleotide transhydrogenase subunit beta:nad:p transhydrogenase subunit beta:pntb) (gn:pntb) (gtcfc:2.8) (ec:1.6.1.1) (pntb_haein) (keggfc:11.1) (ti) HI1363 HI1363 Haemophilus influenzae 727 10032306

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877401	14065	36221	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877432	14066	36222	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877434	14067	36223	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877435	14068	36224	978	326

Description

GTC ORF with score 1296 to: (sr:baker's yeast) (db:genpept-pln1)
 (de:saccharomyces cerevisiae splicing factor prp43p (prp43) gene,complete
 cds.) (nt:proposed function in spliceosome disassembly; deah) (le:379)
 (re:2682) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877439	14069	36225	381	126

Description

GTC ORF with score 153 to: (sr:baker's yeast) (db:genpept-pln1)
 (de:saccharomyces cerevisiae splicing factor prp43p (prp43) gene,complete
 cds.) (nt:proposed function in spliceosome disassembly; deah) (le:379)
 (re:2682) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877442	14070	36226	201	66

Description

6500733067 fabg:hi0155 3-ketoacyl-acyl carrier protein
 reductase:3-oxoacyl-acyl-carrier protein reductase (gtcfc:3.1:3.2)
 (ec:1.1.1.100) (keggfc:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae)
 HI0155 HI0155 Haemophilus influenzae 727 -11536925 70992 fabg:hi0155
 (ec:1.1.1.100) (de:acyl carrier protein reductase)) (db:swissprot)
 FABG_HAEIN P43713 HAEMOPHILUS INFLUENZAE 727 -11536925 136080 fabg
 3-oxoacyl-acyl-carrier-protein reductase,) (cl:ribitol
 dehydrogenase:short-chain alcohol dehydrogenase homology) (ec:1.1.1.100)
 (db:pir2.dat) D64051 D64051 Haemophilus influenzae 727 -11536925 7500881308
 hi0155 3-ketoacyl-acyl carrier protein reductase (db:genpept-bct1)
 (de:haemophilus influenzae rd section 16 of 163 of the complete genome.)
 (nt:similar to gb:m84991 sp:p25716 pid:145881) (le:5582) (re:6310)
 (di:complement) U32701 U32701 g1573112 Haemophilus influenzae Rd 71421
 -11536925 5000694189 (de:(hi0155) (pn:3-oxoacyl-:3-ketoacyl-acyl carrier
 protein reductase:fabg) (gn:fabg) (gtcfc:3.1) (ec:1.1.1.100) (fabg_haein)
 (keggfc:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae)) HI0155 HI0155
 Haemophilus influenzae 727 10013567

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877443	14071	36227	1218	406

Description

6500733068 fabd:hi0156 malonyl coenzyme a-acyl carrier protein transacylase:malonyl coa-acyl carrier protein transacylase:mct (gtcfc:3.1:3.2) (ec:2.3.1.39) (keggfc:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0156 HI0156 Haemophilus influenzae 727 -11536926 70980 fabd:hi0156 (ec:2.3.1.39) (de:malonyl coa-acyl carrier protein transacylase, (mct)) (db:swissprot) FABD_HAEIN P43712 HAEMOPHILUS INFLUENZAE 727 -11536926 137943 fabd acyl-carrier-protein s-malonyltransferase,) (cl:(acyl-carrier-protein) s-malonyltransferase:(acyl-carrier-protein) s-malonyltransferase homology) (ec:2.3.1.39) (db:pir2.dat) E64051 E64051 Haemophilus influenzae 727 -11536926 7500881305 hi0156 malonyl coa-acyl carrier protein transacylase (db:genpept-bct1) (de:haemophilus influenzae rd section 16 of 163 of the complete genome.) (nt:similar to gb:m87040 sp:p25715 gb:z11565 pid:145887) (le:6327) (re:7265) (di:complement) U32701 U32701 g1573113 Haemophilus influenzae Rd 71421 -11536926 5000694190 (de:(hi0156) (pn:malonyl coa-acyl carrier protein transacylase:mct:malonyl coenzyme a-acyl carrier protein transacylase:fabd) (gn:fabd) (gtcfc:3.1) (ec:2.3.1.39) (fabd_haein) (keggfc:3.1) (tigrfc:7.1) (db:gtc-haemophilus influen) HI0156 HI0156 Haemophilus influenzae 727 10013555

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877451	14072	36228	681	226

Description

6500733069 fabh:hi0157 beta-ketoacyl-acyl carrier protein synthase iii:3-oxoacyl-acyl-carrier-protein synthase:beta-ketoacyl-acp synthase iii:kas iii (gtcfc:3.1:3.2) (ec:2.3.1.41) (keggfc:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0157 HI0157 Haemophilus influenzae 727 -11536927 70999 fabh:hi0157 (ec:2.3.1.41) (de:ketoacyl-acp synthase iii) (kas iii) (db:swissprot) FABH_HAEIN P43711 HAEMOPHILUS INFLUENZAE 727 -11536927 137963 fabh 3-oxoacyl-acyl-carrier-protein synthase, iii) (cl:3-oxoacyl-(acyl-carrier-protein) synthase iii) (ec:2.3.1.41) (db:pir2.dat) F64051 F64051 Haemophilus influenzae 727 -11536927 7500881312 hi0157 beta-ketoacyl-acp synthase iii fabh (db:genpept-bct1) (de:haemophilus influenzae rd section 16 of 163 of the complete genome.) (nt:similar to gb:m77744 sp:p24249 gb:z11565 pid:145886) (le:7893) (re:8843) (di:complement) U32701 U32701 g1573114 Haemophilus influenzae Rd 71421 -11536927 5000694191 (de:(hi0157) (pn:3-oxoacyl-:beta-ketoacyl-acyl carrier protein synthase iii:fabh) (gn:fabh) (gtcfc:3.1) (ec:2.3.1.41) (fabh_haein) (keggfc:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae)) HI0157 HI0157 Haemophilus influenzae 727 10013574

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877455	14073	36229	369	122

Description

6500733070 faba:hi1325 3-hydroxydecanoyl-acyl-carrier-protein
dehydratase:beta-hydroxydecanoyl thioester dehydrase (gtcfc:3.1:3.2)
(ec:4.2.1.60) (keggfc:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae)
HI1325 HI1325 Haemophilus influenzae 727 -11536928 70969 faba:hi1325
(ec:4.2.1.60) (de:(beta-hydroxydecanoyl thioester dehydrase)) (db:swissprot)
FABA_HAEIN P45159 HAEMOPHILUS INFLUENZAE 727 -11536928 141937 faba
3-hydroxydecanoyl-acyl-carrier-protein dehydratase,)
(cl:3-hydroxydecanoyl-(acyl-carrier-protein) dehydratase) (ec:4.2.1.60)
(db:pir2.dat) G64116 G64116 Haemophilus influenzae 727 -11536928 7500881301
hi1325 3-hydroxydecanoyl-acyl carrier-protein (db:genpept-bct1)
(de:haemophilus influenzae rd section 127 of 163 of the completegenome.)
(nt:similar to gb:j03186 sp:p18391 pid:1045606) (le:2053) (re:2586)
(di:direct) U32812 U32812 g1574786 Haemophilus influenzae Rd 71421 -11536928
5000694192 (de:(hi1325) (pn:3-hydroxydecanoyl-:d-3-hydroxydecanoyl-:acyl
carrier-protein dehydratase:faba) (gn:faba) (gtcfc:3.1) (ec:4.2.1.60)
(faba_haein) (keggfc:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae))
HI1325 HI1325 Haemophilus influenzae 727 10013544

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877456	14074	36230	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877462	14075	36231	468	155

Description

6500733071 fabb:hi1533 beta-ketoacyl-acp synthase
i:3-oxoacyl-acyl-carrier-protein synthase i:kas i (gtcfc:3.1:3.2)
(ec:2.3.1.41) (keggfc:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae)
HI1533 HI1533 Haemophilus influenzae 727 -11536929 70975 fabb:hi1533
(ec:2.3.1.41) (de:ketoacyl-acp synthase i) (kas i)) (db:swissprot)
FABB_HAEIN P43710 HAEMOPHILUS INFLUENZAE 727 -11536929 137944
3-oxoacyl-acyl-carrier-protein synthase, i:beta-ketoacyl-acp synthase i)
(cl:3-oxoacyl-(acyl-carrier-protein) synthase
i:3-oxoacyl-(acyl-carrier-protein) synthase i homology) (ec:2.3.1.41)
(db:pir2.dat) A64128 A64128 Haemophilus influenzae 727 -11536929 7500881303
hi1533 beta-ketoacyl-acp synthase i fabb (db:genpept-bct1) (de:haemophilus
influenzae rd section 144 of 163 of the completegenome.) (nt:similar to
gb:m24427 sp:p14926 pid:145884 gb:u00096) (le:419) (re:1639) (di:complement)
U32829 U32829 g1574377 Haemophilus influenzae Rd 71421 -11536929 5000694193
(de:hi1533) (pn:3-oxoacyl-:beta-ketoacyl-acp synthase i:fabb) (gn:fabb)
(gtcfc:3.1) (ec:2.3.1.41) (fabb_haein) (keggfc:3.1) (tigrfc:7.1)
(db:gtc-haemophilus influenzae)) HI1533 HI1533 Haemophilus influenzae 727
10013550

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877464	14076	36232	330	109

Description

5000694194 fabi:envm:hi1734 short chain alcohol dehydrogenase
homolog:enoyl-acyl-carrier-protein reductase:nadh-dependent enoyl-acp
reductase (gtcfc:1.1:3.1:2.2) (ec:1.3.1.9) (keggfc:3.1) (tigrfc:7.1)
(db:gtc-haemophilus influenzae) HI1734 HI1734 Haemophilus influenzae 727
-11536930 167158 fabi:envm enoyl-acyl-carrier-protein reductase (nadh),)
(cl:enoyl-(acyl-carrier-protein) reductase (nadh):short-chain alcohol
dehydrogenase homology) (ec:1.3.1.9) (db:pir2.dat) B64139 B64139 Haemophilus
influenzae 727 -11536930 7500953789 hi1734 enoyl-acyl-carrier-protein
reductase fabi (db:genpept-bct1) (de:haemophilus influenzae rd section 161
of 163 of the completegenome.) (nt:similar to gb:m97219 sp:p29132 gb:x78733
pid:145851) (le:6538) (re:7425) (di:complement) U32846 U32846 g1574591
Haemophilus influenzae Rd 71421 -11536930 6500733072 fabi:envm short chain
alcohol dehydrogenase homolog:enoyl-acyl-carrier-protein
reductase:nadh-dependent enoyl-acp reductase (gtcfc:1.1:3.1:2.2)
(ec:1.3.1.9) (keggfc:3.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae)
HI1734 HI1734 Haemophilus influenzae 727 -11536930

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877465	14077	36233	789	262

Description

6500733073 long chain fatty acid coa ligase:putative
long-chain-fatty-acid--coa ligase:long-chain acyl-coa synthetase:lacs
(gtcfc:3.1:3.2) (ec:6.2.1.3) (keggfc:3.2) (tigrfc:7.1) (db:gtc-haemophilus
influenzae) HI0002 HI0002 Haemophilus influenzae 727 -11536931 81591 hi0002
(ec:6.2.1.3) (de:acyl-coa synthetase) (lacs)) (db:swissprot) LCFH_HAEIN
P44446 HAEMOPHILUS INFLUENZAE 727 -11536931 166963
long-chain-fatty-acid--coa ligase homolog (cl:acetate--coa ligase homology)
(db:pir2.dat) H64041 H64041 Haemophilus influenzae 727 -11536931 7500884826
hi0002 long chain fatty acid coa ligase:putative (db:genpept-bct1)
(de:haemophilus influenzae rd section 1 of 163 of the complete genome.)
(nt:similar to gb:ae000782 percent identity: 34.58;) (le:1190) (re:3013)
(di:direct) U32686 U32686 g1572946 Haemophilus influenzae Rd 71421 -11536931
5000694195 (de:(hi0002) (pn:putative long-chain-fatty-acid--coa
ligase:long-chain acyl-coa synthetase:lacs:long chain fatty acid coa ligase)
(gtcfc:3.2) (ec:6.2.1.3) (lcfh_haein) (keggfc:3.2) (tigrfc:7.1)
(db:gtc-haemophilus influenzae)) HI0002 HI0002 Haemophilus influenzae 727
10023827

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877468	14078	36234	579	192

Description

6500733074 tesb:hi0076 acyl-coa thioesterase ii (gtcfc:3.1:3.2) (ec:3.1.2.-)
(keggfc:14.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0076 HI0076
Haemophilus influenzae 727 -11536932 101055 tesb:hi0076 (ec:3.1.2.-)
(de:acyl-coa thioesterase ii,) (db:swissprot) TESB_HAEIN P44498 HAEMOPHILUS
INFLUENZAE 727 -11536932 165979 tesb acyl-coa thiolesterase:ii (cl:acyl-coa
thiolesterase ii) (ec:3.1.2.-) (db:pir2.dat) B64047 B64047 Haemophilus
influenzae 727 -11536932 7500892939 hi0076 acyl-coa thioesterase ii tesb
(db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the
complete genome.) (nt:similar to gb:m63308 sp:p23911 pid:147932 gb:u00096)
(le:4078) (re:4938) (di:direct) U32693 U32693 g1573025 Haemophilus
influenzae Rd 71421 -11536932 5000694202 (de:(hi0076) (pn:acyl-coa
thioesterase ii:tesb) (gn:tesb) (gtcfc:3.8:8.2:8.3) (ec:3.1.2.-)
(tesb_haein) (keggfc:11.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae))
HI0076 HI0076 Haemophilus influenzae 727 10042897

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877469	14079	36235	189	62

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877498	14080	36236	2964	987

Description

6500733075 pgsa:hi0123 cdp-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase:phosphatidylglycerophosphate synthase:pgp synthase (gtcfc:3.1:3.2:8.1) (ec:2.7.8.5) (keggfc:8.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0123 HI0123 Haemophilus influenzae 727 -11536933 89370 pgsa:hi0123 (ec:2.7.8.5) (de:(ec 2.7.8.5) (phosphatidylglycerophosphate synthase) (pgp synthase)) (db:swissprot) PGSA_HAEIN P44528 HAEMOPHILUS INFLUENZAE 727 -11536933 139386 cdpdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (cl:cdpdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase) (ec:2.7.8.5) (db:pir2.dat) F64049 F64049 Haemophilus influenzae 727 -11536933 7500887988 hi0123 phosphatidylglycerophosphate synthase pgsa (db:genpept-bct1) (de:haemophilus influenzae rd section 13 of 163 of the complete genome.) (nt:similar to gb:m12299 sp:p06978 pid:473749 gb:u00096) (le:7061) (re:7618) (di:direct) U32698 U32698 g1573078 Haemophilus influenzae Rd 71421 -11536933 5000694393 (de:(hi0123) (pn:cdp-diacylglycerol--glycerol-3-phosphate 3- phosphatidyltransferase:pgp synthase:phosphatidylglycerophosphate synthase:pgsa) (gn:pgsa) (gtcfc:8.1) (ec:2.7.8.5) (pgsa_haein) (keggfc:8.1) (tigrfc:7.1) (db:gtc-haem) HI0123 HI0123 Haemophilus influenzae 727 10031493

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877509	14081	36237	3393	1131

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877516	14082	36238	567	188

Description

6500733076 acpp:hi0154 acyl carrier protein:acp (gtcfc:3.1:3.2) (keggfc:14.2) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0154 HI0154 Haemophilus influenzae 727 -11536934 58274 acpp:hi0154 (de:acyl carrier protein (acp)) (db:swissprot) ACP_HAEIN P43709 HAEMOPHILUS INFLUENZAE 727 -11536934 152959 acpp acyl carrier protein (cl:acyl carrier protein:acyl carrier protein homology) (db:pir2.dat) C64051 C64051 Haemophilus influenzae 727 -11536934 7500876360 hi0154 acyl carrier protein acpp (db:genpept-bct1) (de:haemophilus influenzae rd section 16 of 163 of the complete genome.) (nt:similar to pid:1173841 sp:p55337 pid:1173842) (le:5096) (re:5326) (di:complement) U32701 U32701 g1573111 Haemophilus influenzae Rd 71421 -11536934 5000694203 (de:(hi0154) (pn:acp:acyl carrier protein:acpp) (gn:acpp) (gtcfc:3.8:8.2:8.3) (ec:) (acp_haein) (keggfc:11.2) (tigrfc:7.1) (db:gtc-haemophilus influenzae)) HI0154 HI0154 Haemophilus influenzae 727 10001054

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877519	14083	36239	3468	1155

Description

GTC ORF with score 493 to: (db:genpept-inv) (de:caenorhabditis elegans cosmid zk1067, complete sequence.) (nt:cdna est embl:d32579 comes from this gene; cdna est) (le:30592:31120:31487:32254) (re:31008:31440:32209:33142) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877536	14084	36240	531	176

Description

GTC ORF with score 216 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana bac t10m13 from chromosome iv short arm, mapsat 11.6 cm, complete sequence.) (nt:similar to plant and fission yeast hexose (glucose)) (le:24652:25815:26216) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877537	14085	36241	255	84

Description

6500733077 psd:hi0160 psd:phosphatidylserine decarboxylase proenzyme (gtcfc:3.1:3.2:5.3:8.1) (ec:4.1.1.65) (keggfc:5.3:8.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0160 HI0160 Haemophilus influenzae 727 -11536935 69249 psd:hi0160 (ec:4.1.1.65) (de:phosphatidylserine decarboxylase proenzyme,) (db:swissprot) DPSD_HAEIN P43789 HAEMOPHILUS INFLUENZAE 727 -11536935 167089 phosphatidylserine decarboxylase (ec:4.1.1.65) (db:pir2.dat) I64051 I64051 Haemophilus influenzae 727 -11536935 241611 psd phosphatidylserine decarboxylase (fn:lipid metabolism) (db:genpept-bct1) (de:haemophilus influenzae bola (bola), glutathione reductase (gor),phosphatidylserine decarboxylase (psd), 30k protein (rpmf), genes,complete cds.) (le:3218) (re:4090) (di:complement) HIU20229 U20229 g644855 Haemophilus influenzae 727 -11536935 7500880609 hi0160 phosphatidylserine decarboxylase proenzyme (db:genpept-bct1) (de:haemophilus influenzae rd section 16 of 163 of the complete genome.) (nt:similar to sp:p10740 gb:j03916 pid:537004) (le:9903) (re:10775) (di:direct) U32701 U32701 g1573117 Haemophilus influenzae Rd 71421 -11536935 5000694332 (de:(hi0160) (pn:phosphatidylserine decarboxylase proenzyme:psd) (gn:psd) (gtcfc:5.3:8.1) (ec:4.1.1.65) (dpsd_haein) (keggfc:5.3:8.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae)) HI0160 HI0160 Haemophilus influenzae 727 10011832

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877552	14086	36242	510	169

Description

6500733078 pgpb:hi0211 phosphatidylglycerophosphate phosphatase
b:phosphatidylglycerophosphatase b (gtcfc:3.1:3.2:8.1) (ec:3.1.3.27)
(keggfc:8.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0211 HI0211
Haemophilus influenzae 727 -11536936 89357 pgpb:hi0211 (ec:3.1.3.27)
(de:phosphatidylglycerophosphatase b,) (db:swissprot) PGPB_HAEIN P44570
HAEMOPHILUS INFLUENZAE 727 -11536936 167088 phosphatidylglycerophosphatase
b homolog (db:pir2.dat) I64054 I64054 Haemophilus influenzae 727 -11536936
7500887982 hi0211 phosphatidylglycerophosphatase b pgpb (db:genpept-bct1)
(de:haemophilus influenzae rd section 21 of 163 of the complete genome.)
(nt:similar to gb:m23628 sp:p18201 pid:450384 gb:u00096) (le:644) (re:1369)
(di:complement) U32706 U32706 g1573171 Haemophilus influenzae Rd 71421
-11536936 5000694394 (de:(hi0211) (pn:phosphatidylglycerophosphatase
b:phosphatidylglycerophosphate phosphatase b:pgpb) (gn:pgpb) (gtcfc:8.1)
(ec:3.1.3.27) (pgpb_haein) (keggfc:8.1) (tigrfc:7.1) (db:gtc-haemophilus
influenzae)) HI0211 HI0211 Haemophilus influenzae 727 10031480

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877570	14087	36243	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877571	14088	36244	414	137

Description

6500733079 dgka:hi0335 diacylglycerol kinase:dagk:diglyceride kinase:dgk
(gtcfc:3.1:3.2:8.1) (ec:2.7.1.107) (keggfc:8.1) (tigrfc:7.1)
(db:gtc-haemophilus influenzae) HI0335 HI0335 Haemophilus influenzae 727
-11536937 80583 dgka:hi0335 (ec:2.7.1.107) (de:(dgk)) (db:swissprot)
KDGL_HAEIN P44424 HAEMOPHILUS INFLUENZAE 727 -11536937 166091
diacylglycerol kinase homolog hi0335 (db:pir2.dat) E64062 E64062 Haemophilus
influenzae 727 -11536937 7500884547 hi0335 diacylglycerol kinase dgka
(db:genpept-bct1) (de:haemophilus influenzae rd section 33 of 163 of the
complete genome.) (nt:similar to gb:u00006 sp:p00556 gb:k00127 pid:396377)
(le:6192) (re:6548) (di:direct) U32718 U32718 g1573304 Haemophilus
influenzae Rd 71421 -11536937 5000694395 (de:(hi0335) (pn:dagk:diglyceride
kinase:dgk:diacylglycerol kinase:dgka) (gn:dgka) (gtcfc:8.1) (ec:2.7.1.107)
(kdgl_haein) (keggfc:8.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae))
HI0335 HI0335 Haemophilus influenzae 727 10022825

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877574	14089	36245	855	284

Description

GTC ORF with score 678 to: (fn:major diagnostic antigen and laminin receptor) (db:genpept-pln2) (de:paracoccidioides brasiliensis 43 kda secreted glycoproteinprecursor (gp43) gene, complete cds.) (nt:major diagnostic antigen of paracoccidioidomycosis,...)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877580	14090	36246	531	176

Description

GTC ORF with score 435 to: (fn:major diagnostic antigen and laminin receptor) (db:genpept-pln2) (de:paracoccidioides brasiliensis 43 kda secreted glycoproteinprecursor (gp43) gene, complete cds.) (nt:major diagnostic antigen of paracoccidioidomycosis,...)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877586	14091	36247	1143	380

Description

6500733080 pssa:hi0425 cdp-diacylglycerol--serine
o-phosphatidyltransferase:phosphatidylserine synthase
(gtcfc:3.1:3.2:5.3:8.1) (ec:2.7.8.8) (keggfc:5.3:8.1) (tigrfc:7.1)
(db:gtc-haemophilus influenzae) HI0425 HI0425 Haemophilus influenzae 727
-11536938 92033 pssa:hi0425 (ec:2.7.8.8) (de:(phosphatidylserine synthase))
(db:swissprot) PSS_HAEIN P44704 HAEMOPHILUS INFLUENZAE 727 -11536938 167090
cdpdiacylglycerol--serine o-phosphatidyltransferase homolog (cl:escherichia
coli cdpdiacylglycerol--serine o-phosphatidyltransferase) (db:pir2.dat)
I64066 I64066 Haemophilus influenzae 727 -11536938 7500888872 hi0425
phosphatidylserine synthase pssa (db:genpept-bct1) (de:haemophilus
influenzae rd section 41 of 163 of the complete genome.) (nt:similar to
gb:m58699 sp:p23830 pid:147389 gb:u00096) (le:104) (re:1471) (di:direct)
U32726 U32726 g1573400 Haemophilus influenzae Rd 71421 -11536938 5000694333
(de:(hi0425) (pn:cdp-diacylglycerol--serine
o-phosphatidyltransferase:phosphatidylserine synthase:pssa) (gn:pssa)
(gtcfc:5.3:8.1) (ec:2.7.8.8) (pss_haein) (keggfc:5.3:8.1) (tigrfc:7.1)
(db:gtc-haemophilus influenzae)) HI0425 HI0425 Haemophilus influenzae 727
10034067

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877590	14092	36248	309	102

Description

6500733081 fadr:hi0426 fatty acid metabolism protein:fatty acid metabolism regulator protein (gtcfc:3.1:3.2) (keggfc:14.2) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0426 HI0426 Haemophilus influenzae 727 -11536939 71045 fadr:hi0426 (de:fatty acid metabolism regulator protein) (db:swissprot) FADR_HAEIN P44705 HAEMOPHILUS INFLUENZAE 727 -11536939 166127 regulatory protein fadr homolog (cl:regulatory protein fadr) (db:pir2.dat) A64067 A64067 Haemophilus influenzae 727 -11536939 7500881320 hi0426 fatty acid metabolism regulator protein fadr (db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the complete genome.) (nt:similar to gb:x08087 sp:p09371 pid:992991 gb:u00096) (le:1516) (re:2241) (di:complement) U32726 U32726 g1573401 Haemophilus influenzae Rd 71421 -11536939 5000694204 (de:(hi0426) (pn:fatty acid metabolism regulator protein:fatty acid metabolism protein:fadr) (gn:fadr) (gtcfc:3.8:8.2:8.3) (ec:) (fadr_haein) (keggfc:11.2) (tigrfc:7.1) (db:gtc-haemophilus influenzae)) HI0426 HI0426 Haemophilus influenzae 727 10013620

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877598	14093	36249	1488	495

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877612	14094	36250	231	76

Description

5000694399 glpq:hpdi:hi0689 hpd:glycerophosphoryl diester phosphodiesterase precursor:glycerophosphodiester phosphodiesterase:surface-exposed lipoprotein d:protein d:immunoglobulin d-binding protein:igd-binding protein (gtcfc:3.1:3.2:8.1:8.4) (ec:3.1.4.46) (keggfc:8.1:8.4) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0689 HI0689 Haemophilus influenzae 727 -11536940 74047 glpq:hpdi:hi0689 (ec:3.1.4.46) (de:protein)) (db:swissprot) GLPQ_HAEIN Q06282 HAEMOPHILUS INFLUENZAE 727 -11536940 167182 glycerophosphodiester phosphodiesterase::igd-binding protein:protein d (ec:3.1.4.46) (db:pir2.dat) G64086 G64086 Haemophilus influenzae 727 -11536940 7500882516 hi0689 glycerophosphoryl diester phosphodiesterase (db:genpept-bct1) (de:haemophilus influenzae rd section 66 of 163 of the complete genome.) (nt:similar to gb:l42023 sp:q06282 pid:1005591) (le:9396) (re:10490) (di:direct) U32751 U32751 g1573690 Haemophilus influenzae Rd 71421 -11536940 6500733082 glpq:hpdi hpd:glycerophosphoryl diester phosphodiesterase precursor:glycerophosphodiester phosphodiesterase:surface-exposed lipoprotein d:protein d:immunoglobulin d-binding protein:igd-binding protein (gtcfc:3.1:3.2:8.1:8.4) (ec:3.1.4.46) (keggfc:8.1:8.4) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0689 HI0689 Haemophilus influenzae 727 -11536940

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877619	14095	36251	456	151

Description

6500733083 plsc:hi0734 1-acyl-glycerol-3-phosphate acyltransferase:1-acyl-sn-glycerol-3-phosphate acyltransferase (gtcfc:3.1:3.2:8.1) (ec:2.3.1.51) (keggfc:8.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0734 HI0734 Haemophilus influenzae 727 -11536941 90017 plsc:hi0734 (ec:2.3.1.51) (de:(lpaat)) (db:swissprot) PLSC_HAEIN P44848 HAEMOPHILUS INFLUENZAE 727 -11536941 165955 1-acylglycerol-3-phosphate o-acyltransferase (ec:2.3.1.51) (db:pir2.dat) D64089 D64089 Haemophilus influenzae 727 -11536941 7500888171 hi0734 1-acyl-glycerol-3-phosphate acyltransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 71 of 163 of the complete genome.) (nt:similar to gb:m63491 sp:p26647 pid:147298) (le:10333) (re:11055) (di:complement) U32756 U32756 g1573737 Haemophilus influenzae Rd 71421 -11536941 5000694401 (de:(hi0734) (pn:1-acyl-sn-glycerol-3-phosphate acyltransferase:1-acyl-glycerol-3-phosphate acyltransferase:plsc) (gn:plsc) (gtcfc:8.1) (ec:2.3.1.51) (plsc_haein) (keggfc:8.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae)) HI0734 HI0734 Haemophilus influenzae 727 10032137

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877622	14096	36252	1665	554

Description

6500733084 plsb:hi0748 glycerol-3-phosphate acyltransferase (gtcfc:3.1:3.2:8.1) (ec:2.3.1.15) (keggfc:8.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0748 HI0748 Haemophilus influenzae 727 -11536942 90014 plsb:hi0748 (ec:2.3.1.15) (de:glycerol-3-phosphate acyltransferase, (gpat)) (db:swissprot) PLSB_HAEIN P44857 HAEMOPHILUS INFLUENZAE 727 -11536942 137909 glycerol-3-phosphate o-acyltransferase (cl:glycerol-3-phosphate acyltransferase) (ec:2.3.1.15) (db:pir2.dat) D64090 D64090 Haemophilus influenzae 727 -11536942 7500888169 hi0748 glycerol-3-phosphate acyltransferase plsb (db:genpept-bct1) (de:haemophilus influenzae rd section 73 of 163 of the complete genome.) (nt:similar to sp:p00482 gb:k00127 pid:147295) (le:7589) (re:10021) (di:complement) U32758 U32758 g1573755 Haemophilus influenzae Rd 71421 -11536942 5000694402 (de:(hi0748) (pn:glycerol-3-phosphate acyltransferase:plsb) (gn:plsb) (gtcfc:8.1) (ec:2.3.1.15) (plsb_haein) (keggfc:8.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae)) HI0748 HI0748 Haemophilus influenzae 727 10032134

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877623	14097	36253	246	81

Description

6500733085 cdsa:hi0919 phosphatidate cytidyltransferase:cdp-diglyceride synthetase:cdp-diglyceride pyrophosphorylase:cdp-diacylglycerol synthase (gtcfc:3.1:3.2:8.1) (ec:2.7.7.41) (keggfc:8.1) (tigrfc:7.1) (db:gtc-haemophilus influenzae) HI0919 HI0919 Haemophilus influenzae 727 -11536943 63721 cdsa:cds:hi0919 (ec:2.7.7.41) (de:synthase)) (db:swissprot) CDSA_HAEIN P44937 HAEMOPHILUS INFLUENZAE 727 -11536943 166041 phosphatidate cytidyltransferase homolog (db:pir2.dat) G64102 G64102 Haemophilus influenzae 727 -11536943 7500878463 hi0919 cdp-diglyceride synthetase cdsa (db:genpept-bct1) (de:haemophilus influenzae rd section 88 of 163 of the complete genome.) (nt:similar to gb:m11330 sp:p06466 pid:1208947) (le:8396) (re:9262) (di:complement) U32773 U32773 g1573940 Haemophilus influenzae Rd 71421 -11536943 5000694403 (de:(hi0919) (pn:phosphatidate cytidyltransferase:cdp-diglyceride pyrophosphorylase:cdp-diacylglycerol synthase:cdp-diglyceride synthetase:cdsa) (gn:cdsa) (gtcfc:8.1) (ec:2.7.7.41) (cdsa_haein) (keggfc:8.1) (tigrfc:7.1) (db:gt) HI0919 HI0919 Haemophilus influenzae 727 10006390

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877636	14098	36254	819	273

Description

6500733086 usg:hi1433 hist operon protein:usg1:1 protein homolog
 (gtcfc:3.1:3.2) (keggfc:14.2) (tigrfc:7.1) (db:gtc-haemophilus influenzae)
 HI1433 HI1433 Haemophilus influenzae 727 -11536944 104005 usg:hi1433
 (de:usg-1 protein homolog) (db:swissprot) USG_HAEIN P45201 HAEMOPHILUS
 INFLUENZAE 727 -11536944 166201 usg1 protein homolog
 (cl:aspartate-semialdehyde dehydrogenase) (db:pir2.dat) B64123 B64123
 Haemophilus influenzae 727 -11536944 7500893868 hi1433 usg-1 protein usg1
 (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the
 completegenome.) (nt:similar to sp:p08390 gb:x02743 pid:147125 pid:41717)
 (le:4892) (re:5845) (di:complement) U32822 U32822 g1574271 Haemophilus
 influenzae Rd 71421 -11536944 5000694205 (de:(hi1433) (pn:-1 protein
 homolog:hist operon protein:usg1) (gn:usg) (gtcfc:3.8:8.2:8.3) (ec:)
 (usg_haein) (keggfc:11.2) (tigrfc:7.1) (db:gtc-haemophilus influenzae))
 HI1433 HI1433 Haemophilus influenzae 727 10045775

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877637	14099	36255	1158	385

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877673	14100	36256	735	244

Description

6500733087 fadd:hi0389b long-chain-fatty-acid--coa ligase:long-chain
 acyl-coa synthetase (gtcfc:3.2) (ec:6.2.1.3) (keggfc:3.2)
 (db:gtc-haemophilus influenzae) HI0389B HI0389B Haemophilus influenzae 727
 -11536945 81585 fadd:hi0389.1 (ec:6.2.1.3) (de:synthetase)) (db:swissprot)
 LCFA_HAEIN P46450 HAEMOPHILUS INFLUENZAE 727 -11536945 7500884825 hi0390.1
 long chain fatty acid coenzyme a ligase fadd (db:genpept-bct1)
 (de:haemophilus influenzae rd section 37 of 163 of the complete genome.)
 (nt:similar to sp:p29212 gb:l02649 gb:x70994 pid:581070) (le:9870)
 (re:11558) (di:direct) U32722 U32722 g1573360 Haemophilus influenzae Rd
 71421 -11536945 5000694196 (de:(hi03891) (pn:long-chain-fatty-acid--coa
 ligase:long-chain acyl-coa synthetase) (gn:fadd) (gtcfc:3.2) (ec:6.2.1.3)
 (lcfa_haein) (keggfc:3.2) (db:gtc-haemophilus influenzae)) HI03891 HI03891
 Haemophilus influenzae 727 10023821

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877674	14101	36257	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877675	14102	36258	906	301

Description

6500733088 ispa:hi1438 farnesyldiphosphate synthase:geranyltranstransferase:farnesyl-diphosphate synthase:fpp synthase (gtcfc:3.4:9.12:9.13) (ec:2.5.1.10) (keggfc:3.4:9.11) (tigrfc:2.5) (db:gtc-haemophilus influenzae) HI1438 HI1438 Haemophilus influenzae 727 -11536946 79993 ispa:hi1438 (ec:2.5.1.10) (de:(fpp synthase)) (db:swissprot) ISPA_HAEIN P45204 HAEMOPHILUS INFLUENZAE 727 -11536946 166126 ispa geranyltranstransferase (cl:dimethylallyltranstransferase) (ec:2.5.1.10) (db:pir2.dat) C64123 C64123 Haemophilus influenzae 727 -11536946 7500884297 hi1438 geranyltranstransferase ispa (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to gb:d00694 sp:p22939 pid:216584 gb:u00096) (le:9977) (re:10864) (di:direct) U32822 U32822 g1574277 Haemophilus influenzae Rd 71421 -11536946 5000694197 (de:(hi1438) (pn:geranyltranstransferase:farnesyl-diphosphate synthase:fpp synthase:farnesyldiphosphate synthase:ispa) (gn:ispa) (gtcfc:3.4:9.11) (ec:2.5.1.10) (ispa_haein) (keggfc:3.4:9.11) (tigrfc:2.5) (db:gtc-haemophilus infl) HI1438 HI1438 Haemophilus influenzae 727 10022243

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877679	14103	36259	420	139

Description

6500733089 hin1462:hi0333 hypothetical protein:gb:u13769_1:hypothetical rna methyltransferase hi0333 (gtcfc:3.7:5.11:5.14:9.12:14.1) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0333 HI0333 Haemophilus influenzae 727 -11536947 112279 hi0333 (ec:2.1.1.-) (de:hypothetical rna methyltransferase hi0333,) (db:swissprot) YGCA_HAEIN P44643 HAEMOPHILUS INFLUENZAE 727 -11536947 166367 hypothetical protein hi0333 (cl:hypothetical protein hi0333) (db:pir2.dat) C64148 C64148 Haemophilus influenzae 727 -11536947 7500924058 hi0333 rna methyltransferase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 33 of 163 of the complete genome.) (nt:similar to pid:882679 sp:p55135 gb:u00096) (le:2552) (re:3868) (di:direct) U32718 U32718 g1573302 Haemophilus influenzae Rd 71421 -11536947 5000694198 (de:(hi0333) (pn:hypothetical rna methyltransferase hi0333:hypothetical protein:gb:u13769_1) (gn:hin1462) (gtcfc:3.7:5.13:9.12) (ec:2.1.1.-) (ygca_haein) (keggfc:3.7:5.13:5.14:9.13) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0333 HI0333 Haemophilus influenzae 727 10054007

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877694	14104	36260	1686	561

Description

6500733090 ksga:hi0549 16s
rrna:adenosine-n6:n6--dimethyltransferase:dimethyladenosine
transferase:s-adenosylmethionine-6-n:n-adenosyl:rrna dimethyltransferase:16s
rrna dimethylase:high level kasugamycin resistance protein ksga:kasugamycin
dimethyltransferase (gtcfc:3.7:5.11:5.14:9.12:13.3) (ec:2.1.1.-)
(keggfc:3.7:5.11:5.14:9.13) (tigrfc:14.3) (db:gtc-haemophilus influenzae)
HI0549 HI0549 Haemophilus influenzae 727 -11536948 81178 ksga:hi0549
(ec:2.1.1.-) (de:dimethyltransferase) (db:swissprot) KSGA_HAEIN P44749
HAEMOPHILUS INFLUENZAE 727 -11536948 137794 rrna
adenine-n6:n6--dimethyltransferase (cl:rrna (adenine-n6-)-methyltransferase)
(ec:2.1.1.-) (db:pir2.dat) I64076 I64076 Haemophilus influenzae 727
-11536948 7500884748 hi0549 dimethyladenosine transferase ksga
(db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the
complete genome.) (nt:similar to gb:d10483 sp:p06992 gb:m11054 gb:m68521)
(le:9864) (re:10727) (di:direct) U32736 U32736 g1573534 Haemophilus
influenzae Rd 71421 -11536948 5000694199 (de:(hi0549) (pn:dimethyladenosine
transferase:s-adenosylmethionine-6-n", n"- adenosyl:rrna
dimethyltransferase:16s rrna dimethylase:high level kasugamycin resistance
protein ksga:kasugamycin dimethyltransferase:16s rrna:adenosine-n6,n6)
HI0549 HI0549 Haemophilus influenzae 727 10023414

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877701	14105	36261	960	320

Description

GTC ORF with score 142 to: (sr:thale cress) (db:genpept-pln2)
(de:arabidopsis thaliana bac t10m13 from chromosome iv short arm, mapsat
11.6 cm, complete sequence.) (nt:similar to c. elegans protein b0414.8,
genbank) (le:18527:19163:19428:19571) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877703	14106	36262	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877713	14107	36263	945	314

Description

GTC ORF with score 1278 to: (sr:schizosaccharomyces pombe (strain:972 h-) dna, clone_lib:mizukam) (db:genpept-pln2) (de:schizosaccharomyces pombe 42.8 kb genomic dna, clone c973.) (nt:similar to arabidopsis thaliana prl1 gene: genbank) (le:21296) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877727	14108	36264	1587	528

Description

GTC ORF with score 866 to: (sr:fission yeast) (db:genpept-pln2) (de:schizosaccharomyces pombe orcl-related protein (orpl) gene, complete cds.) (nt:related to s.cerevisiae orcl, cdc6 and to s.pombe) (le:478:1417) (re:1364:2653) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877735	14109	36265	708	235

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877736	14110	36266	219	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877750	14111	36267	909	303

Description

6500733091 hypothetical rna methyltransferase hi0958
 (gtcfc:3.7:5.11:5.14:9.12) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13)
 (db:gtc-haemophilus influenzae) HI0958 HI0958 Haemophilus influenzae 727
 -11536949 109331 hi0958 (ec:2.1.1.-) (de:hypothetical rna methyltransferase
 hi0958,) (db:swissprot) YBJF_HAEIN P44083 HAEMOPHILUS INFLUENZAE 727
 -11536949 166579 probable rna methyltransferase hi0958 (db:pir2.dat) B64017
 B64017 Haemophilus influenzae 727 -11536949 7500896858 hi0958 rna
 methyltransferase:putative (db:genpept-bct1) (de:haemophilus influenzae rd
 section 92 of 163 of the complete genome.) (nt:similar to gb:u00096
 sp:p75817 pid:1787083 percent) (le:213) (re:1391) (di:complement) U32777
 U32777 g1573984 Haemophilus influenzae Rd 71421 -11536949 5000694200
 (de:(hi0958) (pn:hypothetical rna methyltransferase hi0958)
 (gtcfc:3.7:5.13:9.12) (ec:2.1.1.-) (y958_haein) (keggfc:3.7:5.13:5.14:9.13)
 (db:gtc-haemophilus influenzae)) HI0958 HI0958 Haemophilus influenzae 727
 10051063

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877763	14112	36268	432	143

Description

6500733092 prma:hi0978 ribosomal protein l11 methyltransferase
 (gtcfc:3.7:5.11:5.14:9.12:10.4) (ec:2.1.1.-) (keggfc:3.7:5.11:5.14:9.13)
 (tigrfc:12.5) (db:gtc-haemophilus influenzae) HI0978 HI0978 Haemophilus
 influenzae 727 -11536950 91122 prma:hi0978 (ec:2.1.1.-) (de:ribosomal
 protein l11 methyltransferase,) (db:swissprot) PRMA_HAEIN P44402 HAEMOPHILUS
 INFLUENZAE 727 -11536950 167144 prma ribosomal protein l11
 methyltransferase (cl:ribosomal protein l11 methyltransferase:bioc homology)
 (ec:2.1.1.-) (db:pir2.dat) I64105 I64105 Haemophilus influenzae 727
 -11536950 7500888512 hi0978 ribosomal protein l11 methyltransferase prma
 (db:genpept-bct1) (de:haemophilus influenzae rd section 93 of 163 of the
 complete genome.) (nt:similar to pid:606199 gb:u00096 pid:2367208 percent)
 (le:8052) (re:8942) (di:direct) U32778 U32778 g1574006 Haemophilus
 influenzae Rd 71421 -11536950 5000694201 (de:(hi0978) (pn:ribosomal protein
 l11 methyltransferase:ribosomal protein l11 methyltransferase:prma)
 (gn:prma) (gtcfc:3.7:5.13:9.12) (ec:2.1.1.-) (prma_haein)
 (keggfc:3.7:5.13:5.14:9.13) (tigrfc:12.5) (db:gtc-haemophilus influ) HI0978
 HI0978 Haemophilus influenzae 727 10033222

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877787	14113	36269	2787	928

Description

6500733093 hold:hi0011 dna polymerase iii:psi subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0011 HI0011 Haemophilus influenzae 727 -11536951 77469 hold:hi0011 (ec:2.7.7.7) (de:dna polymerase iii, psi subunit,) (db:swissprot) HOLD_HAEIN P43750 HAEMOPHILUS INFLUENZAE 727 -11536951 166106 dna-directed dna polymerase iii psi chain homolog (db:pir2.dat) E64042 E64042 Haemophilus influenzae 727 -11536951 7500883464 hi0011 dna polymerase iii:psi subunit hold (db:genpept-bct1) (de:haemophilus influenzae rd section 1 of 163 of the complete genome.) (nt:similar to sp:p28632 gb:l04575 gb:l05387 pid:146390) (le:11857) (re:12261) (di:complement) U32686 U32686 g1572954 Haemophilus influenzae Rd 71421 -11536951 5000694206 (de:(hi0011) (pn:dna polymerase iii, psi subunit:hold) (gn:hold) (gtcfc:4.1:4.2) (ec:2.7.7.7) (hold_haein) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0011 HI0011 Haemophilus influenzae 727 10019829

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877788	14114	36270	459	152

Description

6500733094 nrdd:hi0075 anaerobic ribonucleoside-triphosphate reductase (gtcfc:4.1:4.2) (ec:1.17.4.2) (keggfc:4.1:4.2) (tigrfc:8.1) (db:gtc-haemophilus influenzae) (tigrfc:2'-deoxyribonucleotide metabolism) HI0075 HI0075 Haemophilus influenzae 727 -11536952 86495 nrdd:hi0075 (ec:1.17.4.2) (de:anaerobic ribonucleoside-triphosphate reductase,) (db:swissprot) NRDD_HAEIN P43752 HAEMOPHILUS INFLUENZAE 727 -11536952 123180 ribonucleoside-triphosphate reductase:oxygen-sensitive (cl:escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase:oxygen-sensitive ribonucleoside-triphosphate reductase carboxyl-terminal homology:oxygen-sensitive ribonucleoside-triphosphate reductase middle homology:rubredoxin homology) (e... A64047 A64047 Haemophilus influenzae 727 -11536952 7500886575 hi0075 anaerobic ribonucleoside-triphosphate reductase (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:similar to sp:p28903 gb:l06097 gb:u06195 gb:z46865) (le:1837) (re:3960) (di:direct) U32693 U32693 g1573024 Haemophilus influenzae Rd 71421 -11536952 5000694207 (de:(hi0075) (pn:anaerobic ribonucleoside-triphosphate reductase:nrdd) (gn:nrdd) (gtcfc:4.1:4.2) (ec:1.17.4.2) (nrdd_haein) (keggfc:4.1:4.2) (tigrfc:8.1) (db:gtc-haemophilus influenzae)) HI0075 HI0075 Haemophilus influenzae 727 10028660

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877796	14115	36271	237	78

Description

6500733095 dnaq:hi0137 dna polymerase iii epsilon subunit:dna polymerase iii:epsilon chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0137 HI0137 Haemophilus influenzae 727 -11536953 69075 dnaq:hi0137 (ec:2.7.7.7) (de:dna polymerase iii, epsilon chain,) (db:swissprot) DP3E_HAEIN P43745 HAEMOPHILUS INFLUENZAE 727 -11536953 154424 dnaq dna-directed dna polymerase:iii epsilon chain (cl:dnaq protein) (ec:2.7.7.7) (db:pir2.dat) B64050 B64050 Haemophilus influenzae 727 -11536953 7500880555 hi0137 dna polymerase iii:epsilon subunit dnaq (db:genpept-bct1) (de:haemophilus influenzae rd section 14 of 163 of the complete genome.) (nt:similar to gb:k00985 sp:p03007 gb:x04027) (le:7398) (re:8168) (di:complement) U32699 U32699 g1573090 Haemophilus influenzae Rd 71421 -11536953 5000694208 (de:(hi0137) (pn:dna polymerase iii, epsilon chain:dna polymerase iii epsilon subunit:dnaq) (gn:dnaq) (gtcfc:4.1:4.2) (ec:2.7.7.7) (dp3e_haein) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0137 HI0137 Haemophilus influenzae 727 10011658

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877805	14116	36272	519	172

Description

6500733096 5-nucleotidase:usha:probable 5-nucleotidase precursor (gtcfc:4.1:4.2:4.3:9.4) (ec:3.1.3.5) (keggfc:4.1:4.2:9.4) (tigrfc:8.6) (db:gtc-haemophilus influenzae) HI0206 HI0206 Haemophilus influenzae 727 -11536954 57605 hi0206 (ec:3.1.3.5) (de:probable 5'-nucleotidase precursor,) (db:swissprot) 5NTD_HAEIN P44569 HAEMOPHILUS INFLUENZAE 727 -11536954 165973 probable 5-nucleotidase:precursor:5-ribonucleotide phosphohydrolase (cl:5'-nucleotidase:5'-nucleotidase homology:phosphoesterase core homology) (ec:3.1.3.5) (db:pir1.dat) E64054 E64054 Haemophilus influenzae 727 -11536954 7500876131 hi0206 5-nucleotidase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 20 of 163 of the complete genome.) (nt:similar to sp:p29240 pid:62772 percent identity:) (le:7002) (re:8813) (di:direct) U32705 U32705 g1573165 Haemophilus influenzae Rd 71421 -11536954 5000694209 (de:(hi0206) (pn:probable 5"-nucleotidase precursor:5"-nucleotidase:usha) (gtcfc:4.1:4.2:9.4) (ec:3.1.3.5) (5ntd_haein) (keggfc:4.1:4.2:9.4) (tigrfc:8.6) (db:gtc-haemophilus influenzae)) HI0206 HI0206 Haemophilus influenzae 727 10000388

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877806	14117	36273	204	67

Description

6500733097 guab:hi0221 inosine-5-monophosphate dehydrogenase:imp
dehydrogenase:impdh:impd (gtcfc:4.1) (ec:1.1.1.205) (keggfc:4.1)
(tigrfc:8.3) (db:gtc-haemophilus influenzae) HI0221 HI0221 Haemophilus
influenzae 727 -11536955 79299 guab:hi0221 (ec:1.1.1.205)
(de:dehydrogenase) (impdh) (impd)) (db:swissprot) IMDH_HAEIN P44334
HAEMOPHILUS INFLUENZAE 727 -11536955 122585 guab imp
dehydrogenase::inosine-5-monophosphate dehydrogenase (cl:imp
dehydrogenase:cbs homology) (ec:1.1.1.205) (db:pir1.dat) H64055 H64055
Haemophilus influenzae 727 -11536955 7500884113 hi0221
inosine-5-monophosphate dehydrogenase guab (db:genpept-bct1) (de:haemophilus
influenzae rd section 23 of 163 of the complete genome.) (nt:similar to
sp:p06981 gb:x02209 pid:146275 pid:41627) (le:3308) (re:4774) (di:direct)
U32708 U32708 g1573185 Haemophilus influenzae Rd 71421 -11536955 5000694210
(de:(hi0221) (pn:imp dehydrogenase:impdh:impd:inosine-5"-monophosphate
dehydrogenase:guab) (gn:guab) (gtcfc:4.1) (ec:1.1.1.205) (imd_haein)
(keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae)) HI0221 HI0221
Haemophilus influenzae 727 10021627

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877813	14118	36274	306	101

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877825	14119	36275	1824	607

Description

6500733098 guaa:hi0222 gmp synthase:glutamine-hydrolyzing:glutamine
amidotransferase:gmp synthetase (gtcfc:4.1:5.1) (ec:6.3.5.2)
(keggfc:4.1:5.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae) HI0222 HI0222
Haemophilus influenzae 727 -11536956 74990 guaa:hi0222 (ec:6.3.5.2)
(de:amidotransferase) (gmp synthetase)) (db:swissprot) GUAA_HAEIN P44335
HAEMOPHILUS INFLUENZAE 727 -11536956 142424 gmp synthase
glutamine-hydrolyzing (cl:gmp synthase (glutamine-hydrolyzing):trpg
homology) (ec:6.3.5.2) (db:pir2.dat) I64055 I64055 Haemophilus influenzae
727 -11536956 7500882840 hi0222 gmp synthase guaa (db:genpept-bct1)
(de:haemophilus influenzae rd section 23 of 163 of the complete genome.)
(nt:similar to gb:m10101 sp:p04079 pid:146276 gb:u00096) (le:5485) (re:7056)
(di:direct) U32708 U32708 g1573186 Haemophilus influenzae Rd 71421 -11536956
5000694211 (de:(hi0222) (pn:gmp synthase:glutamine-hydrolyzing:glutamine
amidotransferase:gmp synthetase:guaa) (gn:guaa) (gtcfc:4.1:5.1) (ec:6.3.5.2)
(guaa_haein) (keggfc:4.1:5.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae))
HI0222 HI0222 Haemophilus influenzae 727 10017502

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877865	14120	36276	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877867	14121	36277	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877870	14122	36278	603	200

Description

6500733099 pnp:hi0229 polyribonucleotide
nucleotidyltransferase:polynucleotide phosphorylase:pnpase
(gtcfc:4.1:4.2:10.2) (ec:2.7.7.8) (keggfc:4.1:4.2) (tigrfc:11.2)
(db:gtc-haemophilus influenzae) HI0229 HI0229 Haemophilus influenzae 727
-11536957 90177 pnp:hi0229 (ec:2.7.7.8) (de:phosphorylase) (pnpase))
(db:swissprot) PNP_HAEIN P44584 HAEMOPHILUS INFLUENZAE 727 -11536957 167095
polyribonucleotide nucleotidyltransferase:alpha chain (cl:polyribonucleotide
nucleotidyltransferase alpha chain) (ec:2.7.7.8) (db:pir2.dat) E64056 E64056
Haemophilus influenzae 727 -11536957 7500888233 hi0229 polynucleotide
phosphorylase pnp (db:genpept-bct1) (de:haemophilus influenzae rd section 24
of 163 of the complete genome.) (nt:similar to gb:j02638 sp:p05055 gb:m14425
gb:x00761) (le:2758) (re:4887) (di:direct) U32709 U32709 g1573193
Haemophilus influenzae Rd 71421 -11536957 5000694212 (de:(hi0229)
(pn:polyribonucleotide nucleotidyltransferase:pnpase:polynucleotide
phosphorylase:pnp) (gn:pnp) (gtcfc:4.1:4.2) (ec:2.7.7.8) (pnp_haein)
(keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae)) HI0229
HI0229 Haemophilus influenzae 727 10032297

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877871	14123	36279	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877874	14124	36280	420	139

Description

6500733100 rela:hi0334 gtp pyrophosphokinase:atp:gtp
 3-pyrophosphotransferase:ppgpp synthetase i (gtcfc:4.1:12.13) (ec:2.7.6.5)
 (keggfc:4.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0334 HI0334
 Haemophilus influenzae 727 -11536958 93881 rela:hi0334 (ec:2.7.6.5)
 (de:(ppgpp synthetase i)) (db:swissprot) RELA HAEIN P44644 HAEMOPHILUS
 INFLUENZAE 727 -11536958 139826 gtp pyrophosphokinase (cl:guanosine
 3',5'-bis(diphosphate) 3'-pyrophosphatase) (ec:2.7.6.5) (db:pir2.dat) D64062
 D64062 Haemophilus influenzae 727 -11536958 7500889620 hi0334 gtp
 pyrophosphokinase rela (db:genpept-bct1) (de:haemophilus influenzae rd
 section 33 of 163 of the complete genome.) (nt:similar to gb:j04039
 sp:p11585 pid:147562) (le:3946) (re:6177) (di:direct) U32718 U32718 g1573303
 Haemophilus influenzae Rd 71421 -11536958 5000694213 (de:(hi0334) (pn:gtp
 pyrophosphokinase:ppgpp synthetase i:atp:gtp 3"-pyrophosphotransferase:rela)
 (gn:rela) (gtcfc:4.1) (ec:2.7.6.5) (rela_haein) (keggfc:4.1) (tigrfc:9.1)
 (db:gtc-haemophilus influenzae)) HI0334 HI0334 Haemophilus influenzae 727
 10035868

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877875	14125	36281	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877879	14126	36282	309	102

Description

GTC ORF with score 124 to: (sr:drosophila melanogaster cdna to mrna)
 (db:genpept-inv) (de:drosophila melanogaster ethanolamine kinase (easily
 shocked) mrna,complete cds.) (nt:mutant phenotype includes paralysis,
 excitability) (le:223) (re:1710) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877881	14127	36283	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877882	14128	36284	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877892	14129	36285	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877895	14130	36286	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877903	14131	36287	552	183

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877911	14132	36288	597	198

Description

6500733101 adk:hi0349 adenylate kinase:atp-amp transphosphorylase (gtcfc:4.1) (ec:2.7.4.3) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae) HI0349 HI0349 Haemophilus influenzae 727 -11536959 80329 adk:hi0349 (ec:2.7.4.3) (de:adenylate kinase, (atp-amp transphosphorylase)) (db:swissprot) KAD_HAEIN P24323 HAEMOPHILUS INFLUENZAE 727 -11536959 139028 adk adenylate kinase::atp-amp transphosphorylase (cl:adenylate kinase) (ec:2.7.4.3) (db:pir2.dat) I64062 I64062 Haemophilus influenzae 727 -11536959 7500884459 hi0349 adenylate kinase adk (db:genpept-bct1) (de:haemophilus influenzae rd section 34 of 163 of the complete genome.) (nt:similar to sp:p24323 gb:l42023 pid:1003588) (le:7754) (re:8398) (di:complement) U32719 U32719 g1573319 Haemophilus influenzae Rd 71421 -11536959 5000694214 (de:(hi0349) (pn:adenylate kinase:atp-amp transphosphorylase:adk) (gn:adk) (gtcfc:4.1) (ec:2.7.4.3) (kad_haein) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae)) HI0349 HI0349 Haemophilus influenzae 727 10022579

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877916	14133	36289	789	262

Description

6500733102 holb:hi0455 dna polymerase iii delta prime subunit:dna polymerase iii:delta subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0455 HI0455 Haemophilus influenzae 727 -11536960 77464 holb:hi0455 (ec:2.7.7.7) (de:dna polymerase iii, delta' subunit,) (db:swissprot) HOLB_HAEIN P43748 HAEMOPHILUS INFLUENZAE 727 -11536960 7500883461 hi0455 dna polymerase iii:delta subunit holb (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to gb:l01483 sp:p28631 gb:l04577 pid:145783) (le:3973) (re:4956) (di:complement) U32728 U32728 g1573429 Haemophilus influenzae Rd 71421 -11536960 5000694215 (de:(hi0455) (pn:dna polymerase iii, delta" subunit:dna polymerase iii delta prime subunit:holb) (gn:holb) (gtcfc:4.1:4.2) (ec:2.7.7.7) (holb_haein) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0455 HI0455 Haemophilus influenzae 727 10126686

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877918	14134	36290	525	174

Description

6500733103 rpoc:hi0514 dna-directed rna polymerase beta chain:transcriptase beta chain:rna polymerase beta subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0514 HI0514 Haemophilus influenzae 727 -11536961 96229 rpoc:hi0514 (ec:2.7.7.6) (de:beta' chain) (rna polymerase beta' subunit)) (db:swissprot) RPOC_HAEIN P43739 HAEMOPHILUS INFLUENZAE 727 -11536961 139094 dna-directed rna polymerase:beta chain (cl:escherichia coli dna-directed rna polymerase beta' chain) (ec:2.7.7.6) (db:pir1.dat) G64073 G64073 Haemophilus influenzae 727 -11536961 7500890628 hi0514 dna-directed rna polymerase:beta chain rpoc (db:genpept-bct1) (de:haemophilus influenzae rd section 48 of 163 of the complete genome.) (nt:similar to sp:p00577 gb:m38303 gb:m38288 gb:m38293) (le:2541) (re:6788) (di:complement) U32733 U32733 g1573495 Haemophilus influenzae Rd 71421 -11536961 5000694216 (de:(hi0514) (pn:transcriptase beta" chain:rna polymerase beta" subunit:dna-directed rna polymerase beta" chain:rpoc) (gn:rpoc) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpoc_haein) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-haemophilus influen) HI0514 HI0514 Haemophilus influenzae 727 10038172

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877934	14135	36291	513	170

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877945	14136	36292	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877956	14137	36293	1338	446

Description

6500733104 rpob:hi0515 dna-directed rna polymerase beta chain:transcriptase
beta chain:rna polymerase beta subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6)
(keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0515 HI0515
Haemophilus influenzae 727 -11536962 96194 rpob:hi0515 (ec:2.7.7.6)
(de:beta chain) (rna polymerase beta subunit)) (db:swissprot) RPOB_HAEIN
P43738 HAEMOPHILUS INFLUENZAE 727 -11536962 139074 dna-directed rna
polymerase:beta chain (cl:dna-directed rna polymerase beta chain)
(ec:2.7.7.6) (db:pir2.dat) H64073 H64073 Haemophilus influenzae 727
-11536962 7500890617 hi0515 dna-directed rna polymerase:beta chain rpob
(db:genpept-bct1) (de:haemophilus influenzae rd section 48 of 163 of the
complete genome.) (nt:similar to sp:p06173 gb:m38311 pid:154355 pid:47919)
(le:7030) (re:11061) (di:complement) U32733 U32733 g1573496 Haemophilus
influenzae Rd 71421 -11536962 5000694217 (de:(hi0515) (pn:transcriptase
beta chain:rna polymerase beta subunit:dna-directed rna polymerase beta
chain:rpob) (gn:rpob) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpob_haein)
(keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0515 HI0515
Haemophilus influenzae 727 10038137

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877962	14138	36294	1197	398

Description

6500733105 deod:hi0518 purine-nucleoside phosphorylase:purine nucleoside phosphorylase:inosine phosphorylase:pnp (gtcfc:4.1:4.2:4.4:9.4) (ec:2.4.2.1) (keggfc:4.1:4.2:9.4) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI0518 HI0518 Haemophilus influenzae 727 -11536963 68261 deod:hi0518 (ec:2.4.2.1) (de:(pnp)) (db:swissprot) DEOD_HAEIN P44417 HAEMOPHILUS INFLUENZAE 727 -11536963 167124 purine-nucleoside phosphorylase::inosine phosphorylase (cl:purine-nucleoside phosphorylase pnp) (ec:2.4.2.1) (db:pir2.dat) B64074 B64074 Haemophilus influenzae 727 -11536963 7500880173 hi0518 purine-nucleoside phosphorylase deod (db:genpept-bct1) (de:haemophilus influenzae rd section 49 of 163 of the complete genome.) (nt:similar to pid:1732037 percent ident: 88.19;) (le:1517) (re:2233) (di:complement) U32734 U32734 g1573501 Haemophilus influenzae Rd 71421 -11536963 5000694218 (de:(hi0518) (pn:purine nucleoside phosphorylase:inosine phosphorylase:pnp:purine-nucleoside phosphorylase:deod) (gn:deod) (gtcfc:4.1:4.2:9.4) (ec:2.4.2.1) (deod_haein) (keggfc:4.1:4.2:9.4) (tigrfc:8.5) (db:gtc-haemophilus influ) HI0518 HI0518 Haemophilus influenzae 727 10010854

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877967	14139	36295	567	188

Description

GTC ORF with score 554 to: (sr:schizosaccharomyces pombe (strain:pr745) cdna to mrna) (db:genpept-pln1) (de:schizosaccharomyces pombe mrna, partial cds, clone: sy 1028.) (nt:similar to saccharomyces cerevisiae acetyl-coa) (le:49) (re:1236) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877968	14140	36296	516	171

Description

6500733106 urea:hi0539 urease alpha subunit:amidohydrolase (gtcfc:5.16:4.1) (ec:3.5.1.5) (keggfc:4.1:5.16) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0539 HI0539 Haemophilus influenzae 727 -11536964 103811 urec:hi0539 (ec:3.5.1.5) (de:urease alpha subunit, (urea amidohydrolase)) (db:swissprot) URE1_HAEIN P44391 HAEMOPHILUS INFLUENZAE 727 -11536964 140875 urease:62k chain:urease alpha chain (cl:urease 62k chain:urease 62k chain homology) (ec:3.5.1.5) (db:pir2.dat) H64075 H64075 Haemophilus influenzae 727 -11536964 7500893840 hi0539 urease:alpha subunit urec (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to sp:q07397 pid:216362 percent ident:) (le:3136) (re:4854) (di:complement) U32736 U32736 g1573524 Haemophilus influenzae Rd 71421 -11536964 5000694219 (de:(hi0539) (pn:urea amidohydrolase:urease alpha subunit:urea amidohydrolase:urec) (gn:urec) (gtcfc:4.1:5.16) (ec:3.5.1.5) (ure1_haein) (keggfc:4.1:5.16) (tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI0539 HI0539 Haemophilus influenzae 727 10045581

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877974	14141	36297	1203	400

Description

6500733107 ureb:hi0540 urease beta subunit:amidohydrolase (gtcfc:5.16:4.1) (ec:3.5.1.5) (keggfc:4.1:5.16) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0540 HI0540 Haemophilus influenzae 727 -11536965 103832 ureb:hi0540 (ec:3.5.1.5) (de:urease beta subunit, (urea amidohydrolase)) (db:swissprot) URE2_HAEIN P44392 HAEMOPHILUS INFLUENZAE 727 -11536965 125017 ureb urease:12k chain:urease beta chain:urease chain b (cl:urease 12k chain:urease 12k chain homology) (ec:3.5.1.5) (db:pir1.dat) I64075 I64075 Haemophilus influenzae 727 -11536965 7500893843 hi0540 urease:beta subunit ureb (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to gb:l03307 sp:q03283 pid:148153 percent) (le:4866) (re:5171) (di:complement) U32736 U32736 g1573525 Haemophilus influenzae Rd 71421 -11536965 5000694220 (de:(hi0540) (pn:urease beta subunit:urea amidohydrolase:urease subunit b:ureb) (gn:ureb) (gtcfc:4.1:5.16) (ec:3.5.1.5) (ure2_haein) (keggfc:4.1:5.16) (tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI0540 HI0540 Haemophilus influenzae 727 10045602

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877982	14142	36298	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877988	14143	36299	420	139

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501877989	14144	36300	225	75

Description

6500733108 urec:hi0541 urease gamma subunit:amidohydrolase (gtcfc:5.16:4.1) (ec:3.5.1.5) (keggfc:4.1:5.16) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0541 HI0541 Haemophilus influenzae 727 -11536966 103851 urea:hi0541 (ec:3.5.1.5) (de:urease gamma subunit, (urea amidohydrolase)) (db:swissprot) URE3_HAEIN P44393 HAEMOPHILUS INFLUENZAE 727 -11536966 140868 urease:11k chain (cl:urease 11k chain:urease 11k chain homology) (ec:3.5.1.5) (db:pir2.dat) A64076 A64076 Haemophilus influenzae 727 -11536966 7500893847 hi0541 urease:gamma subunit urea (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to sp:q07399 pid:216360 percent ident:.) (le:5247) (re:5549) (di:complement) U32736 U32736 g1573526 Haemophilus influenzae Rd 71421 -11536966 5000694221 (de:(hi0541) (pn:urease gamma subunit: amidohydrolase:urease:urea) (gn:urea) (gtcfc:4.1:5.16) (ec:3.5.1.5) (ure3_haein) (keggfc:4.1:5.16) (tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI0541 HI0541 Haemophilus influenzae 727 10045621

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877991	14145	36301	714	237

Description

6500733109 apah:hi0551
adenosine-tetraphosphatase:bis:5-nucleosyl-tetraphosphatase:symmetrical:diadenosine tetraphosphatase (gtcfc:4.1:4.4) (ec:3.6.1.41) (keggfc:4.1) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI0551 HI0551 Haemophilus influenzae 727 -11536967 59782 apah:hi0551 (ec:3.6.1.41) (de:(diadenosine tetraphosphatase)) (db:swissprot) APAH_HAEIN P44751 HAEMOPHILUS INFLUENZAE 727 -11536967 165981 bis 5-nucleosyl -tetraphosphatase symmetrical::diadenosine tetraphosphatase symmetrical (cl:bis(5'-nucleosyl)-tetraphosphatase (symmetrical):phosphoesterase core homology) (ec:3.6.1.41) (db:pir1.dat) B64077 B64077 Haemophilus influenzae 727 -11536967 7500876980 hi0551 diadenosine-tetraphosphatase apah (db:genpept-bct1) (de:haemophilus influenzae rd section 52 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p05637 gb:x04711 pid:216474) (le:90) (re:917) (di:direct) U32737 U32737 g1573537 Haemophilus influenzae Rd 71421 -11536967 5000694222 (de:(hi0551) (pn:bis:5"-nucleosyl-tetraphosphatase:symmetrical:diadenosine tetraphosphatase:adenosine-tetraphosphatase:apah) (gn:apah) (gtcfc:4.1) (ec:3.6.1.41) (apah_haein) (keggfc:4.1) (tigrfc:8.5) (db:gtc-haemophilus influenz) HI0551 HI0551 Haemophilus influenzae 727 10002515

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877994	14146	36302	318	105

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501877996	14147	36303	480	159

Description

GTC ORF with score 124 to: (or:Boreogadus saida) (db:genpept-vrt) (de:boreogadus saida antifreeze glycopeptide afgp polyprotein precursorgene, complete cds.) (nt:cleavage of polyprotein at conserved spacers r or) (le:209:281) (re:211:1801) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878004	14148	36304	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878015	14149	36305	1035	344

Description

5000694223 cyaa:cya:hi0604 cyaa:adenylate cyclase:atp
pyrophosphate-lyase:adenylyl cyclase (gtcfc:4.1:12.13) (ec:4.6.1.1)
(keggfc:4.1) (tigrfc:9.1) (db:gtc-haemophilus influenzae) HI0604 HI0604
Haemophilus influenzae 727 -11536968 67074 cyaa:cya:hi0604 (ec:4.6.1.1)
(de:cyclase)) (db:swissprot) CYAA_HAEIN P40134 HAEMOPHILUS INFLUENZAE 727
-11536968 165982 cya adenylate cyclase (ec:4.6.1.1) (db:pir2.dat) A49922
A49922 Haemophilus influenzae 727 -11536968 7500879640 adenylate cyclase
(sr:haemophilus influenzae (strain rd) dna) (db:genpept-bct2)
(de:haemophilus influenzae adenylate cyclase gene, complete cds.) (le:315)
(re:2846) (di:direct) HEAADCYC L23824 g388299 Haemophilus influenzae 727
-11536968 241242 hi0604 adenylate cyclase cyaa (db:genpept-bct1)
(de:haemophilus influenzae rd section 57 of 163 of the complete genome.)
(nt:similar to gb:l23824 sp:p40134 pid:1573596 percent) (le:7787) (re:10318)
(di:direct) U32742 U32742 g1573596 Haemophilus influenzae Rd 71421 -11536968
6500733110 cyaa:cya cyaa:adenylate cyclase:atp pyrophosphate-lyase:adenylyl
cyclase (gtcfc:4.1:12.13) (ec:4.6.1.1) (keggfc:4.1) (tigrfc:9.1)
(db:gtc-haemophilus influenzae) HI0604 HI0604 Haemophilus influenzae 727
-11536968

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878044	14150	36306	291	97

Description

6500733111 purb:hi0639 adenylosuccinate lyase:adenylosuccinase:asl
(gtcfc:4.1:5.2) (ec:4.3.2.2) (keggfc:4.1:5.2) (tigrfc:8.3)
(db:gtc-haemophilus influenzae) HI0639 HI0639 Haemophilus influenzae 727
-11536969 92440 purb:hi0639 (ec:4.3.2.2) (de:adenylosuccinate lyase,
(adenylosuccinase) (asl)) (db:swissprot) PUR8_HAEIN P44797 HAEMOPHILUS
INFLUENZAE 727 -11536969 7500889067 hi0639 adenylosuccinate lyase purb
(db:genpept-bct1) (de:haemophilus influenzae rd section 62 of 163 of the
complete genome.) (nt:similar to gb:m74924 sp:p25739 pid:145203 pid:42585)
(le:735) (re:2105) (di:direct) U32747 U32747 g1573637 Haemophilus influenzae
Rd 71421 -11536969 5000694224 (de:(hi0639)
(pn:adenylosuccinase:asl:adenylosuccinate lyase:purb) (gn:purb)
(gtcfc:4.1:5.2) (ec:4.3.2.2) (pur8_haein) (keggfc:4.1:5.2) (tigrfc:8.3)
(db:gtc-haemophilus influenzae) HI0639 HI0639 Haemophilus influenzae 727
10034472

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878050	14151	36307	1719	572

Description

GTC ORF with score 1821 to: (sr:neurospora crassa strain=74-or23-1a) (db:genpept-pln1) (de:neurospora crassa vacuolar atpase 98 kda subunit (vph1) gene,complete cds.) (nt:method: conceptual translation supplied by author) (le:710:953:1091:3164:3450) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878053	14152	36308	207	68

Description

GTC ORF with score 157 to: (sr:neurospora crassa strain=74-or23-1a) (db:genpept-pln1) (de:neurospora crassa vacuolar atpase 98 kda subunit (vph1) gene,complete cds.) (nt:method: conceptual translation supplied by author) (le:710:953:1091:3164:3450) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878056	14153	36309	498	166

Description

GTC ORF with score 562 to: (sr:neurospora crassa strain=74-or23-1a) (db:genpept-pln1) (de:neurospora crassa vacuolar atpase 98 kda subunit (vph1) gene,complete cds.) (nt:method: conceptual translation supplied by author) (le:710:953:1091:3164:3450) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878078	14154	36310	3051	1016

Description

GTC ORF with score 187 to: (db:genpept-inv) (de:caenorhabditis elegans unc-89 (unc-89) gene, complete cds.) (nt:giant ig superfamily member located in the middle) (le:4920:5656:5974:7518) (re:4969:5929:6110:7688) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878079	14155	36311	702	233

Description

6500733112 ppx:hi0695 exopolyphosphatase:putative
exopolyphosphatase:metaphosphatase (gtcfc:4.1:13.10) (ec:3.6.1.11)
(keggfc:4.1) (tigrfc:5.3) (db:gtc-haemophilus influenzae) HI0695 HI0695
Haemophilus influenzae 727 -11536970 90829 ppx:hi0695 (ec:3.6.1.11)
(de:putative exopolyphosphatase, (metaphosphatase)) (db:swissprot) PPX_HAEIN
P44828 HAEMOPHILUS INFLUENZAE 727 -11536970 166122 exopolyphosphatase ppx
homolog (db:pir2.dat) C64087 C64087 Haemophilus influenzae 727 -11536970
7500888381 hi0695 exopolyphosphatase:putative (db:genpept-bct1)
(de:haemophilus influenzae rd section 67 of 163 of the complete genome.)
(nt:similar to gb:106129 sp:p29014 pid:147343 gb:u00096) (le:5109) (re:6080)
(di:complement) U32752 U32752 g1573698 Haemophilus influenzae Rd 71421
-11536970 5000694225 (de:(hi0695) (pn:putative
exopolyphosphatase:metaphosphatase:exopolyphosphatase:ppx) (gn:ppx)
(gtcfc:4.1) (ec:3.6.1.11) (ppx_haein) (keggfc:4.1) (tigrfc:5.3)
(db:gtc-haemophilus influenzae)) HI0695 HI0695 Haemophilus influenzae 727
10032941

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878080	14156	36312	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878090	14157	36313	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878092	14158	36314	1620	540

Description

6500733113 dnae:hi0739 dna polymerase iii:alpha chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0739 HI0739 Haemophilus influenzae 727 -11536971 69044 dnae:hi0739 (ec:2.7.7.7) (de:dna polymerase iii, alpha chain,) (db:swissprot) DP3A_HAEIN P43743 HAEMOPHILUS INFLUENZAE 727 -11536971 139248 dna-directed dna polymerase:iii alpha chain (cl:dna-directed dna polymerase iii alpha chain) (ec:2.7.7.7) (db:pir2.dat) H64089 H64089 Haemophilus influenzae 727 -11536971 7500880544 hi0739 dna polymerase iii:alpha subunit dnae (db:genpept-bct1) (de:haemophilus influenzae rd section 72 of 163 of the complete genome.) (nt:similar to gb:m19334 sp:p10443 gb:s52931) (le:7157) (re:10636) (di:complement) U32757 U32757 g1573746 Haemophilus influenzae Rd 71421 -11536971 5000694226 (de:(hi0739) (pn:dna polymerase iii, alpha chain:dnae) (gn:dnae) (gtcfc:4.1:4.2) (ec:2.7.7.7) (dp3a_haein) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0739 HI0739 Haemophilus influenzae 727 10011627

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878099	14159	36315	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878108	14160	36316	642	213

Description

6500733114 purl:hi0752 formylglycineamide ribonucleotide synthetase:phosphoribosylformylglycinamide synthase:fgam synthase:formylglycineamide ribotide amidotransferase:fgarat (gtcfc:4.1) (ec:6.3.5.3) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae) HI0752 HI0752 Haemophilus influenzae 727 -11536972 142430 phosphoribosylformylglycinamide synthase (cl:phosphoribosylformylglycinamide synthase) (ec:6.3.5.3) (db:pir2.dat) H64090 H64090 Haemophilus influenzae 727 -11536972 7500954514 hi0752 phosphoribosylformylglycinamide synthase (db:genpept-bct1) (de:haemophilus influenzae rd section 74 of 163 of the complete genome.) (nt:similar to gb:m19501 sp:p15254 pid:147423) (le:3047) (re:7009) (di:direct) U32759 U32759 g1573760 Haemophilus influenzae Rd 71421 -11536972 5000694227 (de:(hi0752) (pn:phosphoribosylformylglycinamide synthase:fgam synthase:formylglycineamide ribotide amidotransferase:fgarat:formylglycineamide ribonucleotide synthetase:purl) (gn:purl) (gtcfc:4.1) (ec:6.3.5.3) (purl_haein) (keg) HI0752 HI0752 Haemophilus influenzae 727 10072928

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878109	14161	36317	1059	352

Description

6500733115 rpoa:hi0802 dna-directed rna polymerase alpha chain:transcriptase alpha chain:rna polymerase alpha subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI0802 HI0802 Haemophilus influenzae 727 -11536973 96170 rpoa:hi0802 (ec:2.7.7.6) (de:alpha chain) (rna polymerase alpha subunit)) (db:swissprot) RPOA_HAEIN P43737 HAEMOPHILUS INFLUENZAE 727 -11536973 139063 dna-directed rna polymerase:alpha chain (cl:dna-directed rna polymerase alpha chain) (ec:2.7.7.6) (db:pir2.dat) B64095 B64095 Haemophilus influenzae 727 -11536973 7500890600 hi0802 dna-directed rna polymerase:alpha chain rpoa (db:genpept-bct1) (de:haemophilus influenzae rd section 77 of 163 of the complete genome.) (nt:similar to gb:j01685 sp:p00574 gb:v00353 gb:x00766) (le:8218) (re:9204) (di:direct) U32762 U32762 g1573813 Haemophilus influenzae Rd 71421 -11536973 5000694228 (de:(hi0802) (pn:transcriptase alpha chain:rna polymerase alpha subunit:dna-directed rna polymerase alpha chain:rpoa) (gn:rpoa) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpoa_haein) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-haemophilus influen) HI0802 HI0802 Haemophilus influenzae 727 10038113

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878115	14162	36318	771	256

Description

6500733116 pola:hi0856 dna polymerase i:pol i (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0856 HI0856 Haemophilus influenzae 727 -11536974 69101 pola:hi0856 (ec:2.7.7.7) (de:dna polymerase i, (pol i)) (db:swissprot) DPO1_HAEIN P43741 HAEMOPHILUS INFLUENZAE 727 -11536974 139239 dna-directed dna polymerase:i (cl:dna-directed dna polymerase i) (ec:2.7.7.7) (db:pir2.dat) E64098 E64098 Haemophilus influenzae 727 -11536974 7500880574 hi0856 dna polymerase i pola (db:genpept-bct1) (de:haemophilus influenzae rd section 82 of 163 of the complete genome.) (nt:similar to gb:j01663 sp:p00582 gb:j01664 gb:v00317) (le:3186) (re:5978) (di:complement) U32767 U32767 g1573871 Haemophilus influenzae Rd 71421 -11536974 5000694229 (de:(hi0856) (pn:pol i:dna polymerase i:pola) (gn:pola) (gtcfc:4.1:4.2) (ec:2.7.7.7) (dpol_haein) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0856 HI0856 Haemophilus influenzae 727 10011684

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878117	14163	36319	825	274

Description

6500733117 ndk:hi0876 nucleoside diphosphate kinase:ndp kinase
 (gtcfc:4.1:4.2) (ec:2.7.4.6) (keggfc:4.1:4.2) (tigrfc:8.3)
 (db:gtc-haemophilus influenzae) HI0876 HI0876 Haemophilus influenzae 727
 -11536975 85487 ndk:hi0876 (ec:2.7.4.6) (de:nucleoside diphosphate kinase,
 (ndk) (ndp kinase)) (db:swissprot) NDK_HAEIN P43802 HAEMOPHILUS INFLUENZAE
 727 -11536975 167045 nucleoside-diphosphate kinase
 (cl:nucleoside-diphosphate kinase) (ec:2.7.4.6) (db:pir2.dat) D64099 D64099
 Haemophilus influenzae 727 -11536975 7500886374 hi0876 nucleoside
 diphosphate kinase ndk (db:genpept-bct1) (de:haemophilus influenzae rd
 section 84 of 163 of the complete genome.) (nt:similar to sp:p24233
 gb:x57555 pid:416172 gb:u00096) (le:6773) (re:7198) (di:direct) U32769
 U32769 g1573893 Haemophilus influenzae Rd 71421 -11536975 5000694230
 (de:(hi0876) (pn:ndp kinase:nucleoside diphosphate kinase:ndk) (gn:ndk)
 (gtcfc:4.1:4.2) (ec:2.7.4.6) (ndk_haein) (keggfc:4.1:4.2) (tigrfc:8.3)
 (db:gtc-haemophilus influenzae)) HI0876 HI0876 Haemophilus influenzae 727
 10027664

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878121	14164	36320	219	72

Description

6500733118 purh:hi0887 phosphoribosylaminoimidazolecarboxamide
 formyltransferase:aicar transformylase / imp cyclohydrolase:inosinase:imp
 synthetase:atic (gtcfc:4.1:9.6) (keggfc:4.1:9.8) (tigrfc:8.3)
 (db:gtc-haemophilus influenzae) (gtcfc:nucleotide metabolism-purine
 metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and
 folate biosynthesis) HI0887 HI0887 Haemophilus influenzae 727 -11536976
 92448 purh:hi0887 (ec:2.1.2.3:3.5.4.10) (de:(inosinase) (imp synthetase)
 (atic)) (db:swissprot) PUR9_HAEIN P43852 HAEMOPHILUS INFLUENZAE 727
 -11536976 137835 purh bifunctional enzyme (cl:purh bifunctional enzyme)
 (db:pir2.dat) B64100 B64100 Haemophilus influenzae 727 -11536976 7500889080
 hi0887 phosphoribosylaminoimidazolecarboxamide (db:genpept-bct1)
 (de:haemophilus influenzae rd section 85 of 163 of the complete genome.)
 (nt:similar to sp:p15639 gb:j05126 gb:x51950 pid:147420) (le:7086) (re:8684)
 (di:direct) U32770 U32770 g1573904 Haemophilus influenzae Rd 71421 -11536976
 5000694231 (de:(hi0887) (pn:aicar transformylase
 :phosphoribosylaminoimidazolecarboxamide formyltransferase:purh) (gn:purh)
 (gtcfc:4.1:9.8) (ec:2.1.2.3) (pur9_haein) (keggfc:4.1:9.8) (tigrfc:8.3)
 (db:gtc-haemophilus influenzae)) HI0887 HI0887 Haemophilus influenzae 727
 10034480

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878126	14165	36321	573	191

Description

6500733119 purd:hi0888 phosphoribosylamine--glycine ligase:gars:glycinamide ribonucleotide synthetase:phosphoribosylglycinamide synthetase (gtcfc:4.1) (ec:6.3.4.13) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae) HI0888 HI0888 Haemophilus influenzae 727 -11536977 92392 purd:hi0888 (ec:6.3.4.13) (de:ribonucleotide synthetase) (phosphoribosylglycinamide synthetase)) (db:swissprot) PUR2_HAEIN P43845 HAEMOPHILUS INFLUENZAE 727 -11536977 126039 phosphoribosylamine--glycine ligase::phosphoribosylglycinamide synthetase (cl:phosphoribosylamine--glycine ligase:phosphoribosylamine--glycine ligase homology) (ec:6.3.4.13) (db:pir1.dat) C64100 C64100 Haemophilus influenzae 727 -11536977 7500889036 hi0888 phosphoribosylamine--glycine ligase purd (db:genpept-bct1) (de:haemophilus influenzae rd section 85 of 163 of the complete genome.) (nt:similar to sp:p15640 gb:j05126 gb:x51950 pid:147421) (le:8780) (re:10069) (di:direct) U32770 U32770 g1573905 Haemophilus influenzae Rd 71421 -11536977 5000694232 (de:(hi0888) (pn:gars:glycinamide ribonucleotide synthetase:phosphoribosylglycinamide synthetase:phosphoribosylamine--glycine ligase:purd) (gn:purd) (gtcfc:4.1) (ec:6.3.4.13) (pur2_haein) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemop) HI0888 HI0888 Haemophilus influenzae 727 10034424

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878143	14166	36322	498	165

Description

6500733120 hola:hi0923 dna polymerase iii delta subunit:dna polymerase iii:delta subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0923 HI0923 Haemophilus influenzae 727 -11536978 77462 hola:hi0923 (ec:2.7.7.7) (de:dna polymerase iii, delta subunit,) (db:swissprot) HOLA_HAEIN P43747 HAEMOPHILUS INFLUENZAE 727 -11536978 166104 dna-directed dna polymerase iii delta chain homolog (db:pir2.dat) A64103 A64103 Haemophilus influenzae 727 -11536978 7500883458 hi0923 dna polymerase iii:delta subunit hola (db:genpept-bct1) (de:haemophilus influenzae rd section 89 of 163 of the complete genome.) (nt:similar to gb:l04576 sp:p28630 gb:m94267 pid:145729) (le:3338) (re:4372) (di:direct) U32774 U32774 g1573945 Haemophilus influenzae Rd 71421 -11536978 5000694233 (de:(hi0923) (pn:dna polymerase iii, delta subunit:dna polymerase iii delta subunit:hola) (gn:hola) (gtcfc:4.1:4.2) (ec:2.7.7.7) (hola_haein) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0923 HI0923 Haemophilus influenzae 727 10019822

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878147	14167	36323	384	127

Description

6500733121 dnan:hi0992 dna polymerase iii beta-subunit:dna polymerase iii:beta chain (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI0992 HI0992 Haemophilus influenzae 727 -11536979 69057 dnan:hi0992 (ec:2.7.7.7) (de:dna polymerase iii, beta chain,) (db:swissprot) DP3B_HAEIN P43744 HAEMOPHILUS INFLUENZAE 727 -11536979 124040 dnan dna-directed dna polymerase:iii beta chain (cl:dna-directed dna polymerase iii beta chain) (ec:2.7.7.7) (db:pir1.dat) A64107 A64107 Haemophilus influenzae 727 -11536979 7500880549 hi0992 dna polymerase iii:beta subunit dnan (db:genpept-bct1) (de:haemophilus influenzae rd section 95 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p00583 gb:j01602 gb:k02179) (le:1232) (re:2332) (di:complement) U32780 U32780 g1574022 Haemophilus influenzae Rd 71421 -11536979 5000694234 (de:(hi0992) (pn:dna polymerase iii, beta chain:dna polymerase iii beta-subunit:dnan) (gn:dnan) (gtcfc:4.1:4.2) (ec:2.7.7.7) (dp3b_haein) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI0992 HI0992 Haemophilus influenzae 727 10011640

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878148	14168	36324	360	119

Description

6500733122 hpt:hi1153 hypoxanthine phosphoribosyltransferase:hprt (gtcfc:4.1:14.1) (ec:2.4.2.8) (keggfc:4.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI1153 HI1153 Haemophilus influenzae 727 -11536980 77558 hpt:hi1153 (ec:2.4.2.8) (de:hypoxanthine phosphoribosyltransferase, (hprt)) (db:swissprot) HPRT_HAEIN P45078 HAEMOPHILUS INFLUENZAE 727 -11536980 138135 hypoxanthine phosphoribosyltransferase::protein hi1153 (cl:hypoxanthine phosphoribosyltransferase) (ec:2.4.2.8) (db:pir2.dat) D64168 D64168 Haemophilus influenzae 727 -11536980 7500883504 hi1153 hypoxanthine phosphoribosyltransferase hpt (db:genpept-bct1) (de:haemophilus influenzae rd section 110 of 163 of the completegenome.) (nt:similar to gb:d26562 sp:p36766 pid:473792 gb:u00096) (le:1641) (re:2180) (di:direct) U32795 U32795 g1574710 Haemophilus influenzae Rd 71421 -11536980 5000694235 (de:(hi1153) (pn:hprt:hypoxanthine phosphoribosyltransferase:hpt) (gn:hpt) (gtcfc:4.1) (ec:2.4.2.8) (hprt_haein) (keggfc:4.1) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI1153 HI1153 Haemophilus influenzae 727 10019918

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878152	14169	36325	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878157	14170	36326	3018	1005

Description

6500733123 purf:hi1207 amidophosphoribosyltransferase:glutamine
phosphoribosylpyrophosphate amidotransferase:atase (gtcfc:4.1:5.1)
(ec:2.4.2.14) (keggfc:4.1:5.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae)
HI1207 HI1207 Haemophilus influenzae 727 -11536981 138150
amidophosphoribosyltransferase (cl:amidophosphoribosyltransferase)
(ec:2.4.2.14) (db:pir2.dat) I64189 I64189 Haemophilus influenzae 727
-11536981 7500954019 hi1207 amidophosphoribosyltransferase purf
(db:genpept-bct1) (de:haemophilus influenzae rd section 115 of 163 of the
completegenome.) (nt:similar to gb:x12423 sp:p00496 gb:m26893 gb:v00322)
(le:2516) (re:4033) (di:direct) U32800 U32800 g1574137 Haemophilus
influenzae Rd 71421 -11536981 5000694236 (de:(hi1207) (pn:glutamine
phosphoribosylpyrophosphate
amidotransferase:atase:amidophosphoribosyltransferase:purf) (gn:purf)
(gtcfc:4.1:5.1) (ec:2.4.2.14) (pur1_haein) (keggfc:4.1:5.1) (tigrfc:8.3)
(db:gtc-haemophilus influenzae) HI1207 HI1207 Haemophilus influenzae 727
10070449

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878161	14171	36327	516	171

Description

6500733124 dnax:hi1229 replication protein:dna polymerase iii subunits gamma
and tau (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2)
(db:gtc-haemophilus influenzae) HI1229 HI1229 Haemophilus influenzae 727
-11536982 69079 dnax:hi1229 (ec:2.7.7.7) (de:dna polymerase iii subunits
gamma and tau,) (db:swissprot) DP3X_HAEIN P43746 HAEMOPHILUS INFLUENZAE 727
-11536982 139249 dnax dna-directed dna polymerase:iii gamma/tau chain
(cl:dna-directed dna polymerase iii gamma chain) (ec:2.7.7.7) (db:pir2.dat)
F64111 F64111 Haemophilus influenzae 727 -11536982 7500880557 hi1229 dna
polymerase iii:subunits gamma and tau (db:genpept-bct1) (de:haemophilus
influenzae rd section 117 of 163 of the completegenome.) (nt:similar to
gb:m38777 sp:p06710 gb:x04275 gb:x04487) (le:5866) (re:7932) (di:complement)
U32802 U32802 g1574159 Haemophilus influenzae Rd 71421 -11536982 5000694237
(de:(hi1229) (pn:dna polymerase iii subunits gamma and tau:replication
protein:dnax) (gn:dnax) (gtcfc:4.1:4.2) (ec:2.7.7.7) (dp3x_haein)
(keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1229
HI1229 Haemophilus influenzae 727 10011662

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878174	14172	36328	375	124

Description

6500733125 apt:hi1230 adenine phosphoribosyltransferase:aprt (gtcfc:4.1:4.4) (ec:2.4.2.7) (keggfc:4.1) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI1230 HI1230 Haemophilus influenzae 727 -11536983 59900 apt:hi1230 (ec:2.4.2.7) (de:adenine phosphoribosyltransferase, (aprt)) (db:swissprot) APT_HAEIN P43856 HAEMOPHILUS INFLUENZAE 727 -11536983 138117 apt adenine phosphoribosyltransferase (cl:adenine phosphoribosyltransferase) (ec:2.4.2.7) (db:pir2.dat) G64111 G64111 Haemophilus influenzae 727 -11536983 7500877005 hi1230 adenine phosphoribosyltransferase aprt (db:genpept-bct1) (de:haemophilus influenzae rd section 117 of 163 of the completegenome.) (nt:similar to gb:m14040 sp:p07672 gb:x04487 pid:145294) (le:7944) (re:8486) (di:complement) U32802 U32802 g1574160 Haemophilus influenzae Rd 71421 -11536983 5000694238 (de:(hi1230) (pn:aprt:adenine phosphoribosyltransferase:aprt) (gn:apt) (gtcfc:4.1) (ec:2.4.2.7) (apt_haein) (keggfc:4.1) (tigrfc:8.5) (db:gtc-haemophilus influenzae)) HI1230 HI1230 Haemophilus influenzae 727 10002633

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878177	14173	36329	642	213

Description

6500733126 holc:hi1397 dna polymerase iii:chi subunit (gtcfc:4.1:4.2:10.8) (ec:2.7.7.7) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1397 HI1397 Haemophilus influenzae 727 -11536984 77467 holc:hi1397 (ec:2.7.7.7) (de:dna polymerase iii, chi subunit,) (db:swissprot) HOLC_HAEIN P43749 HAEMOPHILUS INFLUENZAE 727 -11536984 166105 holc dna-directed dna polymerase:chi chain:dna polymerase iii chi chain (ec:2.7.7.7) (db:pir2.dat) I64121 I64121 Haemophilus influenzae 727 -11536984 7500883462 hi1397 dna polymerase iii:chi subunit holc (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:similar to sp:p28905 sp:p11649 gb:l04574 gb:x15130) (le:784) (re:1218) (di:complement) U32820 U32820 g1574233 Haemophilus influenzae Rd 71421 -11536984 5000694239 (de:(hi1397) (pn:dna polymerase iii, chi subunit:holc) (gn:holc) (gtcfc:4.1:4.2) (ec:2.7.7.7) (holc_haein) (keggfc:4.1:4.2) (tigrfc:10.2) (db:gtc-haemophilus influenzae)) HI1397 HI1397 Haemophilus influenzae 727 10019827

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878179	14174	36330	207	68

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878182	14175	36331	486	161

Description

6500733127 purn:hi1428 phosphoribosylglycinamide formyltransferase:gart:gar
transformylase:5-phosphoribosylglycinamide transformylase (gtcfc:4.1:9.6)
(ec:2.1.2.2) (keggfc:4.1:9.8) (tigrfc:8.3) (db:gtc-haemophilus influenzae)
(gtcfc:nucleotide metabolism-purine metabolism:metabolism of cofactors and
vitamins-biotin metabolism (b8) and folate biosynthesis) HI1428 HI1428
Haemophilus influenzae 727 -11536985 92401 purn:hi1428 (ec:2.1.2.2)
(de:transformylase) (5'-phosphoribosylglycinamide transformylase))
(db:swissprot) PUR3_HAEIN P43846 HAEMOPHILUS INFLUENZAE 727 -11536985
137831 phosphoribosylglycinamide formyltransferase
(cl:phosphoribosylglycinamide formyltransferase:phosphoribosylglycinamide
formyltransferase homology) (ec:2.1.2.2) (db:pir2.dat) F64122 F64122
Haemophilus influenzae 727 -11536985 7500889051 hi1428
phosphoribosylglycinamide formyltransferase (db:genpept-bct1)
(de:haemophilus influenzae rd section 137 of 163 of the completegenome.)
(nt:similar to gb:m13747 sp:p08179 pid:147426 gb:u00096) (le:73) (re:711)
(di:complement) U32822 U32822 g1574266 Haemophilus influenzae Rd 71421
-11536985 5000694240 (de:(hi1428) (pn:gart:gar
transformylase:5"-phosphoribosylglycinamide
transformylase:phosphoribosylglycinamide formyltransferase:purn) (gn:purn)
(gtcfc:4.1:9.8) (ec:2.1.2.2) (pur3_haein) (keggfc:4.1:9.8) (tigrfc:8.3)
(db:gtc-hae) HI1428 HI1428 Haemophilus influenzae 727 10034433

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878187	14176	36332	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878188	14177	36333	303	101

Description

6500733128 purm:hi1429 5-phosphoribosyl-5-aminoimidazole synthetase:phosphoribosylformylglycinamide
cyclo-ligase:airs:phosphoribosyl-aminoimidazole synthetase:air synthase (gtcfc:4.1) (ec:6.3.3.1) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae) HI1429 HI1429 Haemophilus influenzae 727 -11536986 92409 purm:hi1429 (ec:6.3.3.1) (de:(phosphoribosyl-aminoimidazole synthetase) (air synthase)) (db:swissprot) PUR5_HAEIN P43848 HAEMOPHILUS INFLUENZAE 727 -11536986 142404 phosphoribosylformylglycinamide cyclo-ligase (cl:phosphoribosylformylglycinamide
cyclo-ligase:phosphoribosylformylglycinamide cyclo-ligase homology) (ec:6.3.3.1) (db:pir2.dat) G64122 G64122 Haemophilus influenzae 727 -11536986 7500889055 hi1429 phosphoribosylaminoimidazole synthetase purm (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to gb:m13747 sp:p08178 pid:147425 gb:u00096) (le:766) (re:1800) (di:complement) U32822 U32822 g1574267 Haemophilus influenzae Rd 71421 -11536986 5000694241 (de:(hi1429) (pn:phosphoribosylformylglycinamide
cyclo-ligase:airs:phosphoribosyl-aminoimidazole synthetase:air synthase:5"-phosphoribosyl-5-aminoimidazole synthetase:purm) (gn:purm) (gtcfc:4.1) (ec:6.3.3.1) (pur5_haein) (keggf) HI1429 HI1429 Haemophilus influenzae 727 10034441

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878218	14178	36334	330	109

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878221	14179	36335	213	70

Description

GTC ORF with score 161 to: (sr:information) (db:genpept-pri2) (de:human bac clone gs025m02 from 7q21-q22, complete sequence.) (nt:similar to adp/atp carrier proteins; 80% similarity) (le:<3621:18436:28320:28572) (re:3761:18574:28478:28662) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878222	14180	36336	567	188

Description

6500733129 pure:hi1615 phosphoribosylaminoimidazole carboxylase catalytic subunit:air carboxylase:airc (gtcfc:4.1) (ec:4.1.1.21) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae) HI1615 HI1615 Haemophilus influenzae 727 -11536987 92417 pure:hi1615 (ec:4.1.1.21) (de:(ec 4.1.1.21) (air carboxylase) (airc)) (db:swissprot) PUR6_HAEIN P43849 HAEMOPHILUS INFLUENZAE 727 -11536987 141464 phosphoribosylaminoimidazole carboxylase:catalytic chain (cl:phosphoribosylaminoimidazole carboxylase catalytic chain:phosphoribosylaminoimidazole carboxylase catalytic chain homology) (ec:4.1.1.21) (db:pir2.dat) G64132 G64132 Haemophilus influenzae 727 -11536987 7500889057 hi1615 phosphoribosylaminoimidazole carboxylase (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:similar to gb:z33502 percent ident: 95.03;) (le:2836) (re:3330) (di:direct) U32835 U32835 g1574461 Haemophilus influenzae Rd 71421 -11536987 5000694242 (de:(hi1615) (pn:air carboxylase:airc:phosphoribosylaminoimidazole carboxylase catalytic subunit:pure) (gn:pure) (gtcfc:4.1) (ec:4.1.1.21) (pur6_haein) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae)) HI1615 HI1615 Haemophilus influenzae 727 10034449

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878223	14181	36337	384	128

Description

6500733130 purk:hi1616 5-phosphoribosyl-5-amino-4-imidazole carboxylase ii:phosphoribosylaminoimidazole carboxylase atpase subunit:air carboxylase:airc (gtcfc:4.1) (ec:4.1.1.21) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae) HI1616 HI1616 Haemophilus influenzae 727 -11536988 92465 purk:hi1616 (ec:4.1.1.21) (de:(air carboxylase) (airc)) (db:swissprot) PURK_HAEIN P43850 HAEMOPHILUS INFLUENZAE 727 -11536988 141465 phosphoribosylaminoimidazole carboxylase:carbon dioxide-fixation chain (cl:phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain:phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain homology) (ec:4.1.1.21) (db:pir2.dat) H64132 H64132 Haemophilus influenzae 727 -11536988 7500889086 hi1616 phosphoribosylaminoimidazole carboxylase:atpase (db:genpept-bct1) (de:haemophilus influenzae rd section 150 of 163 of the completegenome.) (nt:similar to gb:m19657 sp:p09029 gb:x12982 pid:147413) (le:3400) (re:4488) (di:direct) U32835 U32835 g1574462 Haemophilus influenzae Rd 71421 -11536988 5000694243 (de:(hi1616) (pn:phosphoribosylaminoimidazole carboxylase atpase subunit:air carboxylase:airc:5"-phosphoribosyl-5-amino-4-imidazole carboxylase ii:purk) (gn:purk) (gtcfc:4.1) (ec:4.1.1.21) (purk_haein) (keggfc:4.1) (tigrfc:8.3)) HI1616 HI1616 Haemophilus influenzae 727 10034497

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878224	14182	36338	1371	456

Description

6500733131 pura:hi1633 adenylosuccinate synthetase:imp--aspartate ligase (gtcfc:4.1:5.2) (ec:6.3.4.4) (keggfc:4.1:5.2) (tigrfc:8.3) (db:gtc-haemophilus influenzae) HI1633 HI1633 Haemophilus influenzae 727 -11536989 142417 pura adenylosuccinate synthetase::imp--aspartate ligase (cl:adenylosuccinate synthase) (ec:6.3.4.4) (db:pir2.dat) G64133 G64133 Haemophilus influenzae 727 -11536989 7500954506 hi1633 adenylosuccinate synthetase pura (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the completegenome.) (nt:similar to gb:u14003 sp:p12283 gb:j04199 pid:147406) (le:4048) (re:5346) (di:direct) U32836 U32836 g1574479 Haemophilus influenzae Rd 71421 -11536989 5000694244 (de:(hi1633) (pn:imp--aspartate ligase:adenylosuccinate synthetase:pura) (gn:pura) (gtcfc:4.1:5.2) (ec:6.3.4.4) (pura_haein) (keggfc:4.1:5.2) (tigrfc:8.3) (db:gtc-haemophilus influenzae)) HI1633 HI1633 Haemophilus influenzae 727 10072918

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878234	14183	36339	960	319

Description

6500733132 nrda:hi1659 ribonucleoside-diphosphate reductase 1 alpha chain:ribonucleoside-diphosphate reductase alpha chain:ribonucleotide reductase (gtcfc:4.1:4.2) (ec:1.17.4.1) (keggfc:4.1:4.2) (tigrfc:8.1) (db:gtc-haemophilus influenzae) (tigrfc:2'-deoxyribonucleotide metabolism) HI1659 HI1659 Haemophilus influenzae 727 -11536990 137675 ribonucleoside-diphosphate reductase:alpha chain (cl:herpesvirus ribonucleoside-diphosphate reductase large chain) (ec:1.17.4.1) (db:pir2.dat) B64135 B64135 Haemophilus influenzae 727 -11536990 7500953947 hi1659 ribonucleoside-diphosphate reductase:alpha (db:genpept-bct1) (de:haemophilus influenzae rd section 154 of 163 of the completegenome.) (nt:similar to sp:p00452 gb:x06999 pid:42138 gb:u00096) (le:120) (re:2465) (di:direct) U32839 U32839 g1574509 Haemophilus influenzae Rd 71421 -11536990 5000694245 (de:(hi1659) (pn:ribonucleoside-diphosphate reductase alpha chain:ribonucleotide reductase:ribonucleoside-diphosphate reductase 1 alpha chain:nrda) (gn:nrda) (gtcfc:4.1:4.2) (ec:1.17.4.1) (rirl_haein) (keggfc:4.1:4.2) (tigrfc:8.) HI1659 HI1659 Haemophilus influenzae 727 10070207

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878236	14184	36340	834	277

Description

GTC ORF with score 127 to: (sr:caenorhabditis elegans strain=bristol n2)
(db:genpept-inv) (de:caenorhabditis elegans cosmid zc449.) (nt:coded for by
c. elegans cdna yk61e11.3; coded for) (le:30120:30310:30457)
(re:30261:30413:31468) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878253	14185	36341	762	253

Description

6500733133 nrdb:hi1660 ribonucleoside diphosphate reductase b2
subunit:ribonucleoside-diphosphate reductase beta chain:ribonucleotide
reductase (gtcfc:4.1:4.2) (ec:1.17.4.1) (keggfc:4.1:4.2) (tigrfc:8.1)
(db:gtc-haemophilus influenzae) (tigrfc:2'-deoxyribonucleotide metabolism)
HI1660 HI1660 Haemophilus influenzae 727 -11536991 137653
ribonucleoside-diphosphate reductase:beta chain (cl:herpesvirus
ribonucleoside-diphosphate reductase small chain) (ec:1.17.4.1)
(db:pir2.dat) C64135 C64135 Haemophilus influenzae 727 -11536991 7500953946
hi1660 ribonucleoside diphosphate reductase:beta chain (db:genpept-bct1)
(de:haemophilus influenzae rd section 154 of 163 of the completegenome.)
(nt:similar to gb:k02672 sp:p00453 pid:146967 gb:u00096) (le:2607) (re:3737)
(di:direct) U32839 U32839 g1574510 Haemophilus influenzae Rd 71421 -11536991
5000694246 (de:(hi1660) (pn:ribonucleoside-diphosphate reductase beta
chain:ribonucleotide reductase:ribonucleoside diphosphate reductase b2
subunit:nrdb) (gn:nrdb) (gtcfc:4.1:4.2) (ec:1.17.4.1) (rir2_haein)
(keggfc:4.1:4.2) (tigrfc:8.1) () HI1660 HI1660 Haemophilus influenzae 727
10070198

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878257	14186	36342	1428	475

Description

6500733134 purc:hi1726 putative
phosphoribosylaminoimidazole-succinocarboxamide synthase:saicar synthetase
(gtcfc:4.1) (ec:6.3.2.6) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus
influenzae) HI1726 HI1726 Haemophilus influenzae 727 -11536992 92432
purc:hi1726 (ec:6.3.2.6) (de:(ec 6.3.2.6) (saicar synthetase))
(db:swissprot) PUR7_HAEIN P43851 HAEMOPHILUS INFLUENZAE 727 -11536992
167153 phosphoribosylaminoimidazolesuccinocarboxamide synthase homolog
(db:pir2.dat) E64138 E64138 Haemophilus influenzae 727 -11536992 7500889064
hi1726 phosphoribosylaminoimidazole-succinocarboxamide (db:genpept-bct1)
(de:haemophilus influenzae rd section 160 of 163 of the completegenome.)
(nt:similar to pid:1144522 sp:q59566 pid:1550658) (le:5626) (re:6546)
(di:direct) U32845 U32845 g1574582 Haemophilus influenzae Rd 71421 -11536992
5000694247 (de:(hi1726) (pn:putative
phosphoribosylaminoimidazole-succinocarboxamide synthase:saicar
synthetase:purc) (gn:purc) (gtcfc:4.1) (ec:6.3.2.6) (pur7_haein)
(keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae)) HI1726 HI1726
Haemophilus influenzae 727 10034464

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878261	14187	36343	495	164

Description

6500733135 spot:hi1741 guanosine-3:5-bis:diphosphate
3-pyrophosphohydrolase:ppgppase:penta-phosphate
guanosine-3-pyrophosphohydrolase (gtcfc:4.1:12.13) (ec:3.1.7.2) (keggfc:4.1)
(tigrfc:9.1) (db:gtc-haemophilus influenzae) HI1741 HI1741 Haemophilus
influenzae 727 -11536993 99299 spot:hi1741 (ec:3.1.7.2) (de:(ppgppase)
(penta-phosphate guanosine-3'-pyrophosphohydrolase)) (db:swissprot)
SPOT_HAEIN P43811 HAEMOPHILUS INFLUENZAE 727 -11536993 139825 guanosine
3:5-bis diphosphate 3-pyrophosphatase (cl:guanosine 3',5'-bis(diphosphate)
3'-pyrophosphatase) (ec:3.1.7.2) (db:pir2.dat) F64139 F64139 Haemophilus
influenzae 727 -11536993 7500891989 hi1741 guanosine-3:5-bis diphosphate 3-
(db:genpept-bct1) (de:haemophilus influenzae rd section 162 of 163 of the
completegenome.) (nt:similar to gb:l10328 sp:p17580 gb:m24503 pid:290500)
(le:10309) (re:12342) (di:complement) U32847 U32847 g1574600 Haemophilus
influenzae Rd 71421 -11536993 5000694248 (de:(hi1741)
(pn:guanosine-3",5"-bis:diphosphate
3"-pyrophosphohydrolase:ppgppase:penta-phosphate
guanosine-3"-pyrophosphohydrolase:spot) (gn:spot) (gtcfc:4.1) (ec:3.1.7.2)
(spot_haein) (keggfc:4.1) (tigrfc:9.1) (db:gtc-haemophi) HI1741 HI1741
Haemophilus influenzae 727 10041158

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878262	14188	36344	441	146

Description

6500733136 rpoz:hi1742 dna-directed rna polymerase omega chain:transcriptase omega chain:rna polymerase omega subunit (gtcfc:4.1:4.2:10.2) (ec:2.7.7.6) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-haemophilus influenzae) HI1742 HI1742 Haemophilus influenzae 727 -11536994 96310 rpoz:hi1742 (ec:2.7.7.6) (de:omega chain) (rna polymerase omega subunit)) (db:swissprot) RPOZ_HAEIN P43740 HAEMOPHILUS INFLUENZAE 727 -11536994 139213 dna-directed rna polymerase:omega chain (cl:dna-directed rna polymerase omega chain) (ec:2.7.7.6) (db:pir2.dat) G64139 G64139 Haemophilus influenzae 727 -11536994 7500890675 hi1742 dna-directed rna polymerase:omega chain rpoz (db:genpept-bct1) (de:haemophilus influenzae rd section 163 of 163 of the completegenome.) (nt:similar to gb:l10328 sp:p08374 gb:m15266 gb:m24503) (le:161) (re:427) (di:complement) U32848 U32848 g1574602 Haemophilus influenzae Rd 71421 -11536994 5000694249 (de:(hi1742) (pn:dna-directed rna polymerase omega chain:transcriptase omega chain:rna polymerase omega subunit:rpoz) (gn:rpoz) (gtcfc:4.1:4.2) (ec:2.7.7.6) (rpoz_haein) (keggfc:4.1:4.2) (tigrfc:11.2) (db:gtc-haemophilus influen) HI1742 HI1742 Haemophilus influenzae 727 10038253

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878265	14189	36345	471	156

Description

6500733137 gmk:hi1743 5guanylate kinase:guanylate kinase:gmp kinase (gtcfc:4.1) (ec:2.7.4.8) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae) HI1743 HI1743 Haemophilus influenzae 727 -11536995 80656 gmk:hi1743 (ec:2.7.4.8) (de:guanylate kinase, (gmp kinase)) (db:swissprot) KGUA_HAEIN P44310 HAEMOPHILUS INFLUENZAE 727 -11536995 139033 guanylate kinase (cl:guanylate kinase:guanylate kinase homology) (ec:2.7.4.8) (db:pir2.dat) H64139 H64139 Haemophilus influenzae 727 -11536995 7500884603 hi1743 guanylate kinase gmk (db:genpept-bct1) (de:haemophilus influenzae rd section 163 of 163 of the completegenome.) (nt:similar to gb:l10328 sp:p24234 gb:m84400 pid:146230) (le:490) (re:1116) (di:complement) U32848 U32848 g1574603 Haemophilus influenzae Rd 71421 -11536995 5000694250 (de:(hi1743) (pn:guanylate kinase:gmp kinase:5"guanylate kinase:gmk) (gn:gmk) (gtcfc:4.1) (ec:2.7.4.8) (kgua_haein) (keggfc:4.1) (tigrfc:8.3) (db:gtc-haemophilus influenzae)) HI1743 HI1743 Haemophilus influenzae 727 10022897

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878273	14190	36346	210	69

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878274	14191	36347	624	207

Description

6500733138 udk:hi0132 uridine kinase:uridine monophosphokinase:pyrimidine ribonucleoside kinase (gtcfc:4.2:4.4) (ec:2.7.1.48) (keggfc:4.2) (tigrfc:8.2) (db:gtc-haemophilus influenzae) HI0132 HI0132 Haemophilus influenzae 727 -11536996 103930 udk:hi0132 (ec:2.7.1.48) (de:ribonucleoside kinase) (db:swissprot) URK_HAEIN P44533 HAEMOPHILUS INFLUENZAE 727 -11536996 167257 uridine kinase (cl:uridine kinase) (ec:2.7.1.48) (db:pir2.dat) I64049 I64049 Haemophilus influenzae 727 -11536996 7500893864 hi0132 uridine kinase udk (db:genpept-bct1) (de:haemophilus influenzae rd section 14 of 163 of the complete genome.) (nt:similar to sp:p31218 gb:x71492 pid:296947 gb:u00096) (le:1507) (re:2148) (di:direct) U32699 U32699 g1573086 Haemophilus influenzae Rd 71421 -11536996 5000694252 (de:(hi0132) (pn:pyrimidine ribonucleoside kinase:uridine kinase:uridine monophosphokinase:udk) (gn:udk) (gtcfc:4.2) (ec:2.7.1.48) (urk_haein) (keggfc:4.2) (tigrfc:8.2) (db:gtc-haemophilus influenzae)) HI0132 HI0132 Haemophilus influenzae 727 10045700

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878275	14192	36348	624	207

Description

6500733139 dcd:hi0133 deoxycytidine triphosphate deaminase:dctp deaminase (gtcfc:4.2) (ec:3.5.4.13) (keggfc:4.2) (tigrfc:8.1) (db:gtc-haemophilus influenzae) (tigrfc:2'-deoxyribonucleotide metabolism) HI0133 HI0133 Haemophilus influenzae 727 -11536997 67982 dcd:hi0133 (ec:3.5.4.13) (de:deaminase) (db:swissprot) DCD_HAEIN P44534 HAEMOPHILUS INFLUENZAE 727 -11536997 166086 dctp deaminase (cl:dctp deaminase) (ec:3.5.4.13) (db:pir2.dat) A64050 A64050 Haemophilus influenzae 727 -11536997 7500880051 hi0133 deoxycytidine triphosphate deaminase dcd (db:genpept-bct1) (de:haemophilus influenzae rd section 14 of 163 of the complete genome.) (nt:similar to gb:m90069 sp:p28248 pid:145716 gb:u00096) (le:2157) (re:2744) (di:direct) U32699 U32699 g1573087 Haemophilus influenzae Rd 71421 -11536997 5000694253 (de:(hi0133) (pn:dctp deaminase:deoxycytidine triphosphate deaminase:dcd) (gn:dcd) (gtcfc:4.2) (ec:3.5.4.13) (dcd_haein) (keggfc:4.2) (tigrfc:8.1) (db:gtc-haemophilus influenzae)) HI0133 HI0133 Haemophilus influenzae 727 10010575

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878290	14193	36349	363	120

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878292	14194	36350	267	88

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878310	14195	36351	1056	351

Description

6500733140 pyre:hi0272 orotate phosphoribosyltransferase:oprt (gtcfc:4.2) (ec:2.4.2.10) (keggfc:4.2) (tigrfc:8.4) (db:gtc-haemophilus influenzae) HI0272 HI0272 Haemophilus influenzae 727 -11536998 92626 pyre:hi0272 (ec:2.4.2.10) (de:orotate phosphoribosyltransferase, (oprt) (oprtase)) (db:swissprot) PYRE_HAEIN P43855 HAEMOPHILUS INFLUENZAE 727 -11536998 138141 orotate phosphoribosyltransferase (cl:orotate phosphoribosyltransferase:orotate phosphoribosyltransferase homology) (ec:2.4.2.10) (db:pir2.dat) I64058 I64058 Haemophilus influenzae 727 -11536998 7500889167 hi0272 orotate phosphoribosyltransferase pyre (db:genpept-bct1) (de:haemophilus influenzae rd section 28 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p00495 gb:v01578 gb:x00781) (le:6339) (re:6980) (di:complement) U32713 U32713 g1573238 Haemophilus influenzae Rd 71421 -11536998 5000694254 (de:(hi0272) (pn:oprt:orotate phosphoribosyltransferase:pyre) (gn:pyre) (gtcfc:4.2) (ec:2.4.2.10) (pyre_haein) (keggfc:4.2) (tigrfc:8.4) (db:gtc-haemophilus influenzae)) HI0272 HI0272 Haemophilus influenzae 727 10034658

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878311	14196	36352	447	148

Description

GTC ORF with score 341 to: (de:(yhr037w) (pn:delta-1-pyrroline-5-carboxylate dehydrogenase precursor:p5c dehydrogenase:1-pyrroline-5-carboxylate dehydrogenase) (gn:put2) (gtcfc:5.1:5.10) (ec:1.5.1.12) (put2_yeast) (keggfc:5.1:5.10) (sgdgc:1.1.1:9.7.0) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878316	14197	36353	228	75

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878318	14198	36354	1320	439

Description

6500733141 udp:hi0280 udp:uridine phosphorylase (gtcfc:4.2:4.4) (ec:2.4.2.3) (keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI0280 HI0280 Haemophilus influenzae 727 -11536999 103318 udp:hi0280 (ec:2.4.2.3) (de:uridine phosphorylase, (udrpase)) (db:swissprot) UDP_HAEIN P43770 HAEMOPHILUS INFLUENZAE 727 -11536999 167258 uridine phosphorylase (ec:2.4.2.3) (db:pir2.dat) C64059 C64059 Haemophilus influenzae 727 -11536999 7500893752 hi0280 uridine phosphorylase udp (db:genpept-bct1) (de:haemophilus influenzae rd section 29 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p12758 gb:x15689 pid:148229) (le:3941) (re:4720) (di:direct) U32714 U32714 g1573245 Haemophilus influenzae Rd 71421 -11536999 5000694255 (de:(hi0280) (pn:uridine phosphorylase:udp) (gn:udp) (gtcfc:4.2) (ec:2.4.2.3) (_haein) (keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae)) HI0280 HI0280 Haemophilus influenzae 727 10045088

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878326	14199	36355	765	254

Description

6500733142 tmk:hi0456 hypothetical protein:gb:d26185_92:thymidylate kinase:dtmp kinase (gtcfc:4.2:14.1) (ec:2.7.4.9) (keggfc:4.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae) HI0456 HI0456 Haemophilus influenzae 727 -11537000 81197 tmk:hi0456 (ec:2.7.4.9) (de:thymidylate kinase, (dtmp kinase)) (db:swissprot) KTHY_HAEIN P44719 HAEMOPHILUS INFLUENZAE 727 -11537000 7500884760 hi0456 thymidylate kinase (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to sp:p37345 pid:1244710 gb:u00096) (le:4953) (re:5585) (di:complement) U32728 U32728 g1573430 Haemophilus influenzae Rd 71421 -11537000 5000694256 (de:(hi0456) (pn:thymidylate kinase:dtmp kinase:hypothetical protein:gb:d26185_92) (gn:tmk) (gtcfc:4.2) (ec:2.7.4.9) (kthy_haein) (keggfc:4.2) (tigrfc:15.1) (db:gtc-haemophilus influenzae)) HI0456 HI0456 Haemophilus influenzae 727 10023433

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878327	14200	36356	474	157

Description

6500733143 tdk:hi0529 thymidine kinase (gtcfc:4.2:4.4) (ec:2.7.1.21) (keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI0529 HI0529 Haemophilus influenzae 727 -11537001 80755 tdk:hi0529 (ec:2.7.1.21) (de:thymidine kinase,) (db:swissprot) KITH_HAEIN P44309 HAEMOPHILUS INFLUENZAE 727 -11537001 138179 tdk thymidine kinase (cl:phage t4 thymidine kinase) (ec:2.7.1.21) (db:pir2.dat) G64074 G64074 Haemophilus influenzae 727 -11537001 7500884637 hi0529 thymidine kinase tdk (db:genpept-bct1) (de:haemophilus influenzae rd section 50 of 163 of the complete genome.) (nt:similar to sp:p23331 gb:x51523 gb:x53733 gb:x67326) (le:2636) (re:3217) (di:complement) U32735 U32735 g1573513 Haemophilus influenzae Rd 71421 -11537001 5000694257 (de:(hi0529) (pn:thymidine kinase:tdk) (gn:tdk) (gtcfc:4.2) (ec:2.7.1.21) (kith_haein) (keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae)) HI0529 HI0529 Haemophilus influenzae 727 10022996

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878331	14201	36357	894	297

Description

6500733144 thya:hi0905 thymidylate synthetase:probable thymidylate synthase:ts (gtcfc:4.2:9.6) (ec:2.1.1.45) (keggfc:4.2:9.7:9.8) (tigrfc:8.1) (db:gtc-haemophilus influenzae) (gtcfc:nucleotide metabolism-pyrimidine metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis) (tigrfc:2'-deoxyribo... HI0905 HI0905 Haemophilus influenzae 727 -11537002 102943 thya:hi0905 (ec:2.1.1.45) (de:probable thymidylate synthase, (ts)) (db:swissprot) TYSY_HAEIN P44420 HAEMOPHILUS INFLUENZAE 727 -11537002 167192 thymidylate synthase homolog hi0905 (cl:thymidylate synthase homolog) (db:pir2.dat) G64101 G64101 Haemophilus influenzae 727 -11537002 7500893622 hi0905 thymidylate synthetase thya (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:similar to gb:j01710 sp:p00470 pid:147987 pid:42685) (le:4101) (re:4952) (di:direct) U32772 U32772 g1573924 Haemophilus influenzae Rd 71421 -11537002 5000694258 (de:(hi0905) (pn:probable thymidylate synthase:ts:thymidylate synthetase:thya) (gn:thya) (gtcfc:4.2:9.8) (ec:2.1.1.45) (tysy_haein) (keggfc:4.2:9.8) (tigrfc:8.1) (db:gtc-haemophilus influenzae)) HI0905 HI0905 Haemophilus influenzae 727 10044755

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878339	14202	36358	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878373	14203	36359	855	285

Description

6500733145 dut:hi0954 deoxyuridinetriphosphatase:deoxyuridine 5-triphosphate nucleotidohydrolase:dutpase:dutp pyrophosphatase (gtcfc:4.2) (ec:3.6.1.23) (keggfc:4.2) (tigrfc:8.1) (db:gtc-haemophilus influenzae) (tigrfc:2'-deoxyribonucleotide metabolism) HI0954 HI0954 Haemophilus influenzae 727 -11537003 69366 dut:hi0954 (ec:3.6.1.23) (de:(dutpase) (dutp pyrophosphatase)) (db:swissprot) DUT_HAEIN P43792 HAEMOPHILUS INFLUENZAE 727 -11537003 141003 dutp pyrophosphatase (cl:dutp pyrophosphatase) (ec:3.6.1.23) (db:pir2.dat) H64104 H64104 Haemophilus influenzae 727 -11537003 7500880709 hi0954 deoxyuridinetriphosphatase dut (db:genpept-bct1) (de:haemophilus influenzae rd section 91 of 163 of the complete genome.) (nt:similar to gb:l10328 sp:p06968 gb:v01578 gb:x01714) (le:7871) (re:8326) (di:direct) U32776 U32776 g1573979 Haemophilus influenzae Rd 71421 -11537003 5000694259 (de:(hi0954) (pn:deoxyuridine 5"-triphosphate nucleotidohydrolase:dutpase:dutp pyrophosphatase:deoxyuridinetriphosphatase:dut) (gn:dut) (gtcfc:4.2) (ec:3.6.1.23) (dut_haein) (keggfc:4.2) (tigrfc:8.1) (db:gtc-haemophilus influenz) HI0954 HI0954 Haemophilus influenzae 727 10011949

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878391	14204	36360	282	93

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878401	14205	36361	279	92

Description

6500733146 pyrg:hi1077 ctp synthase:utp-ammonia ligase:ctp synthetase (gtcfc:4.2:4.4) (ec:6.3.4.2) (keggfc:4.2) (tigrfc:8.2) (db:gtc-haemophilus influenzae) HI1077 HI1077 Haemophilus influenzae 727 -11537004 92639 pyrg:hi1077 (ec:6.3.4.2) (de:ctp synthase, (utp--ammonia ligase) (ctp synthetase)) (db:swissprot) PYRG_HAEIN P44341 HAEMOPHILUS INFLUENZAE 727 -11537004 142408 ctp synthase (cl:ctp synthase) (ec:6.3.4.2) (db:pir2.dat) F64181 F64181 Haemophilus influenzae 727 -11537004 7500889175 hi1077 ctp synthetase pyrg (db:genpept-bct1) (de:haemophilus influenzae rd section 103 of 163 of the completegenome.) (nt:similar to gb:m12843 sp:p08398 pid:147478) (le:356) (re:1993) (di:direct) U32788 U32788 g1574630 Haemophilus influenzae Rd 71421 -11537004 5000694260 (de:(hi1077) (pn:ctp synthase:utp--ammonia ligase:ctp synthetase:pyrg) (gn:pyrg) (gtcfc:4.2) (ec:6.3.4.2) (pyrg_haein) (keggfc:4.2) (tigrfc:8.2) (db:gtc-haemophilus influenzae)) HI1077 HI1077 Haemophilus influenzae 727 10034671

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878403	14206	36362	237	78

Description

6500733147 trxb:hi1158 thioredoxin reductase (gtcfc:9.13) (ec:1.6.4.5) (keggfc:4.2) (tigrfc:2.10) (db:gtc-haemophilus influenzae) HI1158 HI1158 Haemophilus influenzae 727 -11537005 102508 trxb:hi1158 (ec:1.6.4.5) (de:thioredoxin reductase,) (db:swissprot) TRXB_HAEIN P43788 HAEMOPHILUS INFLUENZAE 727 -11537005 122798 thioredoxin reductase nadph (cl:thioredoxin reductase:thioredoxin reductase homology) (ec:1.6.4.5) (db:pir1.dat) G64186 G64186 Haemophilus influenzae 727 -11537005 7500893533 hi1158 thioredoxin reductase trxb (db:genpept-bct1) (de:haemophilus influenzae rd section 110 of 163 of the completegenome.) (nt:similar to gb:j03762 sp:p09625 pid:148073) (le:8185) (re:9141) (di:complement) U32795 U32795 g1574715 Haemophilus influenzae Rd 71421 -11537005 5000694261 (de:(hi1158) (pn:thioredoxin reductase:trxb) (gn:trxb) (gtcfc:4.2) (ec:1.6.4.5) (trxb_haein) (keggfc:4.2) (tigrfc:2.10) (db:gtc-haemophilus influenzae)) HI1158 HI1158 Haemophilus influenzae 727 10044327

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878406	14207	36363	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878417	14208	36364	933	310

Description

6500733148 cmka:hi1219 cytidylate kinase:cmk:cytidylate kinase 1:ck 1:cytidine monophosphate kinase 1:cmp kinase 1 (gtcfc:4.2:4.4) (ec:2.7.4.14) (keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI1219 HI1219 Haemophilus influenzae 727 -11537006 80550 cmka:hi1219 (ec:2.7.4.14) (de:kinase 1) (cmp kinase 1) (db:swissprot) KCY1_HAEIN P43892 HAEMOPHILUS INFLUENZAE 727 -11537006 166073 cmka cytidylate kinase:a (cl:cytidylate kinase cmk) (ec:2.7.4.14) (db:pir2.dat) I64110 I64110 Haemophilus influenzae 727 -11537006 7500884538 hi1219 cytidylate kinase 1 cmka (db:genpept-bct1) (de:haemophilus influenzae rd section 116 of 163 of the completegenome.) (nt:similar to sp:p23863 pid:42839 gb:u00096) (le:8239) (re:8934) (di:direct) U32801 U32801 g1574149 Haemophilus influenzae Rd 71421 -11537006 5000694262 (de:(hi1219) (pn:cytidylate kinase 1:ck 1:cytidine monophosphate kinase 1:cmp kinase 1:cytidylate kinase:cmk) (gn:cmka) (gtcfc:4.2) (ec:2.7.4.14) (kcy1_haein) (keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae)) HI1219 HI1219 Haemophilus influenzae 727 10022792

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878421	14209	36365	450	149

Description

GTC ORF with score 97 to: (fn:hydrolysis of the beta-1,4 linkages of) (db:genpept-bct2) (de:pseudoalteromonas sp. s9 chitinase c (chic) gene, complete, cds.) (nt:belongs to chitinase class ii (family 18 of) (le:290) (re:2899) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878426	14210	36366	918	305

Description

6500733149 pyrf:hi1224 orotidine 5 monophosphate:orotidine 5-phosphate decarboxylase:omp decarboxylase (gtcfc:4.2) (ec:4.1.1.23) (keggfc:4.2) (tigrfc:8.4) (db:gtc-haemophilus influenzae) HI1224 HI1224 Haemophilus influenzae 727 -11537007 68059 pyrf:hi1224 (ec:4.1.1.23) (de:decarboxylase)) (db:swissprot) DCOP_HAEIN P43812 HAEMOPHILUS INFLUENZAE 727 -11537007 141475 pyrf orotidine-5-phosphate decarboxylase (cl:orotidine-5'-phosphate decarboxylase:orotidine-5'-phosphate decarboxylase homology) (ec:4.1.1.23) (db:pir2.dat) B64111 B64111 Haemophilus influenzae 727 -11537007 7500880061 hi1224 orotidine 5-phosphate decarboxylase pyrf (db:genpept-bct1) (de:haemophilus influenzae rd section 117 of 163 of the completegenome.) (nt:similar to gb:j02768 sp:p08244 pid:147475 gb:u00096) (le:1958) (re:2650) (di:direct) U32802 U32802 g1574155 Haemophilus influenzae Rd 71421 -11537007 5000694263 (de:(hi1224) (pn:orotidine 5"-phosphate decarboxylase:orotidine 5" monophosphate:omp decarboxylase:pyrf) (gn:pyrf) (gtcfc:4.2) (ec:4.1.1.23) (dcop_haein) (keggfc:4.2) (tigrfc:8.4) (db:gtc-haemophilus influenzae)) HI1224 HI1224 Haemophilus influenzae 727 10010652

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878427	14211	36367	768	255

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878430	14212	36368	324	107

Description

6500733150 upp:hi1228 uracil phosphoribosyltransferase:ump
pyrophosphorylase:uprtase (gtcfc:4.2:4.4) (ec:2.4.2.9) (keggfc:4.2)
(tigrfc:8.5) (db:gtc-haemophilus influenzae) HI1228 HI1228 Haemophilus
influenzae 727 -11537008 103784 upp:hi1228 (ec:2.4.2.9) (de:(uprtase))
(db:swissprot) UPP_HAEIN P43857 HAEMOPHILUS INFLUENZAE 727 -11537008 167252
uracil phosphoribosyltransferase:upp-type (cl:uracil
phosphoribosyltransferase upp) (ec:2.4.2.9) (db:pir2.dat) E64111 E64111
Haemophilus influenzae 727 -11537008 7500893827 hi1228 uracil
phosphoribosyltransferase upp (db:genpept-bct1) (de:haemophilus influenzae
rd section 117 of 163 of the completegenome.) (nt:similar to sp:p25532
gb:x57104 pid:43272 gb:u00096) (le:5116) (re:5742) (di:complement) U32802
U32802 g1574158 Haemophilus influenzae Rd 71421 -11537008 5000694264
(de:(hi1228) (pn:ump pyrophosphorylase:uprtase:uracil
phosphoribosyltransferase:upp) (gn:upp) (gtcfc:4.2) (ec:2.4.2.9) (upp_haein)
(keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae)) HI1228 HI1228
Haemophilus influenzae 727 10045554

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878456	14213	36369	1545	514

Description

5000694265 cdd:cda:hi1350 cytidine deaminase:cytidine aminohydrolase:cda
(gtcfc:4.2:4.4) (ec:3.5.4.5) (keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus
influenzae) HI1350 HI1350 Haemophilus influenzae 727 -11537009 63643
cdd:cda:hi1350 (ec:3.5.4.5) (de:cytidine deaminase, (cytidine
aminohydrolase) (cda)) (db:swissprot) CDD_HAEIN P44325 HAEMOPHILUS
INFLUENZAE 727 -11537009 166071 cytidine deaminase homolog (cl:cdd protein)
(db:pir2.dat) D64118 D64118 Haemophilus influenzae 727 -11537009 7500878429
hi1350 cytidine deaminase cdd (db:genpept-bct1) (de:haemophilus influenzae
rd section 129 of 163 of the completegenome.) (nt:similar to gb:x63144
gb:u15410 gb:x16419 pid:41090) (le:2723) (re:3601) (di:direct) U32814 U32814
g1574812 Haemophilus influenzae Rd 71421 -11537009 6500733151 cdd:cda
cytidine deaminase:cytidine aminohydrolase:cda (gtcfc:4.2:4.4) (ec:3.5.4.5)
(keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI1350 HI1350
Haemophilus influenzae 727 -11537009

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878473	14214	36370	1635	544

Description

6500733152 pyrd:hi1401 dihydroorotate dehydrogenase: dihydroorotate oxidase:dhodehase (gtcfc:4.2) (ec:1.3.3.1) (keggfc:4.2) (tigrfc:8.4) (db:gtc-haemophilus influenzae) HI1401 HI1401 Haemophilus influenzae 727 -11537010 92614 pyrd:hi1401 (ec:1.3.3.1) (de:(dhodehase)) (db:swissprot) PYRD_HAEIN P45477 HAEMOPHILUS INFLUENZAE 727 -11537010 136554 pyrd dihydroorotate oxidase::dihydroorotate dehydrogenase (cl:dihydroorotate oxidase) (ec:1.3.3.1) (db:pir2.dat) A64122 A64122 Haemophilus influenzae 727 -11537010 7500889163 hi1401 dihydroorotate dehydrogenase pyrd (db:genpept-bct1) (de:haemophilus influenzae rd section 135 of 163 of the completegenome.) (nt:similar to sp:p05021 gb:x02826 pid:42609 gb:u00096) (le:4506) (re:5525) (di:complement) U32820 U32820 g1574236 Haemophilus influenzae Rd 71421 -11537010 5000694266 (de:(hi1401) (pn:dihydroorotate oxidase:dhodehase:dihydroorotate dehydrogenase:pyrd) (gn:pyrd) (gtcfc:4.2) (ec:1.3.3.1) (pyrd_haein) (keggfc:4.2) (tigrfc:8.4) (db:gtc-haemophilus influenzae)) HI1401 HI1401 Haemophilus influenzae 727 10034646

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878484	14215	36371	2841	947

Description

6500733153 cmkb:hi1646 cytidylate kinase:cmk:cytidylate kinase 2:ck 2:cytidine monophosphate kinase 2:cmp kinase 2 (gtcfc:4.2:4.4) (ec:2.7.4.14) (keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI1646 HI1646 Haemophilus influenzae 727 -11537011 166072 cmkb cytidylate kinase:b (cl:cytidylate kinase cmk) (ec:2.7.4.14) (db:pir2.dat) H64134 H64134 Haemophilus influenzae 727 -11537011 7500960649 hi1646 cytidylate kinase 2 cmkb (db:genpept-bct1) (de:haemophilus influenzae rd section 152 of 163 of the completegenome.) (nt:similar to sp:p23863 pid:42839 gb:u00096) (le:8549) (re:9346) (di:complement) U32837 U32837 g1574494 Haemophilus influenzae Rd 71421 -11537011 5000694267 (de:(hi1646) (pn:cytidylate kinase 2:ck 2:cytidine monophosphate kinase 2:cmp kinase 2:cytidylate kinase:cmk) (gn:cmkb) (gtcfc:4.2) (ec:2.7.4.14) (kcy2_haein) (keggfc:4.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae)) HI1646 HI1646 Haemophilus influenzae 727 10088071

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878520	14216	36372	345	114

Description

5000694251 grxa:grx:hi1532 grx:glutaredoxin (gtcfc:4.2) (keggfc:14.2) (tigrfc:8.1) (db:gtc-haemophilus influenzae) (tigrfc:2'-deoxyribonucleotide metabolism) HI1532 HI1532 Haemophilus influenzae 727 -11537012 74086 grxa:grx:hi1532 (de:glutaredoxin) (db:swissprot) GLRX_HAEIN P45242 HAEMOPHILUS INFLUENZAE 727 -11537012 135833 glutaredoxin (cl:glutaredoxin:glutaredoxin homology) (db:pir2.dat) I64127 I64127 Haemophilus influenzae 727 -11537012 7500882546 hi1532 glutaredoxin grx (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the complete genome.) (nt:similar to gb:m13449 sp:p00277 gb:u18655 pid:146273) (le:89) (re:352) (di:direct) U32829 U32829 g1574376 Haemophilus influenzae Rd 71421 -11537012 6500733154 grxa:grx grx:glutaredoxin (gtcfc:4.2) (keggfc:14.2) (tigrfc:8.1) (db:gtc-haemophilus influenzae) HI1532 HI1532 Haemophilus influenzae 727 -11537012

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878546	14217	36373	240	79

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878551	14218	36374	1716	571

Description

5000694268 uracil phosphoribosyltransferase:pyrr:hypothetical protein (gtcfc:4.2) (keggfc:14.2) (tigrfc:8.4) (db:gtc-haemophilus influenzae) HI0459 HI0459 Haemophilus influenzae 727 -11537013 109183 hi0459 (de:hypothetical protein hi0459) (db:swissprot) Y459_HAEIN P44722 HAEMOPHILUS INFLUENZAE 727 -11537013 167251 purr uracil phosphoribosyltransferase:pyrr (cl:hypoxanthine phosphoribosyltransferase) (ec:2.4.2.9) (db:pir2.dat) G64069 G64069 Haemophilus influenzae 727 -11537013 7500895330 hi0459 pyrimidine operon regulatory protein pyrr (db:genpept-bct1) (de:haemophilus influenzae rd section 43 of 163 of the complete genome.) (nt:similar to gb:x76083 sp:p41007 pid:431230 percent) (le:7727) (re:8266) (di:complement) U32728 U32728 g1573433 Haemophilus influenzae Rd 71421 -11537013 6500733155 uracil phosphoribosyltransferase:pyrr:hypothetical protein (gtcfc:4.2) (keggfc:14.2) (tigrfc:8.4) (db:gtc-haemophilus influenzae) HI0459 HI0459 Haemophilus influenzae 727 -11537013

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878582	14219	36375	744	247

Description

5000694269 pyrF operon encoding orotidine 5-monophosphate:omp
 decarboxylase:hypothetical protein (gtcfc:4.2) (keggfc:14.2) (tigrfc:8.4)
 (db:gtc-haemophilus influenzae) HI1225 HI1225 Haemophilus influenzae 727
 -11537014 110813 hi1225 (de:hypothetical protein hi1225) (db:swissprot)
 YCIH_HAEIN P45116 HAEMOPHILUS INFLUENZAE 727 -11537014 157259 probable
 translation initiation factor hi1225 (cl:pyrF operon conserved hypothetical
 11.4k protein) (db:pir2.dat) C64111 C64111 Haemophilus influenzae 727
 -11537014 7500921827 hi1225 conserved hypothetical protein
 (db:genpept-bct1) (de:haemophilus influenzae rd section 117 of 163 of the
 completegenome.) (nt:similar to gb:j02768 sp:p08245 pid:147476 gb:u00096)
 (le:2657) (re:2977) (di:direct) U32802 U32802 g1574156 Haemophilus
 influenzae Rd 71421 -11537014 6500733156 pyrF operon encoding orotidine
 5-monophosphate:omp decarboxylase:hypothetical protein (gtcfc:4.2)
 (keggfc:14.2) (tigrfc:8.4) (db:gtc-haemophilus influenzae) HI1225 HI1225
 Haemophilus influenzae 727 -11537014

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878596	14220	36376	243	80

Description

GTC ORF with score 100 to: (sr:herpes simplex virus type 1 (strain kos(m))
 dna derived fro) (db:genpept-vrl) (de:herpes simplex virus type one (hsv-1)
 latency associated transcript(lat).) (nt:latency associated transcript (lat)
 orf-2) (le:1160) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878609	14221	36377	234	77

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878621	14222	36378	282	93

Description

6500733157 slt:hi0829 soluble lytic murein transglycosylase:putative soluble lytic murein transglycosylase precursor (gtcfc:4.3:7.1:11.4) (ec:3.2.1.-) (keggfc:4.3:4.4) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0829 HI0829 Haemophilus influenzae 727 -11537015 98633 slt:hi0829 (ec:3.2.1.-) (de:putative soluble lytic murein transglycosylase precursor,) (db:swissprot) SLT_HAEIN P44888 HAEMOPHILUS INFLUENZAE 727 -11537015 167170 probable soluble lytic transglycosylase (cl:soluble lytic transglycosylase) (ec:3.2.1.-) (db:pir2.dat) C64097 C64097 Haemophilus influenzae 727 -11537015 7500891702 hi0829 soluble lytic murein transglycosylase:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p03810 gb:m69185 pid:147836) (le:2193) (re:3974) (di:direct) U32765 U32765 g1573843 Haemophilus influenzae Rd 71421 -11537015 5000694270 (de:(hi0829) (pn:putative soluble lytic murein transglycosylase precursor:soluble lytic murein transglycosylase:slt) (gn:slt) (gtcfc:4.3:7.2) (ec:3.2.1.-) (slt_haein) (keggfc:4.3:7.1) (tigrfc:3.2) (db:gtc-haemophilus influenzae)) HI0829 HI0829 Haemophilus influenzae 727 10040508

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878623	14223	36379	198	65

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878627	14224	36380	555	184

Description

6500733158 glgx:hi1358 glycogen operon protein (gtcfc:4.3:7.1:7.2) (ec:3.2.1.-) (keggfc:4.3:4.4) (tigrfc:5.5) (db:gtc-haemophilus influenzae) HI1358 HI1358 Haemophilus influenzae 727 -11537016 73816 glgx:hi1358 (ec:3.2.1.-) (de:glycogen operon protein glgx,) (db:swissprot) GLGX_HAEIN P45178 HAEMOPHILUS INFLUENZAE 727 -11537016 154416 glyx glyx protein (cl:glyx protein) (ec:3.2.1.-) (db:pir2.dat) A64119 A64119 Haemophilus influenzae 727 -11537016 7500882409 hi1358 glycogen operon protein glgx (db:genpept-bct1) (de:haemophilus influenzae rd section 130 of 163 of the completegenome.) (nt:similar to gb:j01616 sp:p15067 pid:146135) (le:4458) (re:6437) (di:direct) U32815 U32815 g1574821 Haemophilus influenzae Rd 71421 -11537016 5000694271 (de:(hi1358) (pn:glycogen operon protein :glycogen operon protein:glgx) (gn:glgx) (gtcfc:4.3:7.2) (ec:3.2.1.-) (glgx_haein) (keggfc:4.3:7.1) (tigrfc:5.5) (db:gtc-haemophilus influenzae)) HI1358 HI1358 Haemophilus influenzae 727 10016348

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878628	14225	36381	468	155

Description

6500733159 glmu:hi0642 udp-n-acetylglucosamine pyrophosphorylase:n-acetylglucosamine-1-phosphate uridyltransferase (gtcfc:4.3:7.1) (ec:2.7.7.23) (keggfc:4.4) (tigrfc:8.6) (db:gtc-haemophilus influenzae) HI0642 HI0642 Haemophilus influenzae 727 -11537017 73872 glmu:hi0642 (ec:2.7.7.23) (de:acetylglucosamine-1-phosphate uridyltransferase)) (db:swissprot) GLMU_HAEIN P43889 HAEMOPHILUS INFLUENZAE 727 -11537017 167247 glmu protein homolog (cl:n-acetylglucosamine-1-phosphate uridyltransferase) (db:pir2.dat) G64083 G64083 Haemophilus influenzae 727 -11537017 7500882449 hi0642 udp-n-acetylglucosamine pyrophosphorylase (db:genpept-bct1) (de:haemophilus influenzae rd section 62 of 163 of the complete genome.) (nt:similar to sp:p17114 pid:290578 pid:43267) (le:3454) (re:4824) (di:direct) U32747 U32747 g1573640 Haemophilus influenzae Rd 71421 -11537017 5000694377 (de:(hi0642) (pn:n-acetylglucosamine- 1-phosphate uridyltransferase:udp-n-acetylglucosamine pyrophosphorylase:glmu) (gn:glmu) (gtcfc:7.1) (ec:2.7.7.23) (glmu_haein) (keggfc:4.4) (tigrfc:8.6) (db:gtc-haemophilus influenzae)) HI0642 HI0642 Haemophilus influenzae 727 10016402

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878629	14226	36382	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878632	14227	36383	561	186

Description

6500733160 siab:hi1279 cmp-neunac synthetase (gtcfc:4.3) (keggfc:14.2) (tigrfc:8.6) (db:gtc-haemophilus influenzae) HI1279 HI1279 Haemophilus influenzae 727 -11537018 7000685958 neua:hi1279 (ec:2.7.7.43) (de:acid synthetase)) (db:swissprot) NEUA_HAEIN Q57140 HAEMOPHILUS INFLUENZAE 727 -11537018 166058 cmp-neunac synthetase homolog (db:pir2.dat) C64114 C64114 Haemophilus influenzae 727 -11537018 7500886390 hi1279 acylneuraminate cytidyltransferase neua (db:genpept-bct1) (de:haemophilus influenzae rd section 122 of 163 of the completegenome.) (nt:similar to gb:m95053 gb:x78068 gb:u04328 pid:460146) (le:8718) (re:9404) (di:direct) U32807 U32807 g1574734 Haemophilus influenzae Rd 71421 -11537018 5000694272 (de:(hi1279) (pn:cmp-neunac synthetase:siab) (gn:siab) (gtcfc:4.3) (ec:) (keggfc:11.2) (tigrfc:8.6) (db:gtc-haemophilus influenzae)) HI1279 HI1279 Haemophilus influenzae 727 10088066

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878633	14228	36384	585	194

Description

6500733161 cpdb:hi0583 2:3-cyclic-nucleotide
2-phosphodiesterase:2:3-cyclic-nucleotide 2-phosphodiesterase precursor
(gtcfc:4.4) (ec:3.1.4.16) (keggfc:14.1) (tigrfc:8.5) (db:gtc-haemophilus
influenzae) HI0583 HI0583 Haemophilus influenzae 727 -11537019 64893
cpdb:hi0583 (ec:3.1.4.16) (de:2',3'-cyclic-nucleotide 2'-phosphodiesterase
precursor,) (db:swissprot) CN16_HAEIN P44764 HAEMOPHILUS INFLUENZAE 727
-11537019 139803 2:3-cyclic-nucleotide 2-phosphodiesterase:precursor
(cl:2',3'-cyclic-nucleotide 2'-phosphodiesterase:2',3'-cyclic-nucleotide
2'-phosphodiesterase homology:phosphoesterase core homology) (ec:3.1.4.16)
(db:pir1.dat) A64079 A64079 Haemophilus influenzae 727 -11537019 7500878923
hi0583 2:3-cyclic-nucleotide 2-phosphodiesterase (db:genpept-bct1)
(de:haemophilus influenzae rd section 55 of 163 of the complete genome.)
(nt:similar to sp:p08331 gb:m13464 pid:145584 gb:u00096) (le:373) (re:2346)
(di:complement) U32740 U32740 g1573573 Haemophilus influenzae Rd 71421
-11537019 5000694273 (de:(hi0583) (pn:2",3"-cyclic-nucleotide
2"-phosphodiesterase precursor:2",3"-cyclic-nucleotide
2"-phosphodiesterase:cpdb) (gn:cpdb) (gtcfc:4.4) (ec:3.1.4.16) (cn16_haein)
(keggfc:11.1) (tigrfc:8.5) (db:gtc-haemophilus influenza) HI0583 HI0583
Haemophilus influenzae 727 10007554

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878635	14229	36385	318	106

Description

GTC ORF with score 146 to: (sr:thale cress) (db:genpept-pln1)
(de:arabidopsis thaliana dna chromosome 4, essa i contig fragment no.6.)
(nt:similarity to isp4 protein - fission yeast) (le:12085:12896:13233)
(re:12810:13151:13802) (di:complementjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878637	14230	36386	594	198

Description

5000694274 hi0692:gpta:xgprt-a:hi0674:gptb:xgprt-b:hi0674 xanthine guanine phosphoribosyl transferase gpt:xanthine-guanine phosphoribosyltransferase:xgprt (gtcfc:4.4) (ec:2.4.2.22) (keggfc:14.1) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI0674 HI0674 Haemophilus influenzae 727 -11537020 108101 gpta:xgprt-a:hi0674:gptb:xgprt-b:hi0692 (ec:2.4.2.22) (de:xanthine-guanine phosphoribosyltransferase, (xgprt)) (db:swissprot) XGPT_HAEIN P43859 HAEMOPHILUS INFLUENZAE 727 -11537020 138168 xanthine phosphoribosyltransferase (cl:xanthine phosphoribosyltransferase) (ec:2.4.2.22) (db:pir2.dat) A64087 A64087 Haemophilus influenzae 727 -11537020 7500894440 hi0674 xanthine-guanine phosphoribosyltransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to sp:p26972 gb:x52093 gb:x63336 pid:47695) (le:3150) (re:3617) (di:complement) U32750 U32750 g1573682 Haemophilus influenzae Rd 71421 -11537020 7500894441 hi0692 xanthine-guanine phosphoribosyltransferase (db:genpept-bct1) (de:haemophilus influenzae rd section 67 of 163 of the complete genome.) (nt:similar to sp:p26972 gb:x52093 gb:x63336 pid:47695) (le:2546) (re:3013) (di:complement) U32752 U32752 g1573693 Haemophilus influenzae Rd 71421 -11537020 6500733162 hi0692:gpta:xgprt-a:hi0674:gptb:xgprt-b xanthine guanine phosphoribosyl transferase gpt:xanthine-guanine phosphoribosyltransferase:xgprt (gtcfc:4.4) (ec:2.4.2.22) (keggfc:14.1) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI0674 HI0674 Haemophilus influenzae 727 -11537020

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878650	14231	36387	1665	554

Description

6500733163 mrp:hi1277 putative atpase:mrp:protein homolog (gtcfc:4.4) (keggfc:14.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae) HI1277 HI1277 Haemophilus influenzae 727 -11537021 84231 mrp:hi1277 (de:mrp protein homolog) (db:swissprot) MRP_HAEIN P45135 HAEMOPHILUS INFLUENZAE 727 -11537021 167104 mrp probable atpase mrp (cl:conserved probable membrane protein yil003w) (db:pir2.dat) A64114 A64114 Haemophilus influenzae 727 -11537021 7500885883 hi1277 atp-binding protein mrp (db:genpept-bct1) (de:haemophilus influenzae rd section 122 of 163 of the completegenome.) (nt:similar to sp:p21590 gb:u00007 gb:x55791 pid:405896) (le:6744) (re:7904) (di:direct) U32807 U32807 g1574732 Haemophilus influenzae Rd 71421 -11537021 5000694275 (de:(hi1277) (pn:protein homolog:putative atpase:mrp) (gn:mrp) (gtcfc:4.4) (ec:) (_haein) (keggfc:11.2) (tigrfc:8.5) (db:gtc-haemophilus influenzae)) HI1277 HI1277 Haemophilus influenzae 727 10026432

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878652	14232	36388	462	153

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878656	14233	36389	462	153

Description

6500733164 gor:hi0161 glutathione reductase:glutathione reductase:gr:grase
(gtcfc:5.1:6.16) (ec:1.6.4.2) (keggfc:5.1:6.9) (tigrfc:2.10)
(db:gtc-haemophilus influenzae) HI0161 HI0161 Haemophilus influenzae 727
-11537022 74666 gor:hi0161 (ec:1.6.4.2) (de:glutathione reductase, (gr)
(grase)) (db:swissprot) GSHR_HAEIN P43783 HAEMOPHILUS INFLUENZAE 727
-11537022 136647 glutathione reductase nadph (cl:dihydrolipoamide
dehydrogenase:dihydrolipoamide dehydrogenase homology) (ec:1.6.4.2)
(db:pir2.dat) A64052 A64052 Haemophilus influenzae 727 -11537022 241610 gor
glutathione reductase (fn:reduces oxidized glutathione using nadph)
(db:genpept-bct1) (ec:1.6.4.2) (de:haemophilus influenzae bola (bola),
glutathione reductase (gor),phosphatidylserine decarboxylase (psd), 30k
protein (rpmf), genes,complete cds.) (le:1739) (re:3109) (di:di... HIU20229
U20229 g644854 Haemophilus influenzae 727 -11537022 7500882797 hi0161
glutathione reductase gor (db:genpept-bct1) (de:haemophilus influenzae rd
section 17 of 163 of the complete genome.) (nt:similar to sp:p06715
gb:m13141 pid:146248) (le:85) (re:1455) (di:complement) U32702 U32702
g1573119 Haemophilus influenzae Rd 71421 -11537022 5000694276 (de:(hi0161)
(pn:glutathione reductase:gr:grase:glutathione reductase:gor) (gn:gor)
(gtcfc:5.1:6.16) (ec:1.6.4.2) (gshr_haein) (keggfc:5.1:6.9) (tigrfc:2.10)
(db:gtc-haemophilus influenzae)) HI0161 HI0161 Haemophilus influenzae 727
10017180

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878668	14234	36390	558	185

Description

6500733165 gltx:hi0274 glutamyl-trna synthetase:glutamate--trna ligase:glurs
 (gtcfc:5.1:9.10:10.6) (ec:6.1.1.17) (keggfc:5.1:9.10:10.1:10.2)
 (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0274 HI0274 Haemophilus
 influenzae 727 -11537023 100021 gltx:hi0274 (ec:6.1.1.17) (de:(glurs))
 (db:swissprot) SYE_HAEIN P43818 HAEMOPHILUS INFLUENZAE 727 -11537023 142294
 gltx glutamate--trna ligase::glutamyl-trna synthetase (cl:glutamate--trna
 ligase:glutamine--trna ligase homology) (ec:6.1.1.17) (db:pir2.dat) B64059
 B64059 Haemophilus influenzae 727 -11537023 7500892374 hi0274 glutamyl-trna
 synthetase gltx (db:genpept-bct1) (de:haemophilus influenzae rd section 28
 of 163 of the complete genome.) (nt:similar to gb:m13687 sp:p04805 gb:x55737
 gb:x63976) (le:8021) (re:9463) (di:complement) U32713 U32713 g1573240
 Haemophilus influenzae Rd 71421 -11537023 5000694277 (de:(hi0274)
 (pn:glutamate--trna ligase:glurs:glutamyl-trna synthetase:gltx) (gn:gltx)
 (gtcfc:5.1:9.10:10.6) (ec:6.1.1.17) (sy_e_haein) (keggfc:5.1:9.10:10.1:10.2)
 (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0274 HI0274 Haemophilus
 influenzae 727 10041875

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878682	14235	36391	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878686	14236	36392	1617	538

Description

6500733166 glms:hi0429 glutamine
amidotransferase:glucosamine--fructose-6-phosphate
aminotransferase:isomerizing:hexosephosphate
aminotransferase:d-fructose-6-phosphate
amidotransferase:gfat:l-glutamine-d-fructose-6-phosphate amidotransferase
(gtcfc:5.1:7.1) (ec:2.6.1.16) (keggfc:5.1) (tigrfc:5.1) (db:gtc-haemophilus
influenzae) HI0429 HI0429 Haemophilus influenzae 727 -11537024 138408
glutamine--fructose-6-phosphate transaminase isomerizing
(cl:glutamine--fructose-6-phosphate aminotransferase (isomerizing))
(ec:2.6.1.16) (db:pir2.dat) D64067 D64067 Haemophilus influenzae 727
-11537024 7500954057 hi0429 glucosamine--fructose-6-phosphate
(db:genpept-bct1) (de:haemophilus influenzae rd section 41 of 163 of the
complete genome.) (nt:similar to gb:l10328 sp:p17169 pid:290577 pid:43268)
(le:4507) (re:6339) (di:complement) U32726 U32726 g1573404 Haemophilus
influenzae Rd 71421 -11537024 5000694278 (de:(hi0429)
(pn:glucosamine--fructose-6-phosphate
aminotransferase:isomerizing:hexosephosphate aminotransferase:d-fructose-6-
phosphate amidotransferase:gfat:l-glutamine-d-fructose-6- phosphate
amidotransferase:glutamine amidotransfera) HI0429 HI0429 Haemophilus
influenzae 727 10070622

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878687	14237	36393	381	127

Description

6500733167 glns:hi1354 glutaminyl-trna synthetase:glutamine--trna
ligase:glnrs (gtcfc:5.1:10.6) (ec:6.1.1.18) (keggfc:5.1:10.1:10.2)
(tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1354 HI1354 Haemophilus
influenzae 727 -11537025 100151 glns:hi1354 (ec:6.1.1.18) (de:(glnrs))
(db:swissprot) SYQ_HAEIN P43831 HAEMOPHILUS INFLUENZAE 727 -11537025 142296
glns glutamine--trna ligase::glutaminyl-trna synthetase (cl:glutamine--trna
ligase:glutamine--trna ligase homology) (ec:6.1.1.18) (db:pir2.dat) G64118
G64118 Haemophilus influenzae 727 -11537025 7500892552 hi1354
glutaminyl-trna synthetase glns (db:genpept-bct1) (de:haemophilus influenzae
rd section 129 of 163 of the completegenome.) (nt:similar to gb:v01575
sp:p00962 gb:j01617 gb:m10187) (le:8131) (re:9804) (di:direct) U32814 U32814
g1574816 Haemophilus influenzae Rd 71421 -11537025 5000694279 (de:(hi1354)
(pn:glutamine--trna ligase:glnrs:glutaminyl-trna synthetase:glns) (gn:glns)
(gtcfc:5.1:10.6) (ec:6.1.1.18) (syq_haein) (keggfc:5.1:10.1:10.2)
(tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI1354 HI1354 Haemophilus
influenzae 727 10042005

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878688	14238	36394	804	267
<u>Description</u>				
6500733168 argi:hi0596 arc:ornithine carbamoyltransferase:otcase (gtcfc:5.1:5.10:5.16) (ec:2.1.3.3) (keggfc:5.10:5.16) (tigrfc:1.4) (db:gtc-haemophilus influenzae) HI0596 HI0596 Haemophilus influenzae 727 -11537026 87972 arc:hi0596 (ec:2.1.3.3) (de:ornithine carbamoyltransferase, catabolic, (otcase)) (db:swissprot) OTCC_HAEIN P44770 HAEMOPHILUS INFLUENZAE 727 -11537026 137845 ornithine carbamoyltransferase (cl:ornithine carbamoyltransferase:aspartate/ornithine carbamoyltransferase homology) (ec:2.1.3.3) (db:pir2.dat) H64079 H64079 Haemophilus influenzae 727 -11537026 7500887402 hi0596 ornithine carbamoyltransferase arc: (db:genpept-bct1) (de:haemophilus influenzae rd section 56 of 163 of the complete genome.) (nt:similar to gb:x05637 sp:p08308 pid:45288 percent) (le:3467) (re:4471) (di:complement) U32741 U32741 g1573585 Haemophilus influenzae Rd 71421 -11537026 5000694283 (de:(hi0596) (pn:otcase:ornithine carbamoyltransferase:arc) (gn:argi) (gtcfc:5.10:5.16) (ec:2.1.3.3) (otc_haein) (keggfc:5.10:5.16) (tigrfc:1.4) (db:gtc-haemophilus influenzae)) HI0596 HI0596 Haemophilus influenzae 727 10030113				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878697	14239	36395	198	65
<u>Description</u>				
Hypothetical protein				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878701	14240	36396	300	99
<u>Description</u>				
6500733169 arg:hi0811 argininosuccinate lyase:arginosuccinase:asal (gtcfc:5.1:5.10:5.16:5.2) (ec:4.3.2.1) (keggfc:5.2:5.10:5.16) (tigrfc:1.4) (db:gtc-haemophilus influenzae) HI0811 HI0811 Haemophilus influenzae 727 -11537027 60131 arg:hi0811 (ec:4.3.2.1) (de:argininosuccinate lyase, (arginosuccinase) (asal)) (db:swissprot) ARLY_HAEIN P44314 HAEMOPHILUS INFLUENZAE 727 -11537027 166011 argininosuccinate lyase (cl:argininosuccinate lyase) (ec:4.3.2.1) (db:pir2.dat) F64095 F64095 Haemophilus influenzae 727 -11537027 7500877155 hi0811 argininosuccinate lyase arg (db:genpept-bct1) (de:haemophilus influenzae rd section 78 of 163 of the complete genome.) (nt:similar to sp:p11447 gb:j01590 gb:m21446 pid:145335) (le:6589) (re:7962) (di:complement) U32763 U32763 g1573823 Haemophilus influenzae Rd 71421 -11537027 5000694286 (de:(hi0811) (pn:arginosuccinase:asal:argininosuccinate lyase:arg) (gn:argh) (gtcfc:5.10:5.16:5.2) (ec:4.3.2.1) (arly_haein) (keggfc:5.2:5.10:5.16) (tigrfc:1.4) (db:gtc-haemophilus influenzae)) HI0811 HI0811 Haemophilus influenzae 727 10002857				

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878702	14241	36397	402	133

Description

6500733170 prob:hi0900 glutamate 5-kinase:gamma-glutamyl kinase:gk (gtcfc:5.1:5.16) (ec:2.7.2.11) (keggfc:5.16) (tigrfc:1.4) (db:gtc-haemophilus influenzae) HI0900 HI0900 Haemophilus influenzae 727 -11537028 91176 prob:hi0900 (ec:2.7.2.11) (de:glutamate 5-kinase, (gamma-glutamyl kinase) (gk)) (db:swissprot) PROB_HAEIN P43763 HAEMOPHILUS INFLUENZAE 727 -11537028 138969 glutamate 5-kinase (cl:glutamate 5-kinase) (ec:2.7.2.11) (db:pir2.dat) D64101 D64101 Haemophilus influenzae 727 -11537028 7500888527 hi0900 glutamate 5-kinase gamma-glutamyl kinase (db:genpept-bct1) (de:haemophilus influenzae rd section 87 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p07005 pid:1208988) (le:705) (re:1811) (di:direct) U32772 U32772 g1573920 Haemophilus influenzae Rd 71421 -11537028 5000694320 (de:(hi0900) (pn:gk:glutamate 5-kinase:gamma-glutamyl kinase:prob) (gn:prob) (gtcfc:5.16) (ec:2.7.2.11) (prob_haein) (keggfc:5.16) (tigrfc:1.4) (db:gtc-haemophilus influenzae)) HI0900 HI0900 Haemophilus influenzae 727 10033275

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878703	14242	36398	324	107

Description

6500733171 proa:hi1239 gamma-glutamyl phosphate reductase gpr:glutamate-5-semialdehyde dehydrogenase:glutamyl-gamma-semialdehyde dehydrogenase (gtcfc:5.1:9.10) (ec:1.2.1.41) (keggfc:5.16:9.10) (tigrfc:1.4) (db:gtc-haemophilus influenzae) HI1239 HI1239 Haemophilus influenzae 727 -11537029 91163 proa:hi1239 (ec:1.2.1.41) (de:dehydrogenase)) (db:swissprot) PROA_HAEIN P45121 HAEMOPHILUS INFLUENZAE 727 -11537029 136511 glutamate-5-semialdehyde dehydrogenase (cl:glutamate-5-semialdehyde dehydrogenase) (ec:1.2.1.41) (db:pir2.dat) D64112 D64112 Haemophilus influenzae 727 -11537029 7500888519 hi1239 gamma-glutamyl phosphate reductase proa (db:genpept-bct1) (de:haemophilus influenzae rd section 119 of 163 of the complete genome.) (nt:similar to sp:p07004 pid:1208989 pid:42498) (le:70) (re:1323) (di:complement) U32804 U32804 g1574171 Haemophilus influenzae Rd 71421 -11537029 5000694321 (de:(hi1239) (pn:gglutamate-5- semialdehyde dehydrogenase:glutamyl-gamma-semialdehyde dehydrogenase:gamma-glutamyl phosphate reductase:proa) (gn:proa) (gtcfc:5.16:9.10) (ec:1.2.1.41) (proa_haein) (keggfc:5.16:9.10) (tigrfc:1.) HI1239 HI1239 Haemophilus influenzae 727 10033262

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878724	14243	36399	213	70

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878725	14244	36400	351	116

Description

GTC ORF with score 207 to: (sr:chlamydia trachomatis (strain 12/434/bu) dna) (db:genpept-bct1) (de:chlamydia trachomatis alpha-operon, ribosomal protein s13, ribosomal protein s11, rna polymerase alpha-subunit, and ribosomalprotein 117 genes, complete ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878727	14245	36401	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878735	14246	36402	483	160

Description

6500733172 glnd:hi1719 uridylyl transferase (gtcfc:5.1) (ec:2.7.7.59) (keggfc:14.1) (tigrfc:1.4) (db:gtc-haemophilus influenzae) HI1719 HI1719 Haemophilus influenzae 727 -11537030 73981 glnd:hi1719 (ec:2.7.7.59) (de:transferase) (uridylyl removing enzyme) (utase)) (db:swissprot) GLND_HAEIN P43919 HAEMOPHILUS INFLUENZAE 727 -11537030 167259 uridylyltransferase homolog (cl:uridylyltransferase) (db:pir2.dat) B64138 B64138 Haemophilus influenzae 727 -11537030 7500882470 hi1719 uridylyl transferase glnd (db:genpept-bct1) (de:haemophilus influenzae rd section 159 of 163 of the completegenome.) (nt:similar to gb:m96431 sp:p27249 pid:146155 pid:49393) (le:8018) (re:10609) (di:complement) U32844 U32844 g1574572 Haemophilus influenzae Rd 71421 -11537030 5000694280 (de:(hi1719) (pn::uridylyl transferase:glnd) (gn:glnd) (gtcfc:5.1) (ec:2.7.7.59) (glnd_haein) (keggfc:11.1) (tigrfc:1.4) (db:gtc-haemophilus influenzae)) HI1719 HI1719 Haemophilus influenzae 727 10016511

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878739	14247	36403	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878742	14248	36404	309	102

Description

GTC ORF with score 163 to: (sr:caenorhabditis elegans strain=bristol n2) (db:genpept-inv) (de:caenorhabditis elegans cosmid f42g9.) (nt:coded for by c. elegans cdna yk89e10.5; coded for) (le:17600:17844) (re:17797:18251) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878759	14249	36405	195	64

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878772	14250	36406	630	209

Description

6500733173 argg:hi1727 argininosuccinate synthetase:argininosuccinate synthase:citrulline--aspartate ligase (gtcfc:5.1:5.10:5.16:5.2) (ec:6.3.4.5) (keggfc:5.2:5.10:5.16) (tigrfc:1.4) (db:gtc-haemophilus influenzae) HI1727 HI1727 Haemophilus influenzae 727 -11537031 60429 argg:hi1727 (ec:6.3.4.5) (de:ligase)) (db:swissprot) ASSY_HAEIN P44315 HAEMOPHILUS INFLUENZAE 727 -11537031 142420 argininosuccinate synthase::citrulline--aspartate ligase (cl:argininosuccinate synthase) (ec:6.3.4.5) (db:pir2.dat) F64138 F64138 Haemophilus influenzae 727 -11537031 7500877263 hi1727 argininosuccinate synthetase argg (db:genpept-bct1) (de:haemophilus influenzae rd section 160 of 163 of the completegenome.) (nt:similar to gb:m35236 sp:p22767 pid:145342) (le:6702) (re:8036) (di:direct) U32845 U32845 g1574583 Haemophilus influenzae Rd 71421 -11537031 5000694289 (de:(hi1727) (pn:argininosuccinate synthase:citrulline--aspartate ligase:argininosuccinate synthetase:argg) (gn:argg) (gtcfc:5.10:5.16:5.2) (ec:6.3.4.5) (assy_haein) (keggfc:5.2:5.10:5.16) (tigrfc:1.4) (db:gtc-haemophilus influe) HI1727 HI1727 Haemophilus influenzae 727 10003155

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878775	14251	36407	456	151

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878776	14252	36408	540	179

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878788	14253	36409	957	318

Description

6500733174 proc:hi0307 delta-1-pyrroline-5-carboxylate reductase:p5cr:p5c reductase (gtcfc:5.10:5.16:11.1) (ec:1.5.1.2) (keggfc:5.10:5.16) (tigrfc:14.7) (db:gtc-haemophilus influenzae) HI0307 HI0307 Haemophilus influenzae 727 -11537032 91183 proc:hi0307 (ec:1.5.1.2) (de:pyrroline-5-carboxylate reductase, (p5cr) (p5c reductase)) (db:swissprot) PROC_HAEIN P43869 HAEMOPHILUS INFLUENZAE 727 -11537032 166085 pyrroline-5-carboxylate reductase homolog (cl:pyrroline-5-carboxylate reductase) (db:pir2.dat) I64060 I64060 Haemophilus influenzae 727 -11537032 7500888538 hi0307 pyrroline-5-carboxylate reductase proc (db:genpept-bct1) (de:haemophilus influenzae rd section 31 of 163 of the complete genome.) (nt:similar to pid:801880 sp:p52053 pid:801881 percent) (le:6513) (re:7328) (di:direct) U32716 U32716 g1573276 Haemophilus influenzae Rd 71421 -11537032 5000694281 (de:(hi0307) (pn:pyrroline-5-carboxylate reductase:p5cr:p5c reductase:delta-1-pyrroline-5-carboxylate reductase:proc) (gn:proc) (gtcfc:5.10:5.16) (ec:1.5.1.2) (proc_haein) (keggfc:5.10:5.16) (tigrfc:14.7) (db:gtc-haemophilus inf) HI0307 HI0307 Haemophilus influenzae 727 10033282

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878807	14254	36410	465	155

Description

6500733175 spf:hi0591 ornithine decarboxylase (gtcfc:5.10:5.16:13.11) (ec:4.1.1.17) (keggfc:5.10:5.16) (tigrfc:5.4) (db:gtc-haemophilus influenzae) HI0591 HI0591 Haemophilus influenzae 727 -11537033 68085 spf:hi0591 (ec:4.1.1.17) (de:ornithine decarboxylase,) (db:swissprot) DCOR_HAEIN P44317 HAEMOPHILUS INFLUENZAE 727 -11537033 167054 ornithine decarboxylase (ec:4.1.1.17) (db:pir2.dat) F64079 F64079 Haemophilus influenzae 727 -11537033 7500880067 hi0591 ornithine decarboxylase spf (db:genpept-bct1) (de:haemophilus influenzae rd section 55 of 163 of the complete genome.) (nt:similar to gb:m64495 sp:p24169 pid:147331 gb:u00096) (le:9307) (re:11469) (di:complement) U32740 U32740 g1573581 Haemophilus influenzae Rd 71421 -11537033 5000694282 (de:(hi0591) (pn:ornithine decarboxylase:spf) (gn:spf) (gtcfc:5.10:5.16) (ec:4.1.1.17) (dcor_haein) (keggfc:5.10:5.16) (tigrfc:5.4) (db:gtc-haemophilus influenzae)) HI0591 HI0591 Haemophilus influenzae 727 10010678

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878810	14255	36411	543	180
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878812	14256	36412	297	98
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878813	14257	36413	306	101
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878822	14258	36414	234	77
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878827	14259	36415	555	184
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878834	14260	36416	273	90
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878855	14261	36417	528	175

Description

6500733176 pepd:hi0675 aminoacyl-histidine dipeptidase:xaa-his dipeptidase:x-his dipeptidase:beta-alanyl-histidine dipeptidase:carnosinase:peptidase d (gtcfc:5.10:5.11:5.2:6.1:10.11) (ec:3.4.13.3) (keggfc:5.2:5.10:5.11:6.1) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0675 HI0675 Haemophilus influenzae 727 -11537034 167073 x-his dipeptidase::aminoacylhistidine dipeptidase:aminopeptidase d:beta-alanyl-histidine dipeptidase:carnosinase (ec:3.4.13.3) (db:pir2.dat) E64085 E64085 Haemophilus influenzae 727 -11537034 7500960747 hi0675 aminoacyl-histidine dipeptidase pepd (db:genpept-bct1) (de:haemophilus influenzae rd section 65 of 163 of the complete genome.) (nt:similar to gb:m34034 sp:p15288 gb:x14790) (le:3728) (re:5182) (di:direct) U32750 U32750 g1573675 Haemophilus influenzae Rd 71421 -11537034 5000694284 (de:(hi0675) (pn:aminoacyl-histidine dipeptidase:xaa-his dipeptidase:x-his dipeptidase:beta-alanyl-histidine dipeptidase:carnosinase:peptidase d:pepd) (gn:pepd) (gtcfc:5.10:5.11:5.2:6.1) (ec:3.4.13.3) (pepd_haein) (keggfc:5.2:5.1) HI0675 HI0675 Haemophilus influenzae 727 10088278

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878863	14262	36418	837	278

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878864	14263	36419	483	160

Description

6500733177 pros:hi0729 prolyl-trna synthetase:proline--trna ligase:prors (gtcfc:5.10:10.6) (ec:6.1.1.15) (keggfc:5.10:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0729 HI0729 Haemophilus influenzae 727 -11537035 100147 pros:hi0729 (ec:6.1.1.15) (de:prolyl-trna synthetase, (proline--trna ligase) (prors)) (db:swissprot) SYP_HAEIN P43830 HAEMOPHILUS INFLUENZAE 727 -11537035 142292 pros proline--trna ligase::prolyl-trna synthetase (cl:proline--trna ligase) (ec:6.1.1.15) (db:pir2.dat) C64089 C64089 Haemophilus influenzae 727 -11537035 7500892544 hi0729 prolyl-trna synthetase pros (db:genpept-bct1) (de:haemophilus influenzae rd section 71 of 163 of the complete genome.) (nt:similar to gb:m97858 sp:p16659 gb:m32357 gb:x55518) (le:4652) (re:6370) (di:direct) U32756 U32756 g1573733 Haemophilus influenzae Rd 71421 -11537035 5000694285 (de:(hi0729) (pn:proline--trna ligase:prors:prolyl-trna synthetase:pros) (gn:pros) (gtcfc:5.10:10.6) (ec:6.1.1.15) (syp_haein) (keggfc:5.10:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0729 HI0729 Haemophilus influenzae 727 10042001

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878891	14264	36420	369	122

Description

5000694287 lpxc:enva:hi1144 udp-3-0-acyl n-acetylglucosamine deacetylase:enva:udp-3-o- (gtcfc:5.10:5.11:7.1:9.4:9.5:11.2) (ec:3.5.1.-) (keggfc:4.4:5.10:5.11:9.4:9.5) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1144 HI1144 Haemophilus influenzae 727 -11537036 82460 lpxc:enva:hi1144 (ec:3.5.1.-) (de:(ec 3.5.1.-)) (db:swissprot) LPXC_HAEIN P45070 HAEMOPHILUS INFLUENZAE 727 -11537036 154440 enva udp-3-o-3-hydroxymyristoyl n-acetylglucosamine deacetylase,) (cl:enva protein) (ec:3.5.1.-) (db:pir2.dat) A64186 A64186 Haemophilus influenzae 727 -11537036 7500885146 hi1144 udp-3-0-3-hydroxymyristoyl n-acetylglucosamine (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p07652 pid:145848) (le:5966) (re:6883) (di:direct) U32794 U32794 g1574700 Haemophilus influenzae Rd 71421 -11537036 6500733178 lpxc:enva udp-3-0-acyl n-acetylglucosamine deacetylase:enva:udp-3-o- (gtcfc:5.10:5.11:7.1:9.4:9.5:11.2) (ec:3.5.1.-) (keggfc:4.4:5.10:5.11:9.4:9.5) (tigrfc:3.3) (db:gtc-haemophilus influenzae) HI1144 HI1144 Haemophilus influenzae 727 -11537036

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878893	14265	36421	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878899	14266	36422	669	223

Description

6500733179 args:hi1583 arginyl-trna synthetase:arginine--trna ligase:argrs (gtcfc:5.10:10.6) (ec:6.1.1.19) (keggfc:5.10:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1583 HI1583 Haemophilus influenzae 727 -11537037 100165 args:hi1583 (ec:6.1.1.19) (de:arginyl-trna synthetase, (arginine--trna ligase) (argrs)) (db:swissprot) SYR_HAEIN P43832 HAEMOPHILUS INFLUENZAE 727 -11537037 142298 args arginine--trna ligase::arginyl-trna synthetase (cl:arginine--trna ligase) (ec:6.1.1.19) (db:pir2.dat) A64131 A64131 Haemophilus influenzae 727 -11537037 7500892562 hi1583 arginyl-trna synthetase args (db:genpept-bct1) (de:haemophilus influenzae rd section 147 of 163 of the completegenome.) (nt:similar to sp:p11875 gb:x15320 pid:581040 gb:u00096) (le:3236) (re:4969) (di:direct) U32832 U32832 g1574424 Haemophilus influenzae Rd 71421 -11537037 5000694288 (de:(hi1583) (pn:arginine--trna ligase:argrs:arginyl-trna synthetase:args) (gn:args) (gtcfc:5.10:10.6) (ec:6.1.1.19) (syr_haein) (keggfc:5.10:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI1583 HI1583 Haemophilus influenzae 727 10042019

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878915	14267	36423	222	73

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878916	14268	36424	264	87

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878918	14269	36425	405	134

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878919	14270	36426	1182	394

Description

6500733180 hiss:hi0369 histidine-trna synthetase:histidyl-trna synthetase:histidine--trna ligase:hisrs (gtcfc:5.11:10.6) (ec:6.1.1.21) (keggfc:5.11:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0369 HI0369 Haemophilus influenzae 727 -11537038 142304 hiss histidine--trna ligase::histidine-trna synthetase (cl:histidine--trna ligase:amino acid--trna ligase repeat homology:histidine--trna ligase homology) (ec:6.1.1.21) (db:pir2.dat) I64063 I64063 Haemophilus influenzae 727 -11537038 7500954490 hi0369 histidyl-trna synthetase hiss (db:genpept-bct1) (de:haemophilus influenzae rd section 36 of 163 of the complete genome.) (nt:similar to gb:m11843 sp:p04804 pid:146372 gb:u00096) (le:2729) (re:4000) (di:direct) U32721 U32721 g1573338 Haemophilus influenzae Rd 71421 -11537038 5000694290 (de:(hi0369) (pn:histidyl-trna synthetase:histidine--trna ligase:hisrs:histidine-trna synthetase:hiss) (gn:hiss) (gtcfc:5.11:10.6) (ec:6.1.1.21) (syh_haein) (keggfc:5.11:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0369 HI0369 Haemophilus influenzae 727 10072858

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878934	14271	36427	1434	477

Description

6500733181 hisg:hi0468 atp phosphoribosyltransferase (gtcfc:5.11)
(ec:2.4.2.17) (keggfc:5.11) (tigrfc:1.7) (db:gtc-haemophilus influenzae)
HI0468 HI0468 Haemophilus influenzae 727 -11537039 76992 hisg:hi0468
(ec:2.4.2.17) (de:atp phosphoribosyltransferase,) (db:swissprot) HIS1_HAEIN
P43853 HAEMOPHILUS INFLUENZAE 727 -11537039 138160 atp
phosphoribosyltransferase (cl:atp phosphoribosyltransferase) (ec:2.4.2.17)
(db:pir2.dat) D64070 D64070 Haemophilus influenzae 727 -11537039 7500883268
hi0468 atp phosphoribosyltransferase hisg (db:genpept-bct1) (de:haemophilus
influenzae rd section 44 of 163 of the complete genome.) (nt:similar to
sp:p10366 gb:u02070 gb:x63697 pid:41022) (le:8066) (re:8977) (di:direct)
U32729 U32729 g1573446 Haemophilus influenzae Rd 71421 -11537039 5000694291
(de:(hi0468) (pn:atp phosphoribosyltransferase:hisg) (gn:hisg) (gtcfc:5.11)
(ec:2.4.2.17) (his1_haein) (keggfc:5.11) (tigrfc:1.7) (db:gtc-haemophilus
influenzae)) HI0468 HI0468 Haemophilus influenzae 727 10019354

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878937	14272	36428	1476	491

Description

6500733182 hisd:hi0469 histidinol dehydrogenase:hdh (gtcfc:5.11)
(ec:1.1.1.23) (keggfc:5.11) (tigrfc:1.7) (db:gtc-haemophilus influenzae)
HI0469 HI0469 Haemophilus influenzae 727 -11537040 77076 hisd:hi0469
(ec:1.1.1.23) (de:histidinol dehydrogenase, (hdh)) (db:swissprot) HISX_HAEIN
P44001 HAEMOPHILUS INFLUENZAE 727 -11537040 136179 histidinol
dehydrogenase::protein hi0469 (cl:histidinol dehydrogenase:histidinol
dehydrogenase homology) (ec:1.1.1.23) (db:pir2.dat) A64008 A64008
Haemophilus influenzae 727 -11537040 7500883346 hi0469 histidinol
dehydrogenase hisd (db:genpept-bct1) (de:haemophilus influenzae rd section
44 of 163 of the complete genome.) (nt:similar to sp:p06988 gb:x03972
gb:x52656 pid:41698) (le:9070) (re:10353) (di:direct) U32729 U32729 g1573447
Haemophilus influenzae Rd 71421 -11537040 5000694292 (de:(hi0469)
(pn:hdh:histidinol dehydrogenase:hisd) (gn:hisd) (gtcfc:5.11) (ec:1.1.1.23)
(hisx_haein) (keggfc:5.11) (tigrfc:1.7) (db:gtc-haemophilus influenzae))
HI0469 HI0469 Haemophilus influenzae 727 10019438

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878938	14273	36429	1554	517

Description

6500733183 hisc:hi0470 histidinol-phosphate aminotransferase:imidazole acetol-phosphate transaminase (gtcfc:5.11) (ec:2.6.1.9) (keggfc:5.11) (tigrfc:1.7) (db:gtc-haemophilus influenzae) HI0470 HI0470 Haemophilus influenzae 727 -11537041 77054 hisc:hi0470 (ec:2.6.1.9) (de:phosphate transaminase) (db:swissprot) HIS8_HAEIN P44423 HAEMOPHILUS INFLUENZAE 727 -11537041 138401 histidinol-phosphate transaminase (cl:histidinol-phosphate aminotransferase) (ec:2.6.1.9) (db:pir2.dat) E64070 E64070 Haemophilus influenzae 727 -11537041 7500883316 hi0470 histidinol-phosphate aminotransferase hisc (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:similar to sp:p06986 gb:u02071 gb:x03416 pid:41695) (le:65) (re:1168) (di:direct) U32730 U32730 g1573449 Haemophilus influenzae Rd 71421 -11537041 5000694293 (de:(hi0470) (pn:imidazole acetol- phosphate transaminase:histidinol-phosphate aminotransferase:hisc) (gn:hisc) (gtcfc:5.11) (ec:2.6.1.9) (his8_haein) (keggfc:5.11) (tigrfc:1.7) (db:gtc-haemophilus influenzae)) HI0470 HI0470 Haemophilus influenzae 727 10019416

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878941	14274	36430	216	71

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501878942	14275	36431	687	228

Description

6500733184 hisb:hi0471 imidazoleglycerol-phosphate dehydratase:igpd / histidinol-phosphatase (gtcfc:5.11) (keggfc:5.11) (tigrfc:1.7) (db:gtc-haemophilus influenzae) HI0471 HI0471 Haemophilus influenzae 727 -11537042 77040 hisb:hi0471 (ec:4.2.1.19:3.1.3.15) (de:histidinol-phosphatase,) (db:swissprot) HIS7_HAEIN P44327 HAEMOPHILUS INFLUENZAE 727 -11537042 141895 hisb bifunctional enzyme (cl:hisb bifunctional enzyme:imidazoleglycerol-phosphate dehydratase homology) (db:pir2.dat) F64070 F64070 Haemophilus influenzae 727 -11537042 7500883307 hi0471 imidazoleglycerol-phosphate dehydratase / (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the complete genome.) (nt:similar to sp:p06987 gb:x03416 pid:41696 pid:41711) (le:1280) (re:2368) (di:direct) U32730 U32730 g1573450 Haemophilus influenzae Rd 71421 -11537042 5000694294 (de:(hi0471) (pn:igpd :imidazoleglycerol-phosphate dehydratase:hisb) (gn:hisb) (gtcfc:5.11) (ec:4.2.1.19) (his7_haein) (keggfc:5.11) (tigrfc:1.7) (db:gtc-haemophilus influenzae)) HI0471 HI0471 Haemophilus influenzae 727 10019402

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878946	14276	36432	294	97
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878949	14277	36433	1428	475
<u>Description</u>				

6500733185 hish:hi0472 amidotransferase (gtcfc:5.11) (ec:2.4.2.-)
(keggfc:5.11) (tigrfc:1.7) (db:gtc-haemophilus influenzae) HI0472 HI0472
Haemophilus influenzae 727 -11537043 77023 hish:hi0472 (ec:2.4.2.-)
(de:amidotransferase hish,) (db:swissprot) HIS5_HAEIN P44340 HAEMOPHILUS
INFLUENZAE 727 -11537043 138180 amidotransferase hish (cl:amidotransferase
hish) (ec:2.4.2.-) (db:pir2.dat) G64070 G64070 Haemophilus influenzae 727
-11537043 7500883302 hi0472 amidotransferase hish (db:genpept-bct1)
(de:haemophilus influenzae rd section 45 of 163 of the complete genome.)
(nt:similar to sp:p10375 pid:41712 gb:u00096) (le:2434) (re:3033)
(di:direct) U32730 U32730 g1573451 Haemophilus influenzae Rd 71421 -11537043
5000694295 (de:(hi0472) (pn:amidotransferase :amidotransferase:hish)
(gn:hish) (gtcfc:5.11) (ec:2.4.2.-) (his5_haein) (keggfc:5.11) (tigrfc:1.7)
(db:gtc-haemophilus influenzae)) HI0472 HI0472 Haemophilus influenzae 727
10019385

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878957	14278	36434	648	215
<u>Description</u>				

6500733186 hisa:hi0473 phosphoribosylformimino-5-aminoimidazole carboxamide
ribotide isomerase (gtcfc:5.11) (ec:5.3.1.16) (keggfc:5.11) (tigrfc:1.7)
(db:gtc-haemophilus influenzae) HI0473 HI0473 Haemophilus influenzae 727
-11537044 77013 hisa:hi0473 (ec:5.3.1.16) (de:isomerase,) (db:swissprot)
HIS4_HAEIN P44435 HAEMOPHILUS INFLUENZAE 727 -11537044 142149
n-5-phospho-d-ribosylformimino -5-amino-1- 5-phosphoribosyl
-4-imidazolecarboxamide isomerase
(cl:n-(5'-phospho-d-ribosylformimino)-5-amino-1-
(5''-phosphoribosyl)-4-imidazolecarboxamide isomerase) (ec:5.3.1.16)
(db:pir2.dat) H64070 H64070 Haemophilus influenzae 727 -11537044 7500883295
hi0473 phosphoribosylformimino-5-aminoimidazole (db:genpept-bct1)
(de:haemophilus influenzae rd section 45 of 163 of the complete genome.)
(nt:similar to sp:p10371 pid:41713 gb:u00096) (le:3069) (re:3818)
(di:direct) U32730 U32730 g1573452 Haemophilus influenzae Rd 71421 -11537044
5000694296 (de:(hi0473) (pn:phosphoribosylformimino-5-aminoimidazole
carboxamide ribotide isomerase:hisa) (gn:hisa) (gtcfc:5.11) (ec:5.3.1.16)
(his4_haein) (keggfc:5.11) (tigrfc:1.7) (db:gtc-haemophilus influenzae))
HI0473 HI0473 Haemophilus influenzae 727 10019375

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878973	14279	36435	297	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501878981	14280	36436	246	81

Description

5000694297 hisi:hisie:hi0475 phosphoribosyl-amp
cyclohydrolase:hisie:phosphoribosyl-amp cyclohydrolase / phosphoribosyl-atp
pyrophosphohydrolase (gtcfc:5.11) (keggfc:5.11) (tigrfc:1.7)
(db:gtc-haemophilus influenzae) HI0475 HI0475 Haemophilus influenzae 727
-11537045 77002 hisi:hisie:hi0475 (ec:3.5.4.19:3.6.1.31)
(de:pyrophosphohydrolase,) (db:swissprot) HIS2_HAEIN P44434 HAEMOPHILUS
INFLUENZAE 727 -11537045 140982 phosphoribosyl-amp
cyclohydrolase:phosphoribosyl-atp pyrophosphatase (cl:hisi bifunctional
enzyme:hisi bifunctional enzyme homology:hisi protein homology)
(ec:3.5.4.19:3.6.1.31) (db:pir2.dat) A64071 A64071 Haemophilus influenzae
727 -11537045 7500883288 hi0475 phosphoribosyl-amp cyclohydrolase /
(db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of the
complete genome.) (nt:similar to sp:p06989 gb:d43637 gb:u02072 gb:x03974)
(le:4576) (re:5241) (di:direct) U32730 U32730 g1573454 Haemophilus
influenzae Rd 71421 -11537045 6500733187 hisi:hisie phosphoribosyl-amp
cyclohydrolase:hisie:phosphoribosyl-amp cyclohydrolase / phosphoribosyl-atp
pyrophosphohydrolase (gtcfc:5.11) (keggfc:5.11) (tigrfc:1.7)
(db:gtc-haemophilus influenzae) HI0475 HI0475 Haemophilus influenzae 727
-11537045

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879008	14281	36437	252	83

Description

6500733188 gamma-aminobutyric acid transaminase:gabt:hypothetical
aminotransferase hi0949 (gtcfc:5.11:5.16:5.8) (ec:2.6.1.-) (keggfc:5.8:5.11)
(tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0949 HI0949 Haemophilus
influenzae 727 -11537046 109330 hi0949 (ec:2.6.1.-) (de:hypothetical
aminotransferase hi0949,) (db:swissprot) Y949_HAEIN P44951 HAEMOPHILUS
INFLUENZAE 727 -11537046 166150 gamma-aminobutyrate aminotransferase
(ec:2.6.1.-) (db:pir2.dat) C64104 C64104 Haemophilus influenzae 727
-11537046 7500895721 gamma-aminobutyrate aminotransferase (ec:2.6.1.-)
(db:pir) JC5879 JC5879 Haemophilus influenzae 727 -11537046 7500895722
hi0949 aminotransferase (db:genpept-bct1) (de:haemophilus influenzae rd
section 91 of 163 of the complete genome.) (nt:similar to pid:2340815
percent ident: 71.85;) (le:3448) (re:4812) (di:complement) U32776 U32776
g1573974 Haemophilus influenzae Rd 71421 -11537046 5000694298 (de:(hi0949)
(pn:hypothetical aminotransferase hi0949:gamma-aminobutyric acid
transaminase:gabt) (gtcfc:5.11) (ec:2.6.1.-) (y949_haein) (keggfc:5.8:5.11)
(tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI0949 HI0949 Haemophilus
influenzae 727 10051062

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879009	14282	36438	1485	495

Description

6500733189 hisf:hi0474 hisf cyclase:protein:cyclase (gtcfc:5.11)
(keggfc:14.2) (tigrfc:1.7) (db:gtc-haemophilus influenzae) HI0474 HI0474
Haemophilus influenzae 727 -11537047 77030 hisf:hi0474 (de:hisf protein
(cyclase)) (db:swissprot) HIS6_HAEIN P44436 HAEMOPHILUS INFLUENZAE 727
-11537047 142048 hisf cyclase hisf (cl:cyclase hisf) (db:pir2.dat) I64070
I64070 Haemophilus influenzae 727 -11537047 7500883304 hi0474 hisf cyclase
hisf (db:genpept-bct1) (de:haemophilus influenzae rd section 45 of 163 of
the complete genome.) (nt:similar to sp:p10373 pid:41714 pid:598474
gb:u00096) (le:3800) (re:4576) (di:direct) U32730 U32730 g1573453
Haemophilus influenzae Rd 71421 -11537047 5000694299 (de:(hi0474)
(pn:protein:cyclase:hisf cyclase:hisf) (gn:hisf) (gtcfc:5.11) (ec:)
(his6_haein) (keggfc:11.2) (tigrfc:1.7) (db:gtc-haemophilus influenzae))
HI0474 HI0474 Haemophilus influenzae 727 10019392

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879013	14283	36439	552	183

Description

6500733190 hish:hi1166 histidinol-phosphate aminotransferase (gtcfc:5.11) (keggfc:14.2) (tigrfc:1.7) (db:gtc-haemophilus influenzae) HI1166 HI1166 Haemophilus influenzae 727 -11537048 4000707559 hi1166 (ec:2.6.1.-) (de:probable aminotransferase hi1166,) (db:swissprot) YB66_HAEIN Q57004 HAEMOPHILUS INFLUENZAE 727 -11537048 166202 histidinol-phosphate transaminase homolog (cl:probable histidinol-phosphate transaminase) (db:pir2.dat) D64187 D64187 Haemophilus influenzae 727 -11537048 7500896429 hi1166 histidinol-phosphate aminotransferase hish (db:genpept-bct1) (de:haemophilus influenzae rd section 111 of 163 of the completegenome.) (nt:similar to sp:p17731 pid:143814 gb:al009126 percent) (le:7547) (re:8647) (di:complement) U32796 U32796 g1574093 Haemophilus influenzae Rd 71421 -11537048 5000694300 (de:(hi1166) (pn:histidinol-phosphate aminotransferase:hish) (gn:hish) (gtcfc:5.11) (ec:) (keggfc:11.2) (tigrfc:1.7) (db:gtc-haemophilus influenzae)) HI1166 HI1166 Haemophilus influenzae 727 10088105

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879017	14284	36440	1734	577

Description

6500733191 trps:hi0637 tryptophanyl-trna synthetase:tryptophan--trna ligase:trprs (gtcfc:5.14:10.6) (ec:6.1.1.2) (keggfc:5.14:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0637 HI0637 Haemophilus influenzae 727 -11537049 100231 trps:hi0637 (ec:6.1.1.2) (de:(trprs)) (db:swissprot) SYW_HAEIN P43835 HAEMOPHILUS INFLUENZAE 727 -11537049 142244 trps tryptophan--trna ligase::tryptophanyl-trna synthetase (cl:tryptophan--trna ligase) (ec:6.1.1.2) (db:pir2.dat) C64083 C64083 Haemophilus influenzae 727 -11537049 7500892636 hi0637 tryptophanyl-trna synthetase trps (db:genpept-bct1) (de:haemophilus influenzae rd section 61 of 163 of the complete genome.) (nt:similar to sp:p00954 gb:v00370 gb:v00371 gb:z19601) (le:9535) (re:10539) (di:complement) U32746 U32746 g1573633 Haemophilus influenzae Rd 71421 -11537049 5000694585 (de:(hi0637) (pn:tryptophan--trna ligase:trprs:tryptophanyl-trna synthetase:trps) (gn:trps) (gtcfc:10.6) (ec:6.1.1.2) (syw_haein) (keggfc:5.14:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0637 HI0637 Haemophilus influenzae 727 10042085

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879027	14285	36441	948	316

Description

GTC ORF with score 141 to: (sr:caenorhabditis elegans strain=bristol n2)
(db:genpept-inv) (de:caenorhabditis elegans cosmid k06a9.) (nt:partial cds;
coded for by c. elegans cdna yk50c7.5) (le:27212:27374:27536:27666)
(re:27323:27486:27619:27751) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879029	14286	36442	672	223

Description

6500733192 aroc:hi0196 chorismate
synthase:5-enolpyruvylshikimate-3-phosphate phospholyase (gtcfc:5.15)
(ec:4.6.1.4) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae)
HI0196 HI0196 Haemophilus influenzae 727 -11537050 60182 aroc:hi0196
(ec:4.6.1.4) (de:phospholyase)) (db:swissprot) AROC_HAEIN P43875 HAEMOPHILUS
INFLUENZAE 727 -11537050 142051 chorismate synthase (cl:chorismate
synthase) (ec:4.6.1.4) (db:pir2.dat) G64053 G64053 Haemophilus influenzae
727 -11537050 7500877174 hi0196 chorismate synthase aroc (db:genpept-bct1)
(de:haemophilus influenzae rd section 19 of 163 of the complete genome.)
(nt:similar to gb:m27714 sp:p12008 gb:m33021 gb:y00720) (le:11376)
(re:12449) (di:direct) U32704 U32704 g1573154 Haemophilus influenzae Rd
71421 -11537050 5000694301 (de:(hi0196)
(pn:5-enolpyruvylshikimate-3-phosphate phospholyase:chorismate
synthase:aroc) (gn:aroc) (gtcfc:5.15) (ec:4.6.1.4) (aroc_haein)
(keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae)) HI0196 HI0196
Haemophilus influenzae 727 10002908

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879048	14287	36443	354	117

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879068	14288	36444	1191	396

Description

6500733193 arok:hi0207 shikimic acid kinase i:shikimate kinase:sk
 (gtcfc:5.15) (ec:2.7.1.71) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus
 influenzae) HI0207 HI0207 Haemophilus influenzae 727 -11537051 60223
 arok:hi0207 (ec:2.7.1.71) (de:shikimate kinase, (sk)) (db:swissprot)
 AROK_HAEIN P43880 HAEMOPHILUS INFLUENZAE 727 -11537051 138906 shikimate
 kinase (cl:shikimate kinase:shikimate kinase homology) (ec:2.7.1.71)
 (db:pir2.dat) F64054 F64054 Haemophilus influenzae 727 -11537051 7500877191
 hi0207 shikimic acid kinase i arok (db:genpept-bct1) (de:haemophilus
 influenzae rd section 20 of 163 of the complete genome.) (nt:similar to
 sp:p24167 percent identity: 71.93;) (le:9098) (re:9640) (di:direct) U32705
 U32705 g1573166 Haemophilus influenzae Rd 71421 -11537051 5000694302
 (de:(hi0207) (pn:shikimate kinase:sk:shikimic acid kinase i:arok) (gn:arok)
 (gtcfc:5.15) (ec:2.7.1.71) (arok_haein) (keggfc:5.15) (tigrfc:1.1)
 (db:gtc-haemophilus influenzae)) HI0207 HI0207 Haemophilus influenzae 727
 10002949

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879072	14289	36445	321	106

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879079	14290	36446	339	112

Description

6500733194 arob:hi0208 3-dehydroquinate synthase (gtcfc:5.15) (ec:4.6.1.3)
 (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI0208 HI0208
 Haemophilus influenzae 727 -11537052 60176 arob:hi0208 (ec:4.6.1.3)
 (de:3-dehydroquinate synthase,) (db:swissprot) AROB_HAEIN P43879 HAEMOPHILUS
 INFLUENZAE 727 -11537052 142050 3-dehydroquinate synthase
 (cl:3-dehydroquinate synthase:3-dehydroquinate synthase homology)
 (ec:4.6.1.3) (db:pir2.dat) G64054 G64054 Haemophilus influenzae 727
 -11537052 7500877169 hi0208 3-dehydroquinate synthase arob
 (db:genpept-bct1) (de:haemophilus influenzae rd section 20 of 163 of the
 complete genome.) (nt:similar to sp:p07639 gb:x03867 gb:z19601 pid:40968)
 (le:9660) (re:10748) (di:direct) U32705 U32705 g1573167 Haemophilus
 influenzae Rd 71421 -11537052 5000694303 (de:(hi0208) (pn:3-dehydroquinate
 synthase:arob) (gn:arob) (gtcfc:5.15) (ec:4.6.1.3) (arob_haein)
 (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae)) HI0208 HI0208
 Haemophilus influenzae 727 10002902

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879080	14291	36447	879	292

Description

6500733195 aroe:hi0655 shikimate 5-dehydrogenase (gtcfc:5.15) (ec:1.1.1.25) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI0655 HI0655 Haemophilus influenzae 727 -11537053 60199 aroe:hi0655 (ec:1.1.1.25) (de:shikimate 5-dehydrogenase,) (db:swissprot) AROE_HAEIN P43876 HAEMOPHILUS INFLUENZAE 727 -11537053 167157 shikimate 5-dehydrogenase homolog (cl:shikimate dehydrogenase:shikimate dehydrogenase homology) (db:pir2.dat) H64084 H64084 Haemophilus influenzae 727 -11537053 7500877182 hi0655 shikimate 5-dehydrogenase aroe (db:genpept-bct1) (de:haemophilus influenzae rd section 63 of 163 of the complete genome.) (nt:similar to sp:p15770 gb:y00710 pid:40978 pid:606215) (le:7327) (re:8145) (di:complement) U32748 U32748 g1573654 Haemophilus influenzae Rd 71421 -11537053 5000694304 (de:(hi0655) (pn:shikimate 5-dehydrogenase:aro) (gn:aro) (gtcfc:5.15) (ec:1.1.1.25) (aro_haein) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae)) HI0655 HI0655 Haemophilus influenzae 727 10002925

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879100	14292	36448	783	260

Description

6500733196 aroq:hi0970 3-dehydroquinate dehydratase:3-dehydroquinase (gtcfc:5.15) (ec:4.2.1.10) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI0970 HI0970 Haemophilus influenzae 727 -11537054 60192 aroq:hi0970 (ec:4.2.1.10) (de:3-dehydroquinate dehydratase, (3-dehydroquinase)) (db:swissprot) AROD_HAEIN P43878 HAEMOPHILUS INFLUENZAE 727 -11537054 141819 3-dehydroquinate dehydratase (cl:catabolic 3-dehydroquinate dehydratase) (ec:4.2.1.10) (db:pir2.dat) D64105 D64105 Haemophilus influenzae 727 -11537054 7500877178 hi0970 3-dehydroquinase aroq (db:genpept-bct1) (de:haemophilus influenzae rd section 92 of 163 of the complete genome.) (nt:similar to gb:l19895 sp:p43877 pid:469174 percent) (le:11949) (re:12398) (di:direct) U32777 U32777 g1573993 Haemophilus influenzae Rd 71421 -11537054 5000694305 (de:(hi0970) (pn:3-dehydroquinate dehydratase:3-dehydroquinase:aroq) (gn:aroq) (gtcfc:5.15) (ec:4.2.1.10) (arod_haein) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae)) HI0970 HI0970 Haemophilus influenzae 727 10002918

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879103	14293	36449	348	115

Description

GTC ORF with score 424 to: (fn:atp:d-pantothenate 4'-phosphotransferase) (db:genpept) (ec:2.7.1.33) (de:emerella nidulans pantothenate kinase (pank) gene, complete cds.) (le:198:537:883:1429) (re:410:819:1381:1696) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879106	14294	36450	192	63

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879112	14295	36451	387	128

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879119	14296	36452	1224	407

Description

6500733197 phea:hi1145 chorismate mutase/prephenate dehydratase:chorismate mutase:cm / prephenate dehydratase:pdt:p-protein (gtcfc:5.15) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI1145 HI1145 Haemophilus influenzae 727 -11537055 89525 phea:hi1145 (ec:5.4.99.5:4.2.1.51) (de:(ec 4.2.1.51) (pdt) (p-protein)) (db:swissprot) PHEA_HAEIN P43900 HAEMOPHILUS INFLUENZAE 727 -11537055 125845 chorismate mutase:p / prephenate dehydratase (cl:phea bifunctional enzyme:prephenate dehydratase homology) (ec:5.4.99.5:4.2.1.51) (db:pir1.dat) B64186 B64186 Haemophilus influenzae 727 -11537055 7500888017 hi1145 chorismate mutase / prephenate dehydratase (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to sp:q02286 gb:m74134 gb:x60420 pid:148468) (le:7010) (re:8167) (di:direct) U32794 U32794 g1574701 Haemophilus influenzae Rd 71421 -11537055 5000694306 (de:(hi1145) (pn:cm :chorismate mutase) (gn:phea) (gtcfc:5.15) (ec:5.4.99.5) (phea_haein) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae)) HI1145 HI1145 Haemophilus influenzae 727 10031647

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879142	14297	36453	297	98

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879150	14298	36454	1029	342

Description

6500733198 trpg:hi1171 anthranilate synthase glutamine amidotransferase:anthranilate synthase component ii:glutamine amido-transferase (gtcfc:5.15:9.12) (ec:4.1.3.27) (keggfc:5.15:9.13) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI1171 HI1171 Haemophilus influenzae 727 -11537056 102438 trpg:hi1171 (ec:4.1.3.27) (de:transferase)) (db:swissprot) TRPG_HAEIN P44339 HAEMOPHILUS INFLUENZAE 727 -11537056 166003 anthranilate synthase component ii homolog hi1171:trpg protein homolog (cl:glutamine amidotransferase:trpg homology) (db:pir2.dat) G64187 G64187 Haemophilus influenzae 727 -11537056 7500893497 hi1171 anthranilate synthase component ii trpg (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:similar to gb:m36636 sp:p00902 pid:141800 percent) (le:2105) (re:2686) (di:direct) U32797 U32797 g1574098 Haemophilus influenzae Rd 71421 -11537056 5000694307 (de:(hi1171) (pn:anthranilate synthase component ii:glutamine amido-transferase:anthranilate synthase glutamine amidotransferase:trpg) (gn:trpg) (gtcfc:5.15:9.12) (ec:4.1.3.27) (trpg_haein) (keggfc:5.15:9.13) (tigrfc:1.1) (db:g) HI1171 HI1171 Haemophilus influenzae 727 10044257

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879153	14299	36455	813	270

Description

6500733199 tyra:hi1290 chorismate mutase:cm / prephenate dehydrogenase:pdh:t-protein (gtcfc:5.15) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI1290 HI1290 Haemophilus influenzae 727 -11537057 102907 tyra:hi1290 (ec:5.4.99.5:1.3.1.12) (de:(ec 1.3.1.12) (pdh) (t-protein)) (db:swissprot) TYRA_HAEIN P43902 HAEMOPHILUS INFLUENZAE 727 -11537057 125842 chorismate mutase:t / prephenate dehydrogenase (cl:tyra bifunctional enzyme) (ec:5.4.99.5:1.3.1.12) (db:pir1.dat) H64114 H64114 Haemophilus influenzae 727 -11537057 7500893607 hi1290 chorismate mutase / prephenate dehydrogenase (db:genpept-bct1) (de:haemophilus influenzae rd section 124 of 163 of the completegenome.) (nt:similar to sp:q02287 gb:m74135 gb:x60420 pid:415010) (le:1672) (re:2805) (di:direct) U32809 U32809 g1574749 Haemophilus influenzae Rd 71421 -11537057 5000694308 (de:(hi1290) (pn:cm :chorismate mutase:tyra) (gn:tyra) (gtcfc:5.15) (ec:5.4.99.5) (tyra_haein) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae)) HI1290 HI1290 Haemophilus influenzae 727 10044719

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879157	14300	36456	300	99

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879164	14301	36457	2376	791

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879174	14302	36458	633	210

Description

6500733200 phes:hi1311 phenylalanyl-trna synthetase
beta-subunit:phenylalanyl-trna synthetase alpha chain:phenylalanine--trna
ligase alpha chain:phers (gtcfc:5.15:10.6) (ec:6.1.1.20)
(keggfc:5.15:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1311
HI1311 Haemophilus influenzae 727 -11537058 100029 phes:hi1311
(ec:6.1.1.20) (de:-trna ligase alpha chain) (phers)) (db:swissprot)
SYFA_HAEIN P43819 HAEMOPHILUS INFLUENZAE 727 -11537058 142300 phes
phenylalanine--trna ligase:alpha chain:phenylalanyl-trna synthetase alpha
chain (cl:phenylalanine--trna ligase alpha chain) (ec:6.1.1.20)
(db:pir2.dat) H64115 H64115 Haemophilus influenzae 727 -11537058 7500892385
hi1311 phenylalanyl-trna synthetase:alpha subunit (db:genpept-bct1)
(de:haemophilus influenzae rd section 125 of 163 of the completegenome.)
(nt:similar to gb:v00291 sp:p08312 pid:146345 pid:43070) (le:6786) (re:7775)
(di:direct) U32810 U32810 g1574769 Haemophilus influenzae Rd 71421 -11537058
5000694309 (de:(hi1311) (pn:phenylalanyl-trna synthetase alpha
chain:phenylalanine--trna ligase alpha chain:phers:phenylalanyl-trna
synthetase beta-subunit:phes) (gn:phes) (gtcfc:5.15:10.6) (ec:6.1.1.20)
(syfa_haein) (keggfc:5.15:10.1:10.2)) HI1311 HI1311 Haemophilus influenzae
727 10041883

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879177	14303	36459	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879189	14304	36460	498	165

Description

6500733201 phet:hi1312 phenylalanyl-trna synthetase
beta-subunit:phenylalanyl-trna synthetase beta chain:phenylalanine--trna
ligase beta chain:phers (gtcfc:5.15:10.6) (ec:6.1.1.20)
(keggfc:5.15:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1312
HI1312 Haemophilus influenzae 727 -11537059 100036 phet:hi1312
(ec:6.1.1.20) (de:trna ligase beta chain) (phers)) (db:swissprot) SYFB_HAEIN
P43820 HAEMOPHILUS INFLUENZAE 727 -11537059 142302 phet phenylalanine--trna
ligase:beta chain:phenylalanyl-trna synthetase beta chain
(cl:phenylalanine--trna ligase beta chain) (ec:6.1.1.20) (db:pir2.dat)
I64115 I64115 Haemophilus influenzae 727 -11537059 7500892393 hi1312
phenylalanyl-trna synthetase:beta subunit (db:genpept-bct1) (de:haemophilus
influenzae rd section 125 of 163 of the completegenome.) (nt:similar to
gb:k02844 sp:p07395 pid:146346 pid:43071) (le:7809) (re:10196) (di:direct)
U32810 U32810 g1574770 Haemophilus influenzae Rd 71421 -11537059 5000694310
(de:(hi1312) (pn:phenylalanyl-trna synthetase beta chain:phenylalanine--trna
ligase beta chain:phers:phenylalanyl-trna synthetase beta-subunit:phet)
(gn:phet) (gtcfc:5.15:10.6) (ec:6.1.1.20) (syfb_haein)
(keggfc:5.15:10.1:10.2)) HI1312 HI1312 Haemophilus influenzae 727 10041890

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879198	14305	36461	1110	369

Description

6500733202 trpe:hi1387 anthranilate synthase component i (gtcfc:5.15:9.12)
(ec:4.1.3.27) (keggfc:5.15:9.13) (tigrfc:1.1) (db:gtc-haemophilus
influenzae) HI1387 HI1387 Haemophilus influenzae 727 -11537060 102399
trpe:hi1387 (ec:4.1.3.27) (de:anthranilate synthase component i,
(db:swissprot) TRPE_HAEIN P43761 HAEMOPHILUS INFLUENZAE 727 -11537060
141732 trpe anthranilate synthase:component i (cl:anthranilate synthase
component i) (ec:4.1.3.27) (db:pir2.dat) C64121 C64121 Haemophilus
influenzae 727 -11537060 7500893478 hi1387 anthranilate synthase component
i trpe (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of
the completegenome.) (nt:similar to sp:p22099 gb:x17149 pid:48486 percent)
(le:2359) (re:3915) (di:direct) U32819 U32819 g1574221 Haemophilus
influenzae Rd 71421 -11537060 5000694312 (de:(hi1387) (pn:anthranilate
synthase component i:trpe) (gn:trpe) (gtcfc:5.15:9.12) (ec:4.1.3.27)
(trpe_haein) (keggfc:5.15:9.13) (tigrfc:1.1) (db:gtc-haemophilus
influenzae)) HI1387 HI1387 Haemophilus influenzae 727 10044218

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879199	14306	36462	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879219	14307	36463	222	73
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879223	14308	36464	231	76
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879228	14309	36465	390	129
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879229	14310	36466	366	121
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879233	14311	36467	543	180
<u>Description</u>				

6500733203 trpd:hi1389 anthanilate phosphoribosyltransferase:anthranilate phosphoribosyltransferase (gtcfc:8.1:5.15) (ec:2.4.2.18) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI1389 HI1389 Haemophilus influenzae 727 -11537061 102376 trpd:hi1389 (ec:2.4.2.18) (de:anthranilate phosphoribosyltransferase,) (db:swissprot) TRPD_HAEIN P43858 HAEMOPHILUS INFLUENZAE 727 -11537061 166001 anthranilate phosphoribosyltransferase homolog hi1389:trpd protein homolog (cl:anthranilate phosphoribosyltransferase:trpd homology) (db:pir2.dat) E64121 E64121 Haemophilus influenzae 727 -11537061 7500893466 hi1389 anthanilate phosphoribosyltransferase trpd (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the completegenome.) (nt:similar to sp:p22096 gb:x17149 pid:48488 percent) (le:4997) (re:5998) (di:direct) U32819 U32819 g1574223 Haemophilus influenzae Rd 71421 -11537061 5000694313 (de:(hi1389) (pn:anthranilate phosphoribosyltransferase:anthanilate phosphoribosyltransferase:trpd) (gn:trpd) (gtcfc:5.15) (ec:2.4.2.18) (trpd_haein) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae)) HI1389 HI1389 Haemophilus influenzae 727 10044195

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879238	14312	36468	231	76
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879254	14313	36469	1359	452
<u>Description</u>				

6500733204 trpc:hi1389b indole-3-glycerol phosphate
synthase:igps:n-5-phospho-ribosylanthranilate isomerase:prai
(gtcfc:8.1:5.15) (keggfc:5.15) (db:gtc-haemophilus influenzae) HI1389B
HI1389B Haemophilus influenzae 727 -11537062 102352 trpc:hi1389.1
(ec:4.1.1.48:5.3.1.24) (de:n-(5'-phospho-ribosyl)anthranilate isomerase,
(prai)) (db:swissprot) TRPC_HAEIN P46451 HAEMOPHILUS INFLUENZAE 727
-11537062 7500893459 hi1389.1 indole-3-glycerol phosphate synthase /
(db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the
completegenome.) (nt:similar to sp:p22098 gb:x17149 pid:48489 percent)
(le:6035) (re:7468) (di:direct) U32819 U32819 g1574224 Haemophilus
influenzae Rd 71421 -11537062 5000695339 (de:(hi1389b) (gtcfc:13.7) (ec:)
(keggfc:11.1) (db:gtc-haemophilus influenzae)) HI1389B HI1389B Haemophilus
influenzae 727 10044171

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879260	14314	36470	210	69
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879266	14315	36471	447	148

Description

6500733205 trpb:hi1431 tryptophan synthase:beta chain:tryptophan synthase beta chain (gtcfc:5.15) (ec:4.2.1.20) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI1431 HI1431 Haemophilus influenzae 727 -11537063 102325 trpb:hi1431 (ec:4.2.1.20) (de:tryptophan synthase beta chain,) (db:swissprot) TRPB_HAEIN P43760 HAEMOPHILUS INFLUENZAE 727 -11537063 141919 trpb tryptophan synthase:beta chain (cl:tryptophan synthase beta chain:tryptophan synthase beta chain homology) (ec:4.2.1.20) (db:pir2.dat) I64122 I64122 Haemophilus influenzae 727 -11537063 7500893448 hi1431 tryptophan synthase beta subunit trpb (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to pid:733125 sp:p54203 percent ident:) (le:2755) (re:3948) (di:direct) U32822 U32822 g1574269 Haemophilus influenzae Rd 71421 -11537063 5000694314 (de:(hi1431) (pn:tryptophan synthase beta chain:tryptophan synthase, beta chain:trpb) (gn:trpb) (gtcfc:5.15) (ec:4.2.1.20) (trpb_haein) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae)) HI1431 HI1431 Haemophilus influenzae 727 10044144

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879271	14316	36472	798	266

Description

GTC ORF with score 585 to: (sr:thale cress) (db:genpept-pln2) (de:arabidopsis thaliana dna chromosome 4, bac clone f28m20 (essaiiproject).) (nt:strong similarity to rna lariat debranching enzyme,) (le:14905:15121:15359:15647) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879282	14317	36473	660	219

Description

6500733206 trpa:hi1432 tryptophan synthase alpha subunit:tryptophan synthase alpha chain (gtcfc:5.15) (ec:4.2.1.20) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI1432 HI1432 Haemophilus influenzae 727 -11537064 102301 trpa:hi1432 (ec:4.2.1.20) (de:tryptophan synthase alpha chain,) (db:swissprot) TRPA_HAEIN P43759 HAEMOPHILUS INFLUENZAE 727 -11537064 141896 trpa tryptophan synthase:alpha chain (cl:tryptophan synthase alpha chain:tryptophan synthase alpha chain homology) (ec:4.2.1.20) (db:pir2.dat) A64123 A64123 Haemophilus influenzae 727 -11537064 7500893437 hi1432 tryptophan synthase alpha subunit trpa (db:genpept-bct1) (de:haemophilus influenzae rd section 137 of 163 of the completegenome.) (nt:similar to gb:j01714 sp:p00928 gb:u23489 gb:u23490) (le:3948) (re:4754) (di:direct) U32822 U32822 g1574270 Haemophilus influenzae Rd 71421 -11537064 5000694315 (de:(hi1432) (pn:tryptophan synthase alpha chain:tryptophan synthase alpha subunit:trpa) (gn:trpa) (gtcfc:5.15) (ec:4.2.1.20) (trpa_haein) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae)) HI1432 HI1432 Haemophilus influenzae 727 10044120

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879286	14318	36474	642	213

Description

6500733207 arog:hi1547 phenylalanine repressible:phospho-2-dehydro-3-deoxyheptonate aldolase:phospho-2-keto-3-deoxyheptonate aldolase:dahp synthetase:3-deoxy-d-arabino-heptulosonate 7-phosphate synthase (gtcfc:5.15) (ec:4.1.2.15) (keggfc:5.15) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI1547 HI1547 Haemophilus influenzae 727 -11537065 60215 arog:hi1547 (ec:4.1.2.15) (de:d-arabino-heptulosonate 7-phosphate synthase)) (db:swissprot) AROG_HAEIN P44303 HAEMOPHILUS INFLUENZAE 727 -11537065 141658 2-dehydro-3-deoxyphosphoheptonate aldolase:phe-sensitive (cl:phospho-2-dehydro-3-deoxyheptonate aldolase) (ec:4.1.2.15) (db:pir2.dat) I64128 I64128 Haemophilus influenzae 727 -11537065 7500877187 hi1547 phospho-2-dehydro-3-deoxyheptonate aldolase (db:genpept-bct1) (de:haemophilus influenzae rd section 145 of 163 of the completegenome.) (nt:similar to gb:j01591 sp:p00886 pid:145368 gb:u00096) (le:2131) (re:3219) (di:complement) U32830 U32830 g1574392 Haemophilus influenzae Rd 71421 -11537065 5000694316 (de:(hi1547) (pn:phospho-2-dehydro-3-deoxyheptonate aldolase:phospho-2-keto-3- deoxyheptonate aldolase:3-deoxy-d-arabino-heptulosonate 7-phosphate synthase:dahp synthetase:phenylalanine repressible:arog) (gn:arog) (gtcfc:5.15) (ec:4.) HI1547 HI1547 Haemophilus influenzae 727 10002941

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879289	14319	36475	195	64

Description

6500733208 aroa:hi1589
enolpyruvylshikimatephosphatesynthase:3-phosphoshikimate
1-carboxyvinyltransferase:5-enolpyruvylshikimate-3-phosphate synthase:epsp
synthase (gtcfc:5.15) (ec:2.5.1.19) (keggfc:5.15) (tigrfc:1.1)
(db:gtc-haemophilus influenzae) HI1589 HI1589 Haemophilus influenzae 727
-11537066 60160 aroa:hi1589 (ec:2.5.1.19)
(de:enolpyruvylshikimate-3-phosphate synthase) (epsp synthase))
(db:swissprot) AROA_HAEIN Q03421 HAEMOPHILUS INFLUENZAE 727 -11537066
138353 aroa 3-phosphoshikimate 1-carboxyvinyltransferase
(cl:3-phosphoshikimate 1-carboxyvinyltransferase:3-phosphoshikimate
1-carboxyvinyltransferase homology) (ec:2.5.1.19) (db:pir2.dat) F64131
F64131 Haemophilus influenzae 727 -11537066 7500877164 hi1589
3-phosphoshikimate-1-carboxyvinyltransferase (db:genpept-bct1)
(de:haemophilus influenzae rd section 148 of 163 of the completegenome.)
(nt:similar to gb:l04686 sp:q03421 pid:148865 percent) (le:901) (re:2199)
(di:direct) U32833 U32833 g1574434 Haemophilus influenzae Rd 71421 -11537066
5000694317 (de:(hi1589) (pn:3-phosphoshikimate 1-carboxyvinyltransferase:5-
enolpyruvylshikimate-3-phosphate synthase:epsp
synthase:enolpyruvylshikimatephosphatesynthase:aroa) (gn:aroa) (gtcfc:5.15)
(ec:2.5.1.19) (aroa_haein) (keggfc:5.15)) HI1589 HI1589 Haemophilus
influenzae 727 10002886

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879290	14320	36476	1203	400

Description

6500733209 tyrs:hi1610 tyrosyl trna synthetase:tyrosyl-trna
synthetase:tyrosine--trna ligase:tyrrs (gtcfc:5.15:10.6) (ec:6.1.1.1)
(keggfc:5.15:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1610
HI1610 Haemophilus influenzae 727 -11537067 100246 tyrs:hi1610 (ec:6.1.1.1)
(de:tyrosyl-trna synthetase, (tyrosine--trna ligase) (tyrrs)) (db:swissprot)
SYY_HAEIN P43836 HAEMOPHILUS INFLUENZAE 727 -11537067 167240 tyrosine--trna
ligase::tyrosyl-trna synthetase (cl:tyrosine--trna ligase) (ec:6.1.1.1)
(db:pir2.dat) D64132 D64132 Haemophilus influenzae 727 -11537067 7500892657
hi1610 tyrosyl trna synthetase tyrs (db:genpept-bct1) (de:haemophilus
influenzae rd section 149 of 163 of the completegenome.) (nt:similar to
gb:x79010 sp:p41256 pid:505366 percent) (le:9423) (re:10628) (di:complement)
U32834 U32834 g1574452 Haemophilus influenzae Rd 71421 -11537067 5000694318
(de:(hi1610) (pn:tyrosyl-trna synthetase:tyrosine--trna ligase:tyrrs:tyrosyl
trna synthetase:tyrs) (gn:tyrs) (gtcfc:5.15:10.6) (ec:6.1.1.1) (syy_haein)
(keggfc:5.15:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae))
HI1610 HI1610 Haemophilus influenzae 727 10042100

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879291	14321	36477	564	188

Description

6500733210 trpd:hi1388 anthranilate synthase component ii (gtcfc:5.15) (keggfc:14.2) (tigrfc:1.1) (db:gtc-haemophilus influenzae) HI1388 HI1388 Haemophilus influenzae 727 -11537068 7500976282 hi1388 anthranilate synthase component ii trpg (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the completegenome.) (nt:similar to gb:j01787 sp:p00906 pid:152798 percent) (le:3928) (re:4509) (di:direct) U32819 U32819 g1574222 Haemophilus influenzae Rd 71421 -11537068 5000694319 (de:(hi1388) (pn:anthranilate synthase component ii:trpd) (gn:trpd) (gtcfc:5.15) (ec:) (keggfc:11.2) (tigrfc:1.1) (db:gtc-haemophilus influenzae)) HI1388 HI1388 Haemophilus influenzae 727 10126717

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879295	14322	36478	288	95

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879303	14323	36479	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879310	14324	36480	1278	425

Description

6500733211 7-alpha-hydroxysteroid dehydrogenase:hdha:hypothetical oxidoreductase hi0048 (gtcfc:5.16) (ec:1.-.-.-) (keggfc:14.1) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0048 HI0048 Haemophilus influenzae 727 -11537069 108502 hi0048 (ec:1.-.-.-) (de:hypothetical oxidoreductase hi0048,) (db:swissprot) Y048_HAEIN P44481 HAEMOPHILUS INFLUENZAE 727 -11537069 165975 d-arabinitol 2-dehydrogenase homolog (cl:short-chain alcohol dehydrogenase homology) (db:pir2.dat) B64045 B64045 Haemophilus influenzae 727 -11537069 7500894581 hi0048 oxidoreductase (db:genpept-bct1) (de:haemophilus influenzae rd section 5 of 163 of the complete genome.) (nt:similar to gb:al009126 percent identity: 48.39;) (le:1960) (re:2817) (di:complement) U32690 U32690 g1572995 Haemophilus influenzae Rd 71421 -11537069 5000695744 (de:(hi0048) (pn:hypothetical oxidoreductase hi0048:7-alpha-hydroxysteroid dehydrogenase:hdha) (gtcfc:13.7) (ec:1.-.-.-) (y048_haein) (keggfc:11.1) (tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI0048 HI0048 Haemophilus influenzae 727 10050234

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879351	14325	36481	588	195

Description

6500733212 gst:hi0111 glutathione transferase:bphh:glutathione s-transferase (gtcfc:5.16:6.16) (ec:2.5.1.18) (keggfc:6.9) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0111 HI0111 Haemophilus influenzae 727 -11537070 74972 gst:hi0111 (ec:2.5.1.18) (de:glutathione s-transferase,) (db:swissprot) GT_HAEIN P44521 HAEMOPHILUS INFLUENZAE 727 -11537070 166162 glutathione transferase homolog (db:pir2.dat) A64049 A64049 Haemophilus influenzae 727 -11537070 7500882831 hi0111 glutathione transferase bphh (db:genpept-bct1) (de:haemophilus influenzae rd section 11 of 163 of the complete genome.) (nt:similar to gb:x76500 pid:520921 percent identity:) (le:7209) (re:7838) (di:direct) U32696 U32696 g1573063 Haemophilus influenzae Rd 71421 -11537070 5000694363 (de:(hi0111) (pn:glutathione s-transferase:glutathione transferase:bphh) (gn:gst) (gtcfc:6.16) (ec:2.5.1.18) (gt_haein) (keggfc:6.9) (tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI0111 HI0111 Haemophilus influenzae 727 10017484

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879357	14326	36482	654	218

Description

6500733213 ureh:hi0535 urease protein:urease accessory protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0535 HI0535 Haemophilus influenzae 727 -11537071 103905 ureh:hi0535 (de:urease accessory protein ureh) (db:swissprot) UREH_HAEIN P44397 HAEMOPHILUS INFLUENZAE 727 -11537071 167256 ureh protein homolog (db:pir2.dat) D64075 D64075 Haemophilus influenzae 727 -11537071 7500893858 hi0535 urease accessory protein ureh (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to gb:m84338 sp:q09067 pid:485336) (le:119) (re:904) (di:complement) U32736 U32736 g1573520 Haemophilus influenzae Rd 71421 -11537071 5000695745 (de:(hi0535) (pn:urease accessory protein :urease protein:ureh) (gn:ureh) (gtcfc:13.7) (ec:) (ureh_haein) (keggfc:11.2) (tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI0535 HI0535 Haemophilus influenzae 727 10045675

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879362	14327	36483	318	105

Description

6500733214 ureg:hi0536 urease protein:urease accessory protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0536 HI0536 Haemophilus influenzae 727 -11537072 103896 ureg:hi0536 (de:urease accessory protein ureg) (db:swissprot) UREG_HAEIN P44396 HAEMOPHILUS INFLUENZAE 727 -11537072 167255 ureg urease accessory protein ureg (db:pir2.dat) E64075 E64075 Haemophilus influenzae 727 -11537072 7500893855 hi0536 urease accessory protein ureg (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to gb:m84338 sp:q09066 pid:485335) (le:979) (re:1656) (di:complement) U32736 U32736 g1573521 Haemophilus influenzae Rd 71421 -11537072 5000695746 (de:(hi0536) (pn:urease accessory protein :urease protein:ureg) (gn:ureg) (gtcfc:13.7) (ec:) (ureg_haein) (keggfc:11.2) (tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI0536 HI0536 Haemophilus influenzae 727 10045666

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879366	14328	36484	336	111

Description

6500733215 uref:hi0537 urease accessory protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0537 HI0537 Haemophilus influenzae 727 -11537073 103886 uref:hi0537 (de:urease accessory protein uref) (db:swissprot) UREF_HAEIN P44395 HAEMOPHILUS INFLUENZAE 727 -11537073 167253 urease accessory protein homolog (db:pir2.dat) F64075 F64075 Haemophilus influenzae 727 -11537073 7500893852 hi0537 urease accessory protein uref (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to sp:q07402 pid:393298 percent ident:) (le:1759) (re:2343) (di:complement) U32736 U32736 g1573522 Haemophilus influenzae Rd 71421 -11537073 5000695747 (de:(hi0537) (pn:urease accessory protein :urease accessory protein:uref) (gn:uref) (gtcfc:13.7) (ec:) (uref_haein) (keggfc:11.2) (tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI0537 HI0537 Haemophilus influenzae 727 10045656

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879367	14329	36485	2346	781

Description

6500733216 uree:hi0538 urease protein:urease accessory protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0538 HI0538 Haemophilus influenzae 727 -11537074 103878 uree:hi0538 (de:urease accessory protein uree) (db:swissprot) UREE_HAEIN P44394 HAEMOPHILUS INFLUENZAE 727 -11537074 167254 urease accessory protein uree homolog (db:pir2.dat) G64075 G64075 Haemophilus influenzae 727 -11537074 7500893850 hi0538 urease accessory protein uree (db:genpept-bct1) (de:haemophilus influenzae rd section 51 of 163 of the complete genome.) (nt:similar to gb:m84338 sp:q09064 pid:485333) (le:2451) (re:3008) (di:complement) U32736 U32736 g1573523 Haemophilus influenzae Rd 71421 -11537074 5000695748 (de:(hi0538) (pn:urease accessory protein :urease protein:uree) (gn:uree) (gtcfc:13.7) (ec:) (uree_haein) (keggfc:11.2) (tigrfc:5.7) (db:gtc-haemophilus influenzae)) HI0538 HI0538 Haemophilus influenzae 727 10045648

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879404	14330	36486	558	185

Description

5000695749 hippuricase:hipo:hypothetical protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0584 HI0584 Haemophilus influenzae 727 -11537075 109219 hi0584 (de:hypothetical protein hi0584) (db:swissprot) YDAJ_HAEIN P44765 HAEMOPHILUS INFLUENZAE 727 -11537075 166200 probable amidohydrolase:hi0584 (cl:hypothetical protein hi0584) (ec:3.5.-.-) (db:pir2.dat) B64079 B64079 Haemophilus influenzae 727 -11537075 7500922146 hi0584 hydrolase (db:genpept-bct1) (de:haemophilus influenzae rd section 55 of 163 of the complete genome.) (nt:similar to gb:u00096 sp:p77357 pid:1742205) (le:2440) (re:3711) (di:complement) U32740 U32740 g1573574 Haemophilus influenzae Rd 71421 -11537075 6500733217 hippuricase:hipo:hypothetical protein (gtcfc:5.16) (keggfc:14.2) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0584 HI0584 Haemophilus influenzae 727 -11537075

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879415	14331	36487	315	104

Description

6500733218 glpk:hi0691 glycerol kinase:atp:glycerol
 3-phosphotransferase:glycerokinase:gk (gtcfc:5.16:8.1) (ec:2.7.1.30)
 (keggfc:8.1) (tigrfc:5.7) (db:gtc-haemophilus influenzae) HI0691 HI0691
 Haemophilus influenzae 727 -11537076 138463 glycerol kinase
 (cl:xylulokinase) (ec:2.7.1.30) (db:pir2.dat) I64086 I64086 Haemophilus
 influenzae 727 -11537076 7500954068 hi0691 glycerol kinase glpk
 (db:genpept-bct1) (de:haemophilus influenzae rd section 67 of 163 of the
 complete genome.) (nt:similar to gb:l19201 sp:p08859 gb:m18393 gb:m55990)
 (le:960) (re:2471) (di:direct) U32752 U32752 g1573695 Haemophilus influenzae
 Rd 71421 -11537076 5000694400 (de:(hi0691) (pn:atp:glycerol
 3-phosphotransferase:glycerokinase:gk:glycerol kinase:glpk) (gn:glpk)
 (gtcfc:8.1) (ec:2.7.1.30) (glpk_haein) (keggfc:8.1) (tigrfc:5.7)
 (db:gtc-haemophilus influenzae)) HI0691 HI0691 Haemophilus influenzae 727
 10070650

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879417	14332	36488	2094	698

Description

6500733219 asps:hi0317 aspartyl-trna synthetase:aspartate--trna ligase:asprs
 (gtcfc:5.2:10.6) (ec:6.1.1.12) (keggfc:5.2:10.1:10.2) (tigrfc:12.1)
 (db:gtc-haemophilus influenzae) HI0317 HI0317 Haemophilus influenzae 727
 -11537077 100006 asps:hi0317 (ec:6.1.1.12) (de:(asprs)) (db:swissprot)
 SYD_HAEIN P43817 HAEMOPHILUS INFLUENZAE 727 -11537077 142266 asps
 aspartate--trna ligase::aspartyl-trna synthetase (cl:lysine--trna ligase)
 (ec:6.1.1.12) (db:pir2.dat) E64061 E64061 Haemophilus influenzae 727
 -11537077 7500892352 hi0317 aspartyl-trna synthetase asps (db:genpept-bct1)
 (de:haemophilus influenzae rd section 32 of 163 of the complete genome.)
 (nt:similar to sp:p21889 gb:x53863 gb:x53984 pid:41015) (le:2079) (re:3845)
 (di:complement) U32717 U32717 g1573287 Haemophilus influenzae Rd 71421
 -11537077 5000694322 (de:(hi0317) (pn:aspartate--trna
 ligase:asprs:aspartyl-trna synthetase:asps) (gn:asps) (gtcfc:5.2:10.6)
 (ec:6.1.1.12) (syd_haein) (keggfc:5.2:10.1:10.2) (tigrfc:12.1)
 (db:gtc-haemophilus influenzae)) HI0317 HI0317 Haemophilus influenzae 727
 10041860

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879424	14333	36489	753	250

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879432	14334	36490	519	172

Description

6500733220 alas:hi0814 alanyl-trna synthetase:alanine--trna ligase:alars (gtcfc:5.2:10.6) (ec:6.1.1.7) (keggfc:5.2:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0814 HI0814 Haemophilus influenzae 727 -11537078 99978 alas:hi0814 (ec:6.1.1.7) (de:alanyl-trna synthetase, (alanine--trna ligase) (alars)) (db:swissprot) SYA_HAEIN P43815 HAEMOPHILUS INFLUENZAE 727 -11537078 142274 alas alanine--trna ligase::alanyl-trna synthetase (cl:alanine--trna ligase) (ec:6.1.1.7) (db:pir2.dat) I64095 I64095 Haemophilus influenzae 727 -11537078 7500892317 hi0814 alanyl-trna synthetase alas (db:genpept-bct1) (de:haemophilus influenzae rd section 78 of 163 of the complete genome.) (nt:similar to gb:j01581 sp:p00957 pid:145220 gb:u00096) (le:9275) (re:11899) (di:complement) U32763 U32763 g1573826 Haemophilus influenzae Rd 71421 -11537078 5000694323 (de:(hi0814) (pn:alanine--trna ligase:alars:alanyl-trna synthetase:alars) (gn:alars) (gtcfc:5.2:10.6) (ec:6.1.1.7) (sya_haein) (keggfc:5.2:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0814 HI0814 Haemophilus influenzae 727 10041833

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879433	14335	36491	1182	393

Description

6500733221 asns:hi1302 asparaginyl-trna synthetase:asparagine--trna ligase:asnrs (gtcfc:5.2:10.6) (ec:6.1.1.22) (keggfc:5.2:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1302 HI1302 Haemophilus influenzae 727 -11537079 100136 asns:hi1302 (ec:6.1.1.22) (de:(asnrs)) (db:swissprot) SYN_HAEIN P43829 HAEMOPHILUS INFLUENZAE 727 -11537079 142264 asparagine--trna ligase::asparaginyl-trna synthetase (cl:lysine--trna ligase) (ec:6.1.1.22) (db:pir2.dat) B64115 B64115 Haemophilus influenzae 727 -11537079 7500892535 hi1302 asparaginyl-trna synthetase asns (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:similar to gb:m33145 sp:p17242 gb:x68192 pid:147935) (le:68) (re:1501) (di:complement) U32810 U32810 g1574761 Haemophilus influenzae Rd 71421 -11537079 5000694324 (de:(hi1302) (pn:asparagine--trna ligase:asnrs:asparaginyl-trna synthetase:asns) (gn:asns) (gtcfc:5.2:10.6) (ec:6.1.1.22) (syn_haein) (keggfc:5.2:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI1302 HI1302 Haemophilus influenzae 727 10041990

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879458	14336	36492	816	272

Description

6500733222 alr:hi1575 alanine racemase:biosynthetic:alanine racemase (gtcfc:5.2:6.15) (ec:5.1.1.1) (keggfc:5.2:6.8) (tigrfc:1.5) (db:gtc-haemophilus influenzae) HI1575 HI1575 Haemophilus influenzae 727 -11537080 59230 alr:hi1575 (ec:5.1.1.1) (de:alanine racemase,) (db:swissprot) ALR_HAEIN P45257 HAEMOPHILUS INFLUENZAE 727 -11537080 165990 alr alanine racemase::biosynthetic (cl:alanine racemase) (ec:5.1.1.1) (db:pir1.dat) E64130 E64130 Haemophilus influenzae 727 -11537080 7500876779 hi1575 alanine racemase:biosynthetic alr (db:genpept-bct1) (de:haemophilus influenzae rd section 146 of 163 of the complete genome.) (nt:similar to sp:p29743 pid:396388 gb:u00096) (le:11163) (re:12245) (di:direct) U32831 U32831 g1574412 Haemophilus influenzae Rd 71421 -11537080 5000694325 (de:(hi1575) (pn:alanine racemase:alanine racemase, biosynthetic:alr) (gn:alr) (gtcfc:5.2:6.15) (ec:5.1.1.1) (alr_haein) (keggfc:5.2:6.8) (tigrfc:1.5) (db:gtc-haemophilus influenzae)) HI1575 HI1575 Haemophilus influenzae 727 10001969

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879460	14337	36493	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879463	14338	36494	1734	577

Description

6500733223 thrc:hi0087 threonine synthase (gtcfc:5.2:5.3:9.3) (ec:4.2.99.2) (keggfc:5.3:9.3) (tigrfc:1.2) (db:gtc-haemophilus influenzae) (gtcfc:l-amino acid metabolism-alanine and aspartate metabolism:l-amino acid metabolism-glycine--serine and threonine metabolism:metabolism of cofactors and... HI0087 HI0087 Haemophilus influenzae 727 -11537081 101441 thrc:hi0087 (ec:4.2.99.2) (de:threonine synthase,) (db:swissprot) THRC_HAEIN P44503 HAEMOPHILUS INFLUENZAE 727 -11537081 141952 threonine synthase (cl:threonine synthase) (ec:4.2.99.2) (db:pir2.dat) H64047 H64047 Haemophilus influenzae 727 -11537081 7500893113 hi0087 threonine synthase thrc (db:genpept-bct1) (de:haemophilus influenzae rd section 9 of 163 of the complete genome.) (nt:similar to gb:d10387 sp:p27735 pid:216968 pid:47275) (le:3056) (re:4333) (di:complement) U32694 U32694 g1573038 Haemophilus influenzae Rd 71421 -11537081 5000694328 (de:(hi0087) (pn:threonine synthase:thrc) (gn:thrc) (gtcfc:5.3:9.3) (ec:4.2.99.2) (thrc_haein) (keggfc:5.3:9.3) (tigrfc:1.2) (db:gtc-haemophilus influenzae)) HI0087 HI0087 Haemophilus influenzae 727 10043280

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879469	14339	36495	501	166

Description

6500733224 thrb:hi0088 homoserine kinase:hk (gtcfc:5.2:5.3) (ec:2.7.1.39) (keggfc:5.3) (tigrfc:1.2) (db:gtc-haemophilus influenzae) HI0088 HI0088 Haemophilus influenzae 727 -11537082 80669 thrb:hi0088 (ec:2.7.1.39) (de:homoserine kinase, (hk)) (db:swissprot) KHSE_HAEIN P44504 HAEMOPHILUS INFLUENZAE 727 -11537082 138850 homoserine kinase (cl:homoserine kinase) (ec:2.7.1.39) (db:pir2.dat) I64047 I64047 Haemophilus influenzae 727 -11537082 7500884608 hi0088 homoserine kinase thrb (db:genpept-bct1) (de:haemophilus influenzae rd section 9 of 163 of the complete genome.) (nt:similar to gb:d10387 sp:p27722 pid:216967 pid:47274) (le:4376) (re:5320) (di:complement) U32694 U32694 g1573039 Haemophilus influenzae Rd 71421 -11537082 5000694329 (de:(hi0088) (pn:hk:homoserine kinase:thrb) (gn:thrb) (gtcfc:5.3) (ec:2.7.1.39) (khse_haein) (keggfc:5.3) (tigrfc:1.2) (db:gtc-haemophilus influenzae)) HI0088 HI0088 Haemophilus influenzae 727 10022910

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879481	14340	36496	237	78

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879487	14341	36497	312	103

Description

6500733225 thra:hi0089 aspartokinase i / homoserine dehydrogenase i:aspartokinase / homoserine dehydrogenase (gtcfc:5.2:5.3:5.8) (keggfc:5.3:5.8) (tigrfc:1.2) (db:gtc-haemophilus influenzae) HI0089 HI0089 Haemophilus influenzae 727 -11537083 59043 thra:hi0089 (ec:2.7.2.4:1.1.1.3) (de:aspartokinase, / homoserine dehydrogenase,) (db:swissprot) AKH_HAEIN P44505 HAEMOPHILUS INFLUENZAE 727 -11537083 138968 aspartate kinase:i / homoserine dehydrogenase (cl:thra bifunctional enzyme:aspartate kinase homology:homoserine dehydrogenase homology) (ec:2.7.2.4:1.1.1.3) (db:pir2.dat) A64048 A64048 Haemophilus influenzae 727 -11537083 7500876716 hi0089 aspartokinase i / homoserine dehydrogenase i (db:genpept-bct1) (de:haemophilus influenzae rd section 9 of 163 of the complete genome.) (nt:similar to sp:p00561 gb:m10644 gb:v00360 gb:v00361) (le:5333) (re:7780) (di:complement) U32694 U32694 g1573040 Haemophilus influenzae Rd 71421 -11537083 5000694330 (de:(hi0089) (pn:aspartokinase :aspartokinase i) (gn:thra) (gtcfc:5.3) (ec:2.7.2.4) (akh_haein) (keggfc:5.3:5.8) (tigrfc:1.2) (db:gtc-haemophilus influenzae)) HI0089 HI0089 Haemophilus influenzae 727 10001785

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879498	14342	36498	1893	631

Description

6500733226 dape:hi0102 succinyl-diaminopimelate desuccinylase:sdap
(gtcfc:5.2:5.8) (ec:3.5.1.18) (keggfc:5.8) (tigrfc:1.2) (db:gtc-haemophilus
influenzae) HI0102 HI0102 Haemophilus influenzae 727 -11537084 67883
dape:hi0102 (ec:3.5.1.18) (de:succinyl-diaminopimelate desuccinylase,
(sdap)) (db:swissprot) DAPE_HAEIN P44514 HAEMOPHILUS INFLUENZAE 727
-11537084 167179 succinyl-diaminopimelate desuccinylase (ec:3.5.1.18)
(db:pir2.dat) F64048 F64048 Haemophilus influenzae 727 -11537084 7500880000
hi0102 succinyl-diaminopimelate desuccinylase dape (db:genpept-bct1)
(de:haemophilus influenzae rd section 10 of 163 of the complete genome.)
(nt:similar to gb:u00096 pid:1788816 pid:1799895) (le:8301) (re:9434)
(di:complement) U32695 U32695 g1573051 Haemophilus influenzae Rd 71421
-11537084

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879515	14343	36499	720	239

Description

6500733227 dapa:hi0255 dihydrodipicolinate synthetase:dihydrodipicolinate
synthase:dhdps (gtcfc:5.2:5.8) (ec:4.2.1.52) (keggfc:5.8) (tigrfc:1.2)
(db:gtc-haemophilus influenzae) HI0255 HI0255 Haemophilus influenzae 727
-11537085 67867 dapa:hi0255 (ec:4.2.1.52) (de:dihydrodipicolinate synthase,
(dhdps)) (db:swissprot) DAPA_HAEIN P43797 HAEMOPHILUS INFLUENZAE 727
-11537085 141672 dihydrodipicolinate synthase (cl:n-acetylneuraminate
lyase) (ec:4.2.1.52) (db:pir2.dat) A64058 A64058 Haemophilus influenzae 727
-11537085 7500879991 hi0255 dihydrodipicolinate synthetase dapa
(db:genpept-bct1) (de:haemophilus influenzae rd section 26 of 163 of the
complete genome.) (nt:similar to gb:m12844 sp:p05640 pid:145708 gb:u00096)
(le:6316) (re:7212) (di:direct) U32711 U32711 g1573221 Haemophilus
influenzae Rd 71421 -11537085

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879531	14344	36500	183	60

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879537	14345	36501	249	82

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879565	14346	36502	1683	560

Description

6500733228 asd:hi0646 aspartate-semialdehyde dehydrogenase:asa dehydrogenase (gtcfc:5.2) (ec:1.2.1.11) (keggfc:5.3:5.8) (tigrfc:1.2) (db:gtc-haemophilus influenzae) HI0646 HI0646 Haemophilus influenzae 727 -11537086 68419 asd:hi0646 (ec:1.2.1.11) (de:dehydrogenase)) (db:swissprot) DHAS_HAEIN P44801 HAEMOPHILUS INFLUENZAE 727 -11537086 136435 aspartate-semialdehyde dehydrogenase (cl:aspartate-semialdehyde dehydrogenase) (ec:1.2.1.11) (db:pir2.dat) B64084 B64084 Haemophilus influenzae 727 -11537086 7500880237 hi0646 aspartate-semialdehyde dehydrogenase asd (db:genpept-bct1) (de:haemophilus influenzae rd section 62 of 163 of the complete genome.) (nt:similar to sp:p00353 gb:v00262 pid:40992 pid:606368) (le:10638) (re:11753) (di:complement) U32747 U32747 g1573644 Haemophilus influenzae Rd 71421 -11537086 5000694335 (de:(hi0646) (pn:asa dehydrogenase:aspartate-semialdehyde dehydrogenase:asd) (gn:asd) (gtcfc:5.3) (ec:1.2.1.11) (dhas_haein) (keggfc:5.3:5.8) (tigrfc:1.2) (db:gtc-haemophilus influenzae)) HI0646 HI0646 Haemophilus influenzae 727 10011011

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879577	14347	36503	273	90

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879584	14348	36504	252	83

Description

6500733229 lysa:hi0727 diaminopimelate decarboxylase:dap decarboxylase (gtcfc:5.2:5.8) (ec:4.1.1.20) (keggfc:5.8) (tigrfc:1.2) (db:gtc-haemophilus influenzae) HI0727 HI0727 Haemophilus influenzae 727 -11537087 67972 lysa:hi0727 (ec:4.1.1.20) (de:diaminopimelate decarboxylase, (dap decarboxylase)) (db:swissprot) DCDA_HAEIN P44316 HAEMOPHILUS INFLUENZAE 727 -11537087 166092 diaminopimelate decarboxylase (cl:diaminopimelate decarboxylase) (ec:4.1.1.20) (db:pir2.dat) B64089 B64089 Haemophilus influenzae 727 -11537087 7500880048 hi0727 diaminopimelate decarboxylase lysa (db:genpept-bct1) (de:haemophilus influenzae rd section 71 of 163 of the complete genome.) (nt:similar to sp:p19572 percent ident: 57.59;) (le:893) (re:2140) (di:complement) U32756 U32756 g1573731 Haemophilus influenzae Rd 71421 -11537087

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879586	14349	36505	237	78

Description

6500733230 dapf:hi0750 diaminopimelate epimerase (gtcfc:5.2:5.8)
(ec:5.1.1.7) (keggfc:5.8) (tigrfc:1.2) (db:gtc-haemophilus influenzae)
HI0750 HI0750 Haemophilus influenzae 727 -11537088 67886 dapf:hi0750
(ec:5.1.1.7) (de:diaminopimelate epimerase, (dap epimerase)) (db:swissprot)
DAPF_HAEIN P44859 HAEMOPHILUS INFLUENZAE 727 -11537088 166093
diaminopimelate epimerase (cl:diaminopimelate epimerase) (ec:5.1.1.7)
(db:pir2.dat) F64090 Haemophilus influenzae 727 -11537088 7500880001
hi0750 diaminopimelate epimerase dapf (db:genpept-bct1) (de:haemophilus
influenzae rd section 74 of 163 of the complete genome.) (nt:similar to
gb:m87049 sp:p08885 gb:x12968 pid:148208) (le:928) (re:1752) (di:direct)
U32759 U32759 g1573758 Haemophilus influenzae Rd 71421 -11537088

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879588	14350	36506	459	152

Description

GTC ORF with score 284 to: (fn:similar to alpha and gamma adaptins)
(sr:human) (db:genpept-pri3) (de:homo sapiens chromosome 19, cosmid r26634,
complete sequence.) (nt:ap-3 complex delta subunit; human homolog of mouse)
(le:3296:9810:10209) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879590	14351	36507	189	62

Description

6500733231 meth:hi1042 b12-dependent homocysteine-n5-methyltetrahydrofolate
transmethylase (gtcfc:9.6:1.9:4.1) (keggfc:14.2) (tigrfc:1.2)
(db:gtc-haemophilus influenzae) (gtcfc:metabolism of cofactors and
vitamins-biotin metabolism (b8) and folate biosynthesis:carbohydrate
metabolism-glyoxylate and dicarboxylate metabolism:nucleotide metabol...
HI1042 HI1042 Haemophilus influenzae 727 -11537089 4000708219 hi1042
(de:hypothetical protein hi1042) (db:swissprot) YA42_HAEIN Q57195
HAEMOPHILUS INFLUENZAE 727 -11537089 5000694326 (de:(hi1042)
(pn:b12-dependent homocysteine-n5-methyltetrahydrofolate
transmethylase:meth) (gn:meth) (gtcfc:5.2) (ec:) (keggfc:11.2) (tigrfc:1.2)
(db:gtc-haemophilus influenzae)) HI1042 HI1042 Haemophilus influenzae 727
10126706

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879591	14352	36508	252	83

Description

GTC ORF with score 173 to: (fn:required for eye pigment granule biogenesis) (sr:fruit fly) (db:genpept-inv) (de:drosophila melanogaster ap-3 delta-adaptin subunit (garnet) mrna,complete cds.) (nt:mutated in eye color mutant 'garnet'; similar to) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879592	14353	36509	897	299

Description

GTC ORF with score 185 to: (fn:suppresses loss of yck-encoded yeast casein) (sr:baker's yeast) (db:genpept-pln1) (de:saccharomyces cerevisiae putative alpha/gamma adaptin (yks4) gene,complete cds.) (nt:yck suppressor 4; yks4p; putative; predicted ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879651	14354	36510	1368	456

Description

6500733232 dapb:hi1308 dehydrodipicolinate reductase:dihydrodipicolinate reductase (gtcfc:5.2:5.8) (ec:1.3.1.26) (keggfc:5.8) (tigrfc:1.2) (db:gtc-haemophilus influenzae) HI1308 HI1308 Haemophilus influenzae 727 -11537090 67874 dapb:hi1308 (ec:1.3.1.26) (de:dihydrodipicolinate reductase,) (db:swissprot) DAPB_HAEIN P45153 HAEMOPHILUS INFLUENZAE 727 -11537090 136549 hi1308 dihydrodipicolinate reductase (cl:dihydrodipicolinate reductase) (ec:1.3.1.26) (db:pir2.dat) G64115 G64115 Haemophilus influenzae 727 -11537090 7500879995 hi1308 dihydrodipicolinate reductase dapb (db:genpept-bct1) (de:haemophilus influenzae rd section 125 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p04036 gb:m10611 pid:145710) (le:4796) (re:5608) (di:direct) U32810 U32810 g1574767 Haemophilus influenzae Rd 71421 -11537090

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879665	14355	36511	525	174

Description

6500733233 lysc:hi1632 lysine-sensitive aspartokinase iii (gtcfc:5.2) (keggfc:14.2) (tigrfc:1.2) (db:gtc-haemophilus influenzae) HI1632 HI1632 Haemophilus influenzae 727 -11537091 5500686581 hi1632 (de:hypothetical protein hi1632) (db:swissprot) YG32_HAEIN Q57525 HAEMOPHILUS INFLUENZAE 727 -11537091 166973 aspartate kinase iii homolog (cl:aspartate kinase homology) (db:pir2.dat) F64133 F64133 Haemophilus influenzae 727 -11537091 7500923754 hi1632 h. influenzae predicted coding region hi1632 (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the completegenome.) (nt:hypothetical protein; identified by genemark;) (le:3554) (re:3919) (di:direct) U32836 U32836 g1574478 Haemophilus influenzae Rd 71421 -11537091 5000694327 (de:(hi1632) (pn:lysine-sensitive aspartokinase iii:lysc) (gn:lysc) (gtcfc:5.2) (ec:) (keggfc:11.2) (tigrfc:1.2) (db:gtc-haemophilus influenzae)) HI1632 HI1632 Haemophilus influenzae 727 10088223

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879688	14356	36512	498	165

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879708	14357	36513	462	153

Description

6500733234 dapd:hi1634 2:3:4:5-tetrahydropyridine-2-carboxylate n-succinyltransferase:tetrahydrodipicolinate n-succinyltransferase:tetrahydropicolinate succinylase (gtcfc:1.9:5.2:5.8) (ec:2.3.1.117) (keggfc:5.8) (tigrfc:1.2) (db:gtc-haemophilus influenzae) HI1634 HI1634 Haemophilus influenzae 727 -11537092 138412 2:3:4:5-tetrahydropyridine-2-carboxylate n-succinyltransferase (cl:2,3,4,5-tetrahydropyridine-2-carboxylate n-succinyltransferase) (ec:2.3.1.117) (db:pir2.dat) H64133 H64133 Haemophilus influenzae 727 -11537092 7500954000 hi1634 2:3:4:5-tetrahydropyridine-2-carboxylate (db:genpept-bct1) (de:haemophilus influenzae rd section 151 of 163 of the completegenome.) (nt:similar to gb:x63201 sp:p41396 pid:38947 percent) (le:5403) (re:6314) (di:complement) U32836 U32836 g1574480 Haemophilus influenzae Rd 71421 -11537092

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879714	14358	36514	354	117

Description

6500733235 mete:hi1702 tetrahydropteroyltriglutamate
methyltransferase:5-methyltetrahydropteroyltriglutamate--homocysteine
methyltransferase:methionine synthase:vitamin-b12 independent isozyme
(gtcfc:5.4:5.1) (ec:2.1.1.14) (keggfc:5.4) (tigrfc:1.2) (db:gtc-haemophilus
influenzae) HI1702 HI1702 Haemophilus influenzae 727 -11537093 83547
mete:hi1702 (ec:2.1.1.14) (de:(cobalamin-independent methionine synthase))
(db:swissprot) METE_HAEIN P45331 HAEMOPHILUS INFLUENZAE 727 -11537093
137753 5-methyltetrahydropteroyltriglutamate--homocysteine
s-methyltransferase::cobalamin-independent methionine
synthase:tetrahydropteroylglutamate methyltransferase
(cl:cobalamin-independent methionine synthase) (ec:2.1.1.14) (db:pir2.dat)
B64137 B64137 Haemophilus influenzae 727 -11537093 7500885528 hi1702
5-methyltetrahydropteroyltriglutamate- (db:genpept-bct1) (de:haemophilus
influenzae rd section 158 of 163 of the completegenome.) (nt:similar to
gb:m87049 sp:p25665 gb:m87625 gb:u00096) (le:1058) (re:3328) (di:complement)
U32843 U32843 g1574556 Haemophilus influenzae Rd 71421 -11537093 5000694345
(de:(hi1702) (pn:5-methyltetrahydropteroyltriglutamate--homocysteine
methyltransferase:methionine synthase, vitamin-b12 independent
isozyme:tetrahydropteroyltriglutamate methyltransferase:mete) (gn:mete)
(gtcfc:5.4) (ec:2.1.1.14) (sp) HI1702 HI1702 Haemophilus influenzae 727
10025761

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879744	14359	36515	612	203

Description

6500733236 sers:hi0110 seryl-trna synthetase:serine--trna ligase
(gtcfc:5.3:10.6) (ec:6.1.1.11) (keggfc:5.3:10.1:10.2) (tigrfc:12.1)
(db:gtc-haemophilus influenzae) HI0110 HI0110 Haemophilus influenzae 727
-11537094 100177 sers:hi0110 (ec:6.1.1.11) (de:seryl-trna synthetase,
(serine--trna ligase) (serrs)) (db:swissprot) SYS_HAEIN P43833 HAEMOPHILUS
INFLUENZAE 727 -11537094 142289 sers serine--trna ligase::seryl-trna
synthetase (cl:serine--trna ligase) (ec:6.1.1.11) (db:pir2.dat) I64048
I64048 Haemophilus influenzae 727 -11537094 7500892578 hi0110 seryl-trna
synthetase sers (db:genpept-bct1) (de:haemophilus influenzae rd section 11
of 163 of the complete genome.) (nt:similar to sp:p09156 gb:x05017
pid:42950) (le:5585) (re:6874) (di:direct) U32696 U32696 g1573062
Haemophilus influenzae Rd 71421 -11537094 5000694331 (de:(hi0110)
(pn:serine--trna ligase:seryl-trna synthetase:sers) (gn:sers)
(gtcfc:5.3:10.6) (ec:6.1.1.11) (sys_haein) (keggfc:5.3:10.1:10.2)
(tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0110 HI0110 Haemophilus
influenzae 727 10042031

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879745	14360	36516	1329	442

Description

6500733237 sera:hi0465 phosphoglycerate dehydrogenase:d-3-phosphoglycerate dehydrogenase:pgdh (gtcfc:5.3) (ec:1.1.1.95) (keggfc:5.3) (tigrfc:1.6) (db:gtc-haemophilus influenzae) HI0465 HI0465 Haemophilus influenzae 727 -11537095 98414 sera:hi0465 (ec:1.1.1.95) (de:d-3-phosphoglycerate dehydrogenase, (pgdh)) (db:swissprot) SERA_HAEIN P43885 HAEMOPHILUS INFLUENZAE 727 -11537095 136352 phosphoglycerate dehydrogenase (cl:phosphoglycerate dehydrogenase) (ec:1.1.1.95) (db:pir2.dat) C64070 C64070 Haemophilus influenzae 727 -11537095 7500891534 hi0465 d-3-phosphoglycerate dehydrogenase sera (db:genpept-bct1) (de:haemophilus influenzae rd section 44 of 163 of the complete genome.) (nt:similar to gb:u00096 pid:1789279 pid:2294548) (le:4627) (re:5859) (di:direct) U32729 U32729 g1573443 Haemophilus influenzae Rd 71421 -11537095 5000694334 (de:(hi0465) (pn:d-3-phosphoglycerate dehydrogenase:pgdh:phosphoglycerate dehydrogenase:sera) (gn:sera) (gtcfc:5.3) (ec:1.1.1.95) (sera_haein) (keggfc:5.3) (tigrfc:1.6) (db:gtc-haemophilus influenzae)) HI0465 HI0465 Haemophilus influenzae 727 10040291

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879747	14361	36517	387	128

Description

6500733238 ilva:hi0738b threonine dehydratase biosynthetic:threonine deaminase (gtcfc:5.3) (ec:4.2.1.16) (keggfc:5.3) (db:gtc-haemophilus influenzae) HI0738B HI0738B Haemophilus influenzae 727 -11537096 101275 ilva:hi0738.1 (ec:4.2.1.16) (de:deaminase) (db:swissprot) THD1_HAEIN P46493 HAEMOPHILUS INFLUENZAE 727 -11537096 7500893018 hi0738.1 threonine deaminase ilva (db:genpept-bct1) (de:haemophilus influenzae rd section 72 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p04968 gb:k03503 gb:m32253) (le:5577) (re:7118) (di:direct) U32757 U32757 g1573745 Haemophilus influenzae Rd 71421 -11537096 5000694336 (de:(hi07381) (pn:threonine dehydratase biosynthetic:threonine deaminase) (gn:ilva) (gtcfc:5.3) (ec:4.2.1.16) (thd1_haein) (keggfc:5.3) (db:gtc-haemophilus influenzae)) HI07381 HI07381 Haemophilus influenzae 727 10043116

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879748	14362	36518	288	95

Description

6500733239 glys:hi0924 glycyl-trna synthetase beta chain:glycine--trna ligase beta chain:glyrs (gtcfc:5.3:10.6) (ec:6.1.1.14) (keggfc:5.3:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0924 HI0924 Haemophilus influenzae 727 -11537097 100050 glys:hi0924 (ec:6.1.1.14) (de:beta chain) (glyrs)) (db:swissprot) SYGB_HAEIN P43822 HAEMOPHILUS INFLUENZAE 727 -11537097 142291 glycine--trna ligase:beta chain:glycyl-trna synthetase beta chain (cl:glycine--trna ligase beta chain) (ec:6.1.1.14) (db:pir2.dat) B64103 B64103 Haemophilus influenzae 727 -11537097 7500892413 hi0924 glycyl-trna synthetase:beta chain glys (db:genpept-bct1) (de:haemophilus influenzae rd section 89 of 163 of the complete genome.) (nt:similar to sp:p00961 gb:j01622 pid:146223) (le:4607) (re:6673) (di:complement) U32774 U32774 g1573946 Haemophilus influenzae Rd 71421 -11537097 5000694337 (de:(hi0924) (pn:glycine--trna ligase beta chain:glyrs:glycyl-trna synthetase beta chain:glys) (gn:glys) (gtcfc:5.3:10.6) (ec:6.1.1.14) (sygb_haein) (keggfc:5.3:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0924 HI0924 Haemophilus influenzae 727 10041904

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879750	14363	36519	201	66

Description

6500733240 glyq:hi0927 glycyl-trna synthetase alpha chain:glycine--trna ligase alpha chain:glyrs (gtcfc:5.3:10.6) (ec:6.1.1.14) (keggfc:5.3:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0927 HI0927 Haemophilus influenzae 727 -11537098 100046 glyq:hi0927 (ec:6.1.1.14) (de:alpha chain) (glyrs)) (db:swissprot) SYGA_HAEIN P43821 HAEMOPHILUS INFLUENZAE 727 -11537098 142290 glycine--trna ligase:alpha chain:glycyl-trna synthetase alpha chain (cl:glycine--trna ligase alpha chain) (ec:6.1.1.14) (db:pir2.dat) C64103 C64103 Haemophilus influenzae 727 -11537098 7500892405 hi0927 glycyl-trna synthetase:alpha chain glyq (db:genpept-bct1) (de:haemophilus influenzae rd section 89 of 163 of the complete genome.) (nt:similar to sp:p00960 gb:j01622 pid:146222) (le:7724) (re:8632) (di:complement) U32774 U32774 g1573948 Haemophilus influenzae Rd 71421 -11537098 5000694338 (de:(hi0927) (pn:glycine--trna ligase alpha chain:glyrs:glycyl-trna synthetase alpha chain:glyq) (gn:glyq) (gtcfc:5.3:10.6) (ec:6.1.1.14) (syga_haein) (keggfc:5.3:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0927 HI0927 Haemophilus influenzae 727 10041900

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879753	14364	36520	531	176

Description

6500733241 serb:hi1033 phosphoserine phosphatase:psp:o-phosphoserine phosphohydrolase (gtcfc:5.3) (ec:3.1.3.3) (keggfc:5.3) (tigrfc:1.6) (db:gtc-haemophilus influenzae) HI1033 HI1033 Haemophilus influenzae 727 -11537099 98418 serb:hi1033 (ec:3.1.3.3) (de:phosphohydrolase)) (db:swissprot) SERB_HAEIN P44997 HAEMOPHILUS INFLUENZAE 727 -11537099 124275 phosphoserine phosphatase::o-phosphoserine phosphohydrolase:serb protein (cl:phosphoserine phosphatase) (ec:3.1.3.3) (db:pir1.dat) I64108 I64108 Haemophilus influenzae 727 -11537099 7500891554 hi1033 phosphoserine phosphatase serb (db:genpept-bct1) (de:haemophilus influenzae rd section 99 of 163 of the complete genome.) (nt:similar to sp:p06862 gb:x03046 pid:42948 pid:537228) (le:1074) (re:2018) (di:direct) U32784 U32784 g1574066 Haemophilus influenzae Rd 71421 -11537099 5000694339 (de:(hi1033) (pn:po-phosphoserine phosphohydrolase:phosphoserine phosphatase:o-phosphoserine phosphohydrolase:serb) (gn:serb) (gtcfc:5.3) (ec:3.1.3.3) (serb_haein) (keggfc:5.3) (tigrfc:1.6) (db:gtc-haemophilus influenzae)) HI1033 HI1033 Haemophilus influenzae 727 10040295

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879776	14365	36521	1014	338

Description

6500733242 serc:hi1167 phosphoserine aminotransferase (gtcfc:5.3:9.3) (ec:2.6.1.52) (keggfc:5.3:9.3) (tigrfc:1.6) (db:gtc-haemophilus influenzae) (gtcfc:l-amino acid metabolism-glycine--serine and threonine metabolism:metabolism of cofactors and vitamins-pyridoxine metabolism (vitamin b6)) (keggfc:amino a... HI1167 HI1167 Haemophilus influenzae 727 -11537100 98421 serc:hi1167 (ec:2.6.1.52) (de:phosphoserine aminotransferase, (psat)) (db:swissprot) SERC_HAEIN P44336 HAEMOPHILUS INFLUENZAE 727 -11537100 138419 serc phosphoserine transaminase (cl:phosphoserine aminotransferase) (ec:2.6.1.52) (db:pir2.dat) E64187 E64187 Haemophilus influenzae 727 -11537100 7500891559 hi1167 phosphoserine aminotransferase serc (db:genpept-bct1) (de:haemophilus influenzae rd section 111 of 163 of the completegenome.) (nt:similar to sp:p23721 gb:u00096 pid:1651429) (le:8735) (re:9823) (di:complement) U32796 U32796 g1574094 Haemophilus influenzae Rd 71421 -11537100 5000694340 (de:(hi1167) (pn:phosphoserine aminotransferase:serc) (gn:serc) (gtcfc:5.3:9.3) (ec:2.6.1.52) (serc_haein) (keggfc:5.3:9.3) (tigrfc:1.6) (db:gtc-haemophilus influenzae)) HI1167 HI1167 Haemophilus influenzae 727 10040298

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879778	14366	36522	204	67

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879797	14367	36523	1170	389

Description

6500733243 thrs:hi1367 threonyl-trna synthetase:threonine--trna ligase:thrrs (gtcfc:5.3:10.6) (ec:6.1.1.3) (keggfc:5.3:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1367 HI1367 Haemophilus influenzae 727 -11537101 100203 thrs:hi1367 (ec:6.1.1.3) (de:(thrrs)) (db:swissprot) SYT_HAEIN P43014 HAEMOPHILUS INFLUENZAE 727 -11537101 142250 thrs threonine--trna ligase::threonyl-trna synthetase (cl:threonine--trna ligase) (ec:6.1.1.3) (db:pir2.dat) H64119 H64119 Haemophilus influenzae 727 -11537101 7500892605 hi1367 threonyl-trna synthetase thrs (db:genpept-bct1) (de:haemophilus influenzae rd section 131 of 163 of the completegenome.) (nt:similar to sp:p00955 gb:m13549 pid:147985 pid:43066) (le:7765) (re:9696) (di:direct) U32816 U32816 g1574199 Haemophilus influenzae Rd 71421 -11537101 5000694341 (de:(hi1367) (pn:threonine--trna ligase:thrrs:threonyl-trna synthetase:thrs) (gn:thrs) (gtcfc:5.3:10.6) (ec:6.1.1.3) (synt_haein) (keggfc:5.3:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI1367 HI1367 Haemophilus influenzae 727 10042057

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879802	14368	36524	630	209

Description

6500733244 cysz:hi1102 cysteine synthetase:protein homolog (gtcfc:5.3) (keggfc:14.2) (tigrfc:1.6) (db:gtc-haemophilus influenzae) HI1102 HI1102 Haemophilus influenzae 727 -11537102 67720 cysz:hi1102 (de:cysz protein homolog) (db:swissprot) CYSZ_HAEIN P45039 HAEMOPHILUS INFLUENZAE 727 -11537102 153015 cysz cysz protein (cl:cysz protein) (db:pir2.dat) E64182 E64182 Haemophilus influenzae 727 -11537102 7500879932 hi1102 cysteine synthetase:putative cysz (db:genpept-bct1) (de:haemophilus influenzae rd section 105 of 163 of the completegenome.) (nt:similar to gb:m21451 sp:p12610 gb:x12615 pid:145685) (le:1212) (re:2030) (di:direct) U32790 U32790 g1574656 Haemophilus influenzae Rd 71421 -11537102 5000694361 (de:(hi1102) (pn:protein homolog:cysteine synthetase:cysz) (gn:cysz) (gtcfc:6.10) (ec:) (cysz_haein) (keggfc:11.2) (tigrfc:1.6) (db:gtc-haemophilus influenzae)) HI1102 HI1102 Haemophilus influenzae 727 10010318

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879809	14369	36525	1368	455

Description

6500733245 fmt:hi0623 methionyl-trna formyltransferase (gtcfc:5.4:9.6:10.6) (ec:2.1.2.9) (keggfc:5.4:9.8:10.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae) (gtcfc:l-amino acid metabolism-methionine metabolism:metabolism of cofactors and vitamins-biotin metabolism (b8) and folate biosynthesis:metabolism of... HI0623 HI0623 Haemophilus influenzae 727 -11537103 72197 fmt:hi0623 (ec:2.1.2.9) (de:methionyl-trna formyltransferase,) (db:swissprot) FMT_HAEIN P44787 HAEMOPHILUS INFLUENZAE 727 -11537103 166990 methionyl-trna formyltransferase (cl:methionyl-trna formyltransferase:phosphoribosylglycinamide formyltransferase homology) (ec:2.1.2.9) (db:pir2.dat) E64082 E64082 Haemophilus influenzae 727 -11537103 7500881683 hi0623 methionyl-trna formyltransferase fmt (db:genpept-bct1) (de:haemophilus influenzae rd section 60 of 163 of the complete genome.) (nt:similar to gb:x63666 sp:p23882 gb:x00767 pid:581088) (le:4529) (re:5485) (di:direct) U32745 U32745 g1573619 Haemophilus influenzae Rd 71421 -11537103 5000694342 (de:(hi0623) (pn:methionyl-trna formyltransferase:fmt) (gn:fmt) (gtcfc:5.4:9.8:10.6) (ec:2.1.2.9) (fmt_haein) (keggfc:5.4:9.8:10.1) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0623 HI0623 Haemophilus influenzae 727 10014748

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879810	14370	36526	1827	608

Description

6500733246 metk:hi1172 s-adenosylmethionine synthetase 2:metx:s-adenosylmethionine synthetase:methionine adenosyltransferase:adomet synthetase (gtcfc:5.4:6.4:10.8) (ec:2.5.1.6) (keggfc:5.4:6.4) (tigrfc:10.2) (db:gtc-haemophilus influenzae) HI1172 HI1172 Haemophilus influenzae 727 -11537104 83566 metk:hi1172 (ec:2.5.1.6) (de:adenosyltransferase) (adomet synthetase)) (db:swissprot) METK_HAEIN P43762 HAEMOPHILUS INFLUENZAE 727 -11537104 138193 methionine adenosyltransferase (cl:methionine adenosyltransferase) (ec:2.5.1.6) (db:pir2.dat) H64187 H64187 Haemophilus influenzae 727 -11537104 7500885548 hi1172 s-adenosylmethionine synthetase metx (db:genpept-bct1) (de:haemophilus influenzae rd section 112 of 163 of the completegenome.) (nt:similar to sp:p30869 sp:p04384 gb:m98266 pid:146851) (le:2771) (re:3925) (di:direct) U32797 U32797 g1574099 Haemophilus influenzae Rd 71421 -11537104 5000694343 (de:(hi1172) (pn:s-adenosylmethionine synthetase:methionine adenosyltransferase:adomet synthetase:s-adenosylmethionine synthetase 2:metx) (gn:metk) (gtcfc:5.4:6.4) (ec:2.5.1.6) (metk_haein) (keggfc:5.4:6.4) (tigrfc:10.2) (db:gtc) HI1172 HI1172 Haemophilus influenzae 727 10025780

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879833	14371	36527	387	129

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879838	14372	36528	345	114

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879857	14373	36529	792	263

Description

6500733247 metg:hi1276 methionyl-trna synthetase:methionine--trna
ligase:metrs (gtcfc:5.4:6.4:10.6) (ec:6.1.1.10) (keggfc:5.4:6.4:10.1:10.2)
(tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1276 HI1276 Haemophilus
influenzae 727 -11537105 100122 metg:hi1276 (ec:6.1.1.10) (de:(metrs))
(db:swissprot) SYM_HAEIN P43828 HAEMOPHILUS INFLUENZAE 727 -11537105 142286
metg methionine--trna ligase::methionyl-trna synthetase (cl:methionine--trna
ligase) (ec:6.1.1.10) (db:pir2.dat) I64113 I64113 Haemophilus influenzae 727
-11537105 7500892512 hi1276 methionyl-trna synthetase metg
(db:genpept-bct1) (de:haemophilus influenzae rd section 122 of 163 of the
completegenome.) (nt:similar to gb:u00007 sp:p00959 gb:k02671 gb:x55791)
(le:4593) (re:6641) (di:complement) U32807 U32807 g1574731 Haemophilus
influenzae Rd 71421 -11537105 5000694344 (de:(hi1276) (pn:methionine--trna
ligase:metrs:methionyl-trna synthetase:metg) (gn:metg) (gtcfc:5.4:6.4:10.6)
(ec:6.1.1.10) (sym_haein) (keggfc:5.4:6.4:10.1:10.2) (tigrfc:12.1)
(db:gtc-haemophilus influenzae)) HI1276 HI1276 Haemophilus influenzae 727
10041976

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879871	14374	36530	855	285

Description

6500733248 cyss:hi0078 cys-trna synthetase:cysteinyI-trna synthetase:cysteine--trna ligase:cysrs (gtcfc:5.5:10.6) (ec:6.1.1.16) (keggfc:5.5:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0078 HI0078 Haemophilus influenzae 727 -11537106 99997 cyss:hi0078 (ec:6.1.1.16) (de:(cysrs)) (db:swissprot) SYC_HAEIN P43816 HAEMOPHILUS INFLUENZAE 727 -11537106 142293 cyss cysteine--trna ligase::cysteinyI-trna synthetase (cl:cysteine--trna ligase) (ec:6.1.1.16) (db:pir2.dat) C64047 C64047 Haemophilus influenzae 727 -11537106 7500892337 hi0078 cysteinyI-trna synthetase cyss (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:similar to gb:m59381 sp:p21888 gb:x56234 gb:x59293) (le:5891) (re:7270) (di:complement) U32693 U32693 g1573026 Haemophilus influenzae Rd 71421 -11537106 5000694580 (de:(hi0078) (pn:cysteinyI-trna synthetase:cysteine--trna ligase:cysrs:cys-trna synthetase:cyss) (gn:cyss) (gtcfc:10.6) (ec:6.1.1.16) (syc_haein) (keggfc:5.5:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0078 HI0078 Haemophilus influenzae 727 10041851

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879874	14375	36531	372	123

Description

5000694346 ilve:h10602:h1193 branched-chain-amino-acid transaminase:ilve:branched-chain amino acid aminotransferase (gtcfc:5.6:5.7:9.5) (ec:2.6.1.42) (keggfc:5.6:5.7:9.5) (tigrfc:1.3) (db:gtc-haemophilus influenzae) HI1193 HI1193 Haemophilus influenzae 727 -11537107 79260 ilve:h1193 (ec:2.6.1.42) (de:b) (bcat)) (db:swissprot) ILVE_HAEIN P54689 HAEMOPHILUS INFLUENZAE 727 -11537107 166034 amino acid aminotransferase homolog (cl:branched-chain-amino-acid transaminase bat1) (db:pir2.dat) A64189 A64189 Haemophilus influenzae 727 -11537107 7500884050 h1193 branched-chain-amino-acid transaminase ilve (db:genpept-bct1) (de:haemophilus influenzae rd section 113 of 163 of the completegenome.) (nt:similar to gb:ae000511 pid:2314646 percent) (le:9133) (re:10164) (di:complement) U32798 U32798 g1574120 Haemophilus influenzae Rd 71421 -11537107 6500733249 ilve:h10602 branched-chain-amino-acid transaminase:ilve:branched-chain amino acid aminotransferase (gtcfc:5.6:5.7:9.5) (ec:2.6.1.42) (keggfc:5.6:5.7:9.5) (tigrfc:1.3) (db:gtc-haemophilus influenzae) HI1193 HI1193 Haemophilus influenzae 727 -11537107

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879881	14376	36532	228	75

Description

6500733250 ilvc:hi0682 ketol-acid reductoisomerase:acetohydroxy-acid isomeroreductase:alpha-keto-beta-hydroxylacil reductoisomerase (gtcfc:5.7:9.5) (ec:1.1.1.86) (keggfc:5.7:9.5) (tigrfc:1.3) (db:gtc-haemophilus influenzae) HI0682 HI0682 Haemophilus influenzae 727 -11537108 136350 ketol-acid reductoisomerase (cl:escherichia coli ketol-acid reductoisomerase:ketol-acid reductoisomerase homology) (ec:1.1.1.86) (db:pir2.dat) B64086 B64086 Haemophilus influenzae 727 -11537108 7500953814 hi0682 ketol-acid reductoisomerase ilvc (db:genpept-bct1) (de:haemophilus influenzae rd section 66 of 163 of the complete genome.) (nt:similar to gb:m87049 sp:p05793 pid:146477) (le:369) (re:1847) (di:direct) U32751 U32751 g1573684 Haemophilus influenzae Rd 71421 -11537108 5000694347 (de:(hi0682) (pn:acetohydroxy-acid isomeroreductase:alpha-keto-beta-hydroxylacil reductoisomerase:ketol-acid reductoisomerase:ilvc) (gn:ilvc) (gtcfc:5.7:9.5) (ec:1.1.1.86) (ilvc_haein) (keggfc:5.7:9.5) (tigrfc:1.3) (db:gtc-haemo) HI0682 HI0682 Haemophilus influenzae 727 10069425

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879899	14377	36533	1089	362

Description

6500733251 ilvd:hi0738 dihydroxy-acid dehydratase:dad (gtcfc:5.7:9.5) (ec:4.2.1.9) (keggfc:5.7:9.5) (tigrfc:1.3) (db:gtc-haemophilus influenzae) HI0738 HI0738 Haemophilus influenzae 727 -11537109 79254 ilvd:hi0738 (ec:4.2.1.9) (de:dihydroxy-acid dehydratase, (dad)) (db:swissprot) ILVD_HAEIN P44851 HAEMOPHILUS INFLUENZAE 727 -11537109 141812 dihydroxy-acid dehydratase (cl:dihydroxy-acid dehydratase) (ec:4.2.1.9) (db:pir2.dat) G64089 G64089 Haemophilus influenzae 727 -11537109 7500884045 hi0738 dihydroxyacid dehydratase ilvd (db:genpept-bct1) (de:haemophilus influenzae rd section 72 of 163 of the complete genome.) (nt:similar to sp:p05791 gb:m10313 gb:k03503 gb:m32253) (le:3659) (re:5497) (di:direct) U32757 U32757 g1573744 Haemophilus influenzae Rd 71421 -11537109 5000694348 (de:(hi0738) (pn:dihydroxy-acid dehydratase:dad:dihydroxyacid dehydrase:ilvd) (gn:ilvd) (gtcfc:5.7:9.5) (ec:4.2.1.9) (ilvd_haein) (keggfc:5.7:9.5) (tigrfc:1.3) (db:gtc-haemophilus influenzae)) HI0738 HI0738 Haemophilus influenzae 727 10021582

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879908	14378	36534	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879911	14379	36535	462	153

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879922	14380	36536	279	92

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879931	14381	36537	615	204

Description

GTC ORF with score 506 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c31h12.) (nt:spcc31h12.07, len:759, similarity:homo sapiens,) (le:14184:14264:14495:14592) (re:14214:14435:14526:16636) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879932	14382	36538	555	184

Description

GTC ORF with score 379 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c17d11.) (nt:spbc17d11.06, len:459aa, similar eg. to ykl045w,) (le:13651:13875:14270:14905) (re:13816:14070:14861:15330) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879936	14383	36539	849	282

Description

GTC ORF with score 543 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome ii cosmid c17d11.) (nt:spbc17d11.06, len:459aa, similar eg. to ykl045w,) (le:13651:13875:14270:14905) (re:13816:14070:14861:15330) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879937	14384	36540	231	76

Description

GTC ORF with score 177 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c3lh12.) (nt:spcc3lh12.07, len:759, similarity:homo sapiens,) (le:14184:14264:14495:14592) (re:14214:14435:14526:16636) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879938	14385	36541	345	114

Description

GTC ORF with score 349 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c3lh12.) (nt:spcc3lh12.07, len:759, similarity:homo sapiens,) (le:14184:14264:14495:14592) (re:14214:14435:14526:16636) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879940	14386	36542	240	79

Description

GTC ORF with score 217 to: (sr:fission yeast) (db:genpept-pln2) (de:s.pombe chromosome iii cosmid c3lh12.) (nt:spcc3lh12.07, len:759, similarity:homo sapiens,) (le:14184:14264:14495:14592) (re:14214:14435:14526:16636) (di:directjoin)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501879949	14387	36543	186	61

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879978	14388	36544	645	214

Description

6500733252 leus:hi0921 leucyl-trna synthetase:leucine--trna ligase:leurs (gtcfc:5.7:10.6) (ec:6.1.1.4) (keggfc:5.7:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0921 HI0921 Haemophilus influenzae 727 -11537110 100115 leus:hi0921 (ec:6.1.1.4) (de:leucyl-trna synthetase, (leucine--trna ligase) (leurs)) (db:swissprot) SYL_HAEIN P43827 HAEMOPHILUS INFLUENZAE 727 -11537110 142258 leus leucine--trna ligase::leucyl-trna synthetase (cl:leucine--trna ligase) (ec:6.1.1.4) (db:pir2.dat) H64102 H64102 Haemophilus influenzae 727 -11537110 7500892495 hi0921 leucyl-trna synthetase leus (db:genpept-bct1) (de:haemophilus influenzae rd section 89 of 163 of the complete genome.) (nt:similar to sp:p07813 gb:x06331 pid:41916 gb:u00096) (le:155) (re:2740) (di:direct) U32774 U32774 g1573943 Haemophilus influenzae Rd 71421 -11537110 5000694349 (de:(hi0921) (pn:leucine--trna ligase:leurs:leucyl-trna synthetase:leus) (gn:leus) (gtcfc:5.7:10.6) (ec:6.1.1.4) (syl_haein) (keggfc:5.7:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0921 HI0921 Haemophilus influenzae 727 10041969

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879979	14389	36545	441	146

Description

6500733253 ile:hi0962 isoleucyl-trna ligase:isoleucyl-trna synthetase:isoleucine--trna ligase:ilers (gtcfc:5.7:10.6) (ec:6.1.1.5) (keggfc:5.7:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0962 HI0962 Haemophilus influenzae 727 -11537111 142260 ile:hi0962 isoleucine--trna ligase::isoleucyl-trna ligase (cl:isoleucine--trna ligase) (ec:6.1.1.5) (db:pir2.dat) A64105 A64105 Haemophilus influenzae 727 -11537111 5000694350 (de:(hi0962) (pn:isoleucyl-trna synthetase:isoleucine--trna ligase:ilers:isoleucyl-trna ligase:ilers) (gn:ilers) (gtcfc:5.7:10.6) (ec:6.1.1.5) (syi_haein) (keggfc:5.7:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0962 HI0962 Haemophilus influenzae 727 10072843

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879986	14390	36546	216	72

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879988	14391	36547	264	87

Description

6500733254 leub:hi0987 3-isopropylmalate dehydrogenase:beta-ipm dehydrogenase:imd:3-ipm-dh (gtcfc:5.7) (ec:1.1.1.85) (keggfc:5.7) (tigrfc:1.3) (db:gtc-haemophilus influenzae) HI0987 HI0987 Haemophilus influenzae 727 -11537112 81938 leub:hi0987 (ec:1.1.1.85) (de:(imd) (3-ipm-dh)) (db:swissprot) LEU3_HAEIN P43860 HAEMOPHILUS INFLUENZAE 727 -11537112 136337 3-isopropylmalate dehydrogenase (cl:3-isopropylmalate dehydrogenase) (ec:1.1.1.85) (db:pir2.dat) F64106 F64106 Haemophilus influenzae 727 -11537112 7500884947 hi0987 3-isopropylmalate dehydrogenase beta-ipm (db:genpept-bct1) (de:haemophilus influenzae rd section 94 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p30125 gb:d17631 pid:216491) (le:6578) (re:7654) (di:direct) U32779 U32779 g1574016 Haemophilus influenzae Rd 71421 -11537112 5000694351 (de:(hi0987) (pn:imd:3-ipm-dh:3-isopropylmalate dehydrogenase:beta-ipm dehydrogenase:leub) (gn:leub) (gtcfc:5.7) (ec:1.1.1.85) (leu3_haein) (keggfc:5.7) (tigrfc:1.3) (db:gtc-haemophilus influenzae)) HI0987 HI0987 Haemophilus influenzae 727 10024172

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501879992	14392	36548	483	160

Description

6500733255 leuc:hi0988 3-isopropylmalate dehydratase:alpha subunit:3-isopropylmalate dehydratase:isopropylmalate isomerase:alpha-ipm isomerase:ipmi (gtcfc:5.7) (ec:4.2.1.33) (keggfc:5.7) (tigrfc:1.3) (db:gtc-haemophilus influenzae) HI0988 HI0988 Haemophilus influenzae 727 -11537113 166593 leuc 3-isopropylmalate dehydratase:chain leuc (ec:4.2.1.33) (db:pir2.dat) F64163 F64163 Haemophilus influenzae 727 -11537113 7500960645 hi0988 3-isopropylmalate dehydratase:alpha subunit (db:genpept-bct1) (de:haemophilus influenzae rd section 94 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p30127 gb:d17631 gb:d17632) (le:7830) (re:9239) (di:direct) U32779 U32779 g1574017 Haemophilus influenzae Rd 71421 -11537113 5000694352 (de:(hi0988) (pn:3-isopropylmalate dehydratase:isopropylmalate isomerase:alpha-ipm isomerase:ipmi:3-isopropylmalate dehydratase, alpha subunit:leuc) (gn:leuc) (gtcfc:5.7) (ec:4.2.1.33) (leu2_haein) (keggfc:5.7) (tigrfc:1.3) (db:) HI0988 HI0988 Haemophilus influenzae 727 10088165

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880010	14393	36549	1425	474

Description

6500733256 leud:hi0989 3-isopropylmalate dehydratase:isopropylmalate isomerase:alpha-ipm isomerase (gtcfc:5.7) (ec:4.2.1.33) (keggfc:5.7) (tigrfc:1.3) (db:gtc-haemophilus influenzae) HI0989 HI0989 Haemophilus influenzae 727 -11537114 81961 leud:hi0989 (ec:4.2.1.33) (de:(isopropylmalate isomerase) (alpha-ipm isomerase)) (db:swissprot) LEUD_HAEIN P44438 HAEMOPHILUS INFLUENZAE 727 -11537114 165967 leud 3-isopropylmalate dehydratase:small chain (cl:3-isopropylmalate dehydratase small chain) (ec:4.2.1.33) (db:pir2.dat) G64106 G64106 Haemophilus influenzae 727 -11537114 7500884958 hi0989 3-isopropylmalate dehydratase small subunit (db:genpept-bct1) (de:haemophilus influenzae rd section 94 of 163 of the complete genome.) (nt:similar to gb:d10483 sp:p30126 pid:216489 gb:u00096) (le:9263) (re:9865) (di:direct) U32779 U32779 g1574018 Haemophilus influenzae Rd 71421 -11537114 5000694353 (de:(hi0989) (pn:isopropylmalate isomerase:alpha-ipm isomerase:3-isopropylmalate dehydratase:leud) (gn:leud) (gtcfc:5.7) (ec:4.2.1.33) (leud_haein) (keggfc:5.7) (tigrfc:1.3) (db:gtc-haemophilus influenzae)) HI0989 HI0989 Haemophilus influenzae 727 10024195

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880014	14394	36550	222	73

Description

6500733257 vals:hi1391 valyl-trna synthetase:valine--trna ligase:valrs (gtcfc:5.7:10.6) (ec:6.1.1.9) (keggfc:5.7:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1391 HI1391 Haemophilus influenzae 727 -11537115 100216 vals:hi1391 (ec:6.1.1.9) (de:valyl-trna synthetase, (valine--trna ligase) (valrs)) (db:swissprot) SYV_HAEIN P43834 HAEMOPHILUS INFLUENZAE 727 -11537115 142278 vals valine--trna ligase::valyl-trna synthetase (cl:valine--trna ligase) (ec:6.1.1.9) (db:pir2.dat) G64121 G64121 Haemophilus influenzae 727 -11537115 7500892620 hi1391 valyl-trna synthetase vals (db:genpept-bct1) (de:haemophilus influenzae rd section 134 of 163 of the completegenome.) (nt:similar to sp:p07118 gb:j03497 gb:x05891 pid:147906) (le:7836) (re:10700) (di:complement) U32819 U32819 g1574225 Haemophilus influenzae Rd 71421 -11537115 5000694354 (de:(hi1391) (pn:valine--trna ligase:valrs:valyl-trna synthetase:vals) (gn:vals) (gtcfc:5.7:10.6) (ec:6.1.1.9) (syv_haein) (keggfc:5.7:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI1391 HI1391 Haemophilus influenzae 727 10042070

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880017	14395	36551	237	78

Description

6500733258 ilvg:hi0737 acetohydroxy acid synthase ii (gtcfc:5.7) (keggfc:14.2) (tigrfc:1.3) (db:gtc-haemophilus influenzae) HI0737 HI0737 Haemophilus influenzae 727 -11537116 141698 acetolactate synthase:ii (cl:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology) (ec:4.1.3.18) (db:pir2.dat) F64089 F64089 Haemophilus influenzae 727 -11537116 7500954400 hi0737 acetohydroxy acid synthase ii:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 72 of 163 of the complete genome.) (nt:similar to gb:m10313 sp:p00892 gb:m32253 gb:v00290) (le:2790) (re:3587) (di:direct) U32757 U32757 g1573743 Haemophilus influenzae Rd 71421 -11537116 5000694355 (de:(hi0737) (pn:acetohydroxy acid synthase ii:ilvg) (gn:ilvg) (gtcfc:5.7) (ec:) (keggfc:11.2) (tigrfc:1.3) (db:gtc-haemophilus influenzae)) HI0737 HI0737 Haemophilus influenzae 727 10072563

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880019	14396	36552	228	75

Description

6500733259 genx:hi0836 lysyl-trna synthetase analog:hypothetical lysyl-trna synthetase homolog:gx (gtcfc:5.8:10.6) (ec:6.1.1.6) (keggfc:5.8:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI0836 HI0836 Haemophilus influenzae 727 -11537117 166975 genx lysine--trna ligase:genx (ec:6.1.1.6) (db:pir2.dat) I64097 I64097 Haemophilus influenzae 727 -11537117 7500960712 hi0836 lysyl-trna synthetase analog genx (db:genpept-bct1) (de:haemophilus influenzae rd section 80 of 163 of the complete genome.) (nt:similar to gb:u14003 sp:p03812 gb:j01611 gb:x59988) (le:8672) (re:9673) (di:direct) U32765 U32765 g1573850 Haemophilus influenzae Rd 71421 -11537117 5000694586 (de:(hi0836) (pn:hypothetical lysyl-trna synthetase homolog:gx:lysyl-trna synthetase analog:genx) (gn:genx) (gtcfc:10.6) (ec:6.1.1.6) (syk3_haein) (keggfc:5.8:10.1:10.2) (tigrfc:12.1) (db:gtc-haemophilus influenzae)) HI0836 HI0836 Haemophilus influenzae 727 10088224

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880021	14397	36553	663	220

Description

GTC ORF with score 148 to: (sr:drosophila melanogaster (strain iso-1) (library: gt11 embryoni) (db:genpept-inv) (de:drosophila melanogaster brahma protein mrna, complete cds.) (nt:homeotic gene regulator) (le:55) (re:4971) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880030	14398	36554	957	318

Description

6500733260 mure:hi1133 udp-murnac-tripeptide
synthetase:udp-n-acetylmuramoylalanyl-d-glutamate--2:6-diaminopimelate
ligase:udp-n-acetylmuramyl-tripeptide synthetase (gtcfc:5.8:11.4)
(ec:6.3.2.13) (keggfc:5.8:7.3) (tigrfc:3.2) (db:gtc-haemophilus influenzae)
HI1133 HI1133 Haemophilus influenzae 727 -11537118 84713 mure:hi1133
(ec:6.3.2.13) (de:(ec 6.3.2.13) (udp-n-acetylmuramyl-tripeptide synthetase))
(db:swissprot) MURE_HAEIN P45060 HAEMOPHILUS INFLUENZAE 727 -11537118
167244 udp-n-acetylmuramoylalanyl-d-glutamate--2:6-diaminopimelate
ligase::meso-diaminopimelate-adding enzyme:udp-murnac-tripeptide synthetase
mure:udp-n-acetylmuramoyl-tripeptide synthetase (ec:6.3.2.13) (db:pir2.dat)
H64184 H64184 Haemophilus influenzae 727 -11537118 7500886133 hi1133
udp-n-acetylmuramyl-tripeptide synthetase (db:genpept-bct1) (de:haemophilus
influenzae rd section 108 of 163 of the completegenome.) (nt:similar to
gb:d10483 sp:p22188 gb:x55814 pid:285768) (le:3763) (re:5229) (di:direct)
U32793 U32793 g1574688 Haemophilus influenzae Rd 71421 -11537118 5000694382
(de:(hi1133) (pn:udp-n-acetylmuramoylalanyl-d-glutamate--2,6-diaminopimelate
ligase:udp-n-acetylmuramyl-tripeptide synthetase:udp-murnac-tripeptide
synthetase:mure) (gn:mure) (gtcfc:7.2) (ec:6.3.2.13) (mure_haein)
(keggfc:5.8:7.3) HI1133 HI1133 Haemophilus influenzae 727 10026904

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880045	14399	36555	225	74

Description

6500733261 murf:hi1134
 udp-n-acetylmuramoylalanyl-d-glutamyl-2:6-diaminopimelate--d-alanyl-d-alanyl
 ligase:udp-murnac-pentapeptide synthetase:d-alanyl-d-alanine-adding enzyme
 (gtcfc:5.8:11.4) (ec:6.3.2.15) (keggfc:5.8:7.3) (tigrfc:3.2)
 (db:gtc-haemophilus influenzae) HI1134 HI1134 Haemophilus influenzae 727
 -11537119 84715 murf:hi1134 (ec:6.3.2.15) (de:(d-alanyl-d-alanine-adding
 enzyme)) (db:swissprot) MURF_HAEIN P45061 HAEMOPHILUS INFLUENZAE 727
 -11537119 167243
 udp-n-acetylmuramoylalanyl-d-glutamyl-2:6-diaminopimelate--d-alanyl-d-alanin
 e ligase:precursor:udp-n-acetylmuramoyl-pentapeptide synthetase
 (ec:6.3.2.15) (db:pir2.dat) I64184 I64184 Haemophilus influenzae 727
 -11537119 7500886147 hi1134 udp-murnac-pentapeptide synthetase murf
 (db:genpept-bct1) (de:haemophilus influenzae rd section 108 of 163 of the
 completegenome.) (nt:similar to gb:d10483 sp:p11880 pid:216500 pid:40854)
 (le:5243) (re:6616) (di:direct) U32793 U32793 g1574689 Haemophilus
 influenzae Rd 71421 -11537119 5000694383 (de:(hi1134)
 (pn:udp-n-acetylmuramoylalanyl-d-glutamyl-2,6-diaminopimelate--d-
 alanyl-d-alanyl ligase:d- alanyl-d-alanine-adding
 enzyme:udp-murnac-pentapeptide synthetase:murf) (gn:murf) (gtcfc:7.2)
 (ec:6.3.2.15) (murf_haein) (ke) HI1134 HI1134 Haemophilus influenzae 727
 10026906

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880051	14400	36556	1131	376

Description

5000694588 lyss:lysu:hi1211 lysu:lysyl-trna synthetase:lysine--trna
 ligase:lysrs (gtcfc:5.8:10.6) (ec:6.1.1.6) (keggfc:5.8:10.1:10.2)
 (tigrfc:12.1) (db:gtc-haemophilus influenzae) HI1211 HI1211 Haemophilus
 influenzae 727 -11537120 100098 lyss:lysu:hi1211 (ec:6.1.1.6)
 (de:lysyl-trna synthetase, (lysine--trna ligase) (lysrs)) (db:swissprot)
 SYK_HAEIN P43825 HAEMOPHILUS INFLUENZAE 727 -11537120 142262 lysine--trna
 ligase::lysyl-trna synthetase (cl:lysine--trna ligase) (ec:6.1.1.6)
 (db:pir2.dat) D64110 D64110 Haemophilus influenzae 727 -11537120 7500892471
 hi1211 lysyl-trna synthetase lysu (db:genpept-bct1) (de:haemophilus
 influenzae rd section 115 of 163 of the completegenome.) (nt:similar to
 gb:u14003 gb:j03795 sp:p13030 sp:p14825) (le:6660) (re:8168) (di:complement)
 U32800 U32800 g1574141 Haemophilus influenzae Rd 71421 -11537120 6500733262
 lyss:lysu lysu:lysyl-trna synthetase:lysine--trna ligase:lysrs
 (gtcfc:5.8:10.6) (ec:6.1.1.6) (keggfc:5.8:10.1:10.2) (tigrfc:12.1)
 (db:gtc-haemophilus influenzae) HI1211 HI1211 Haemophilus influenzae 727
 -11537120

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880059	14401	36557	303	100

Description

6500733263 hflc:hi0150 lambda cii stability-governing protein:protein
(gtcfc:5.9:10.11) (ec:3.4.-.-) (keggfc:5.9) (tigrfc:12.2)
(db:gtc-haemophilus influenzae) HI0150 HI0150 Haemophilus influenzae 727
-11537121 76909 hflc:hi0150 (ec:3.4.-.-) (de:hflc protein,) (db:swissprot)
HFLC_HAEIN P44545 HAEMOPHILUS INFLUENZAE 727 -11537121 166940 probable
integral membrane proteinase hflc homolog (db:pir2.dat) I64050 I64050
Haemophilus influenzae 727 -11537121 7500883237 hi0150 hflc protein hflc
(db:genpept-bct1) (de:haemophilus influenzae rd section 16 of 163 of the
complete genome.) (nt:similar to sp:p25661 gb:u00005 pid:436158) (le:566)
(re:1453) (di:complement) U32701 U32701 g1573107 Haemophilus influenzae Rd
71421 -11537121 5000694356 (de:(hi0150) (pn:protein:lambda cii
stability-governing protein:hflc) (gn:hflc) (gtcfc:5.9) (ec:3.4.-.-)
(hflc_haein) (keggfc:5.9) (tigrfc:12.2) (db:gtc-haemophilus influenzae))
HI0150 HI0150 Haemophilus influenzae 727 10019271

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880060	14402	36558	270	89

Description

6500733264 collagenase:prtc:putative protease hi0419 (gtcfc:5.9:10.11)
(ec:3.4.-.-) (keggfc:5.9) (tigrfc:12.2) (db:gtc-haemophilus influenzae)
HI0419 HI0419 Haemophilus influenzae 727 -11537122 112650 hi0419
(ec:3.4.-.-) (de:putative protease hi0419,) (db:swissprot) YEQG_HAEIN P44700
HAEMOPHILUS INFLUENZAE 727 -11537122 166062 collagenase prtc homolog
(cl:collagenase prtc) (db:pir2.dat) G64066 G64066 Haemophilus influenzae 727
-11537122 7500923007 hi0419 protease:putative (db:genpept-bct1)
(de:haemophilus influenzae rd section 40 of 163 of the complete genome.)
(nt:similar to gb:u00096 sp:p76403 pid:1736789) (le:4429) (re:5811)
(di:direct) U32725 U32725 g1573393 Haemophilus influenzae Rd 71421 -11537122
5000694357 (de:(hi0419) (pn:putative protease hi0419:collagenase:prtc)
(gtcfc:5.9) (ec:3.4.-.-) (yhbu_haein) (keggfc:5.9) (tigrfc:12.2)
(db:gtc-haemophilus influenzae)) HI0419 HI0419 Haemophilus influenzae 727
10054378

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880093	14403	36559	978	325

Description

6500733265 pepe:hi0587 peptidase e:alpha-aspartyl dipeptidase (gtcfc:5.9:10.11) (ec:3.4.-.-) (keggfc:5.9) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI0587 HI0587 Haemophilus influenzae 727 -11537123 89017 pepe:hi0587 (ec:3.4.-.-) (de:peptidase e, (alpha-aspartyl dipeptidase)) (db:swissprot) PEPE_HAEIN P44766 HAEMOPHILUS INFLUENZAE 727 -11537123 167074 peptidase e homolog (cl:alpha-aspartyl dipeptidase) (db:pir2.dat) C64079 C64079 Haemophilus influenzae 727 -11537123 7500887816 hi0587 peptidase e pepe (db:genpept-bct1) (de:haemophilus influenzae rd section 55 of 163 of the complete genome.) (nt:similar to sp:p32666 pid:396356 gb:u00096) (le:5144) (re:5824) (di:complement) U32740 U32740 g1573577 Haemophilus influenzae Rd 71421 -11537123 5000694358 (de:(hi0587) (pn:alpha-aspartyl dipeptidase:peptidase e:pepe) (gn:pepe) (gtcfc:5.9) (ec:3.4.-.-) (pepe_haein) (keggfc:5.9) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI0587 HI0587 Haemophilus influenzae 727 10031143

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880097	14404	36560	441	146

Description

6500733266 sppa:hi1541 protease iv:endopeptidase iv (gtcfc:5.9:10.11) (ec:3.4.-.-) (keggfc:5.9) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI1541 HI1541 Haemophilus influenzae 727 -11537124 99303 sppa:hi1541 (ec:3.4.-.-) (de:protease iv, (endopeptidase iv)) (db:swissprot) SPPA_HAEIN P45243 HAEMOPHILUS INFLUENZAE 727 -11537124 167111 proteinase iv homolog (cl:proteinase iv) (db:pir2.dat) F64128 F64128 Haemophilus influenzae 727 -11537124 7500891994 hi1541 protease iv sppa (db:genpept-bct1) (de:haemophilus influenzae rd section 144 of 163 of the completegenome.) (nt:similar to gb:m13359 sp:p08395 gb:u13772 gb:u13773) (le:7266) (re:9113) (di:complement) U32829 U32829 g1574383 Haemophilus influenzae Rd 71421 -11537124 5000694359 (de:(hi1541) (pn:endopeptidase iv:protease iv:sppa) (gn:sppa) (gtcfc:5.9) (ec:3.4.-.-) (sppa_haein) (keggfc:5.9) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI1541 HI1541 Haemophilus influenzae 727 10041162

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880106	14405	36561	441	146

Description

6500733267 sohb:hi1682 putative protease:possible protease (gtcfc:5.9:10.11) (ec:3.4.-.-) (keggfc:5.9) (tigrfc:12.2) (db:gtc-haemophilus influenzae) HI1682 HI1682 Haemophilus influenzae 727 -11537125 98948 sohb:hi1682 (ec:3.4.-.-) (de:possible protease sohb,) (db:swissprot) SOHB_HAEIN P45315 HAEMOPHILUS INFLUENZAE 727 -11537125 167108 sohb probable serine proteinase:sohb (ec:3.4.-.-) (db:pir2.dat) D64136 D64136 Haemophilus influenzae 727 -11537125 7500891849 hi1682 protease:putative sohb (db:genpept-bct1) (de:haemophilus influenzae rd section 156 of 163 of the completegenome.) (nt:similar to gb:m73320 sp:p24213 pid:290470 gb:u00096) (le:5274) (re:6335) (di:direct) U32841 U32841 g1574534 Haemophilus influenzae Rd 71421 -11537125 5000694360 (de:(hi1682) (pn:possible protease :putative protease:sohb) (gn:sohb) (gtcfc:5.9) (ec:3.4.-.-) (sohb_haein) (keggfc:5.9) (tigrfc:12.2) (db:gtc-haemophilus influenzae)) HI1682 HI1682 Haemophilus influenzae 727 10040813

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880114	14406	36562	225	74

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880115	14407	36563	201	66

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880117	14408	36564	1317	438

Description

6500733268 ddlb:hi1140 d-alanine-d-alanine ligase:d-alanine--d-alanine
ligase:d-alanylalanine synthetase (gtcfc:6.15:8.1:11.4) (ec:6.3.2.4)
(keggfc:6.8:7.3:8.1) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1140
HI1140 Haemophilus influenzae 727 -11537126 68161 ddlb:hi1140 (ec:6.3.2.4)
(de:d-alanine--d-alanine ligase, (d-alanylalanine synthetase))
(db:swissprot) DDL_HAEIN P44405 HAEMOPHILUS INFLUENZAE 727 -11537126 142382
d-alanine--d-alanine ligase:b (cl:d-alanine--d-alanine ligase) (ec:6.3.2.4)
(db:pir2.dat) F64185 F64185 Haemophilus influenzae 727 -11537126 7500880109
hi1140 d-alanine--d-alanine ligase ddlb (db:genpept-bct1) (de:haemophilus
influenzae rd section 109 of 163 of the completegenome.) (nt:similar to
gb:d10483 sp:p07862 gb:k02668 pid:145724) (le:1598) (re:2518) (di:direct)
U32794 U32794 g1574696 Haemophilus influenzae Rd 71421 -11537126 5000694362
(de:(hi1140) (pn:d-alanine--d-alanine ligase:d-alanylalanine
synthetase:d-alanine-d-alanine ligase:ddlb) (gn:ddlb) (gtcfc:6.15:7.2)
(ec:6.3.2.4) (ddl_haein) (keggfc:6.8:7.3) (tigrfc:3.2) (db:gtc-haemophilus
influenzae)) HI1140 HI1140 Haemophilus influenzae 727 10010754

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880127	14409	36565	216	71

Description

GTC ORF with score 264 to: (sr:fission yeast) (db:genpept-pln1) (ec:1.8.1.4)
(de:schizosaccharomyces pombe dihydrolipoamide dehydrogenase (dl dh)mrna,
complete cds.) (nt:one of the g1 arrest mutant phenotype suppression)
(le:53) (re:1591) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LENGTH</u>	<u>AA</u> <u>LENGTH</u>
7501880128	14410	36566	873	290

Description

GTC ORF with score 985 to: (sr:fission yeast) (db:genpept-pln1) (ec:1.8.1.4)
(de:schizosaccharomyces pombe dihydrolipoamide dehydrogenase (dl dh)mrna,
complete cds.) (nt:one of the g1 arrest mutant phenotype suppression)
(le:53) (re:1591) (di:direct)

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880138	14411	36567	366	121

Description

5000694364 trxa:trxm:hi0084 thioredoxin m (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.10) (db:gtc-haemophilus influenzae) HI0084 HI0084 Haemophilus influenzae 727 -11537127 101382 trxa:trxm:hi0084 (de:thioredoxin (trx)) (db:swissprot) THIO_HAEIN P43785 HAEMOPHILUS INFLUENZAE 727 -11537127 135826 thioredoxin (cl:thioredoxin:thioredoxin homology) (db:pir2.dat) E64047 E64047 Haemophilus influenzae 727 -11537127 7500893083 hi0084 thioredoxin trxm (db:genpept-bct1) (de:haemophilus influenzae rd section 8 of 163 of the complete genome.) (nt:similar to gb:j04475 sp:p12243 pid:142154 percent) (le:10050) (re:10373) (di:complement) U32693 U32693 g1573030 Haemophilus influenzae Rd 71421 -11537127 6500733269 trxa:trxm thioredoxin m (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.10) (db:gtc-haemophilus influenzae) HI0084 HI0084 Haemophilus influenzae 727 -11537127

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880142	14412	36568	570	189

Description

5000694365 thioredoxin:trxa:thioredoxin-like protein hi1115 (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.10) (db:gtc-haemophilus influenzae) HI1115 HI1115 Haemophilus influenzae 727 -11537128 101403 hi1115 (de:thioredoxin-like protein hi1115) (db:swissprot) THIX_HAEIN P43787 HAEMOPHILUS INFLUENZAE 727 -11537128 167190 hypothetical protein hi1115 (cl:thioredoxin homology) (db:pir2.dat) G64183 G64183 Haemophilus influenzae 727 -11537128 7500893099 hi1115 thioredoxin:putative (db:genpept-bct1) (de:haemophilus influenzae rd section 106 of 163 of the completegenome.) (nt:similar to pid:1213065 sp:p52229 percent ident:) (le:7980) (re:8483) (di:complement) U32791 U32791 g1574669 Haemophilus influenzae Rd 71421 -11537128 6500733270 thioredoxin:trxa:thioredoxin-like protein hi1115 (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.10) (db:gtc-haemophilus influenzae) HI1115 HI1115 Haemophilus influenzae 727 -11537128

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880146	14413	36569	378	125

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880153	14414	36570	1566	521

Description

5000694366 thioredoxin:trxa:hypothetical protein (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.10) (db:gtc-haemophilus influenzae) HI1159 HI1159 Haemophilus influenzae 727 -11537129 110094 hi1159 (de:hypothetical protein hi1159) (db:swissprot) YBBN_HAEIN P43786 HAEMOPHILUS INFLUENZAE 727 -11537129 167191 hypothetical protein hi1159 (db:pir2.dat) H64186 H64186 Haemophilus influenzae 727 -11537129 7500896577 hi1159 conserved hypothetical protein (db:genpept-bct1) (de:haemophilus influenzae rd section 110 of 163 of the completegenome.) (nt:similar to gb:u00096 sp:p77395 pid:1773174) (le:9215) (re:9868) (di:complement) U32795 U32795 g1574716 Haemophilus influenzae Rd 71421 -11537129 6500733271 thioredoxin:trxa:hypothetical protein (gtcfc:9.13) (keggfc:14.2) (tigrfc:2.10) (db:gtc-haemophilus influenzae) HI1159 HI1159 Haemophilus influenzae 727 -11537129

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880162	14415	36571	450	149

Description

GTC ORF with score 112 to: (fn:actin patch assembly and localization) (sr:fission yeast) (db:genpept-pln1) (de:schizosaccharomyces pombe wiskott-aldrich syndrome protein homolog(wspl+) gene, complete cds, and btf3/beta-nac gene, partialsequence.) ...

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880185	14416	36572	231	76

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880189	14417	36573	468	155
<u>Description</u>				

6500733272 seld:hi0200 selenium metabolism protein:selenide:water
dikinase:selenophosphate synthetase:selenium donor protein (gtcfc:6.4:10.6)
(ec:2.7.9.3) (keggfc:6.4) (tigrfc:12.1) (db:gtc-haemophilus influenzae)
HI0200 HI0200 Haemophilus influenzae 727 -11537130 167154 selenophosphate
synthase (db:pir2.dat) A64054 A64054 Haemophilus influenzae 727 -11537130
7500960734 hi0200 selenide:water dikinase seld (db:genpept-bct1)
(de:haemophilus influenzae rd section 20 of 163 of the complete genome.)
(nt:similar to gb:m30184 sp:p16456 pid:147806) (le:2848) (re:3819)
(di:direct) U32705 U32705 g1573160 Haemophilus influenzae Rd 71421 -11537130
5000694367 (de:(hi0200) (pn:selenide, water dikinase:selenophosphate
synthetase:selenium donor protein:selenium metabolism protein:seld)
(gn:seld) (gtcfc:6.4) (ec:2.7.9.3) (seld_haein) (keggfc:6.4) (tigrfc:12.1)
(db:gtc-haemophilus influen) HI0200 HI0200 Haemophilus influenzae 727
10088294

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880192	14418	36574	1170	389
<u>Description</u>				

6500733273 sela:hi0708 l-seryl-trna:cysteiny-l-trna:ser selenium
transferase:selenocysteine synthase:selenocysteiny-l-trna:ser synthase
(gtcfc:6.4:10.6) (ec:2.9.1.1) (keggfc:6.4) (tigrfc:12.1) (db:gtc-haemophilus
influenzae) HI0708 HI0708 Haemophilus influenzae 727 -11537131 98382
sela:hi0708 (ec:2.9.1.1) (de:(selenocysteiny-l-trna(sec) synthase))
(db:swissprot) SELA_HAEIN P43910 HAEMOPHILUS INFLUENZAE 727 -11537131
166069 seryl-trna sec selenium transferase (ec:2.9.1.1) (db:pir2.dat)
H64087 H64087 Haemophilus influenzae 727 -11537131 7500891513 hi0708
l-seryl-trna selenium transferase sela (db:genpept-bct1) (de:haemophilus
influenzae rd section 68 of 163 of the complete genome.) (nt:similar to
sp:p23328 gb:m64177 pid:147804) (le:8052) (re:9437) (di:direct) U32753
U32753 g1573709 Haemophilus influenzae Rd 71421 -11537131 5000694368
(de:(hi0708) (pn:l-seryl-trna:ser selenium transferase:selenocysteine
synthase:selenocysteiny-l-trna:ser synthase:cysteiny-l-trna:ser selenium
transferase:sela) (gn:sela) (gtcfc:6.4) (ec:2.9.1.1) (sela_haein)
(keggfc:6.4) (tigrfc) HI0708 HI0708 Haemophilus influenzae 727 10040259

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880215	14419	36575	228	76
<u>Description</u>				

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880218	14420	36576	1404	467

Description

6500733274 murd:hi1136 udp-n-acetylmuramoylalanine-d-glutamate
 ligase:udp-n-acetylmuramoylalanine--d-glutamate
 ligase:udp-n-acetylmuranoyl-l-alanyl-d-glutamate synthetase (gtcfc:6.7:11.4)
 (ec:6.3.2.9) (keggfc:6.6:7.3) (tigrfc:3.2) (db:gtc-haemophilus influenzae)
 HI1136 HI1136 Haemophilus influenzae 727 -11537132 84710 murd:hi1136
 (ec:6.3.2.9) (de:adding enzyme)) (db:swissprot) MURD_HAEIN P45063
 HAEMOPHILUS INFLUENZAE 727 -11537132 142393
 udp-n-acetylmuramoylalanine--d-glutamate ligase
 (cl:udp-n-acetylmuramate--alanine ligase) (ec:6.3.2.9) (db:pir2.dat) B64185
 B64185 Haemophilus influenzae 727 -11537132 7500886123 hi1136
 udp-n-acetylmuramoylalanine--d-glutamate ligase (db:genpept-bct1)
 (de:haemophilus influenzae rd section 108 of 163 of the completegenome.)
 (nt:similar to gb:d10483 sp:p14900 sp:p20100 gb:m30807) (le:7815) (re:9128)
 (di:direct) U32793 U32793 g1574691 Haemophilus influenzae Rd 71421 -11537132
 5000694369 (de:(hi1136) (pn:udp-n-acetylmuramoylalanine--d-glutamate
 ligase:udp-n- acetylmuranoyl-l-alanyl-d-glutamate
 synthetase:udp-n-acetylmuramoylalanine-d-glutamate ligase:murd) (gn:murd)
 (gtcfc:6.7:7.2) (ec:6.3.2.9) (murd_haein) (kegg) HI1136 HI1136 Haemophilus
 influenzae 727 10026901

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880221	14421	36577	366	121

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880222	14422	36578	267	88

Description

6500733275 murc:hi1139 udp-n-acetylmuramate-alanine ligase:udp-n-acetylmuramate--alanine ligase:udp-n-acetylmuranoyl-l-alanine synthetase (gtcfc:6.7:11.4) (ec:6.3.2.8) (keggfc:6.6:7.3) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI1139 HI1139 Haemophilus influenzae 727 -11537133 84707 murc:hi1139 (ec:6.3.2.8) (de:acetylmuranoyl-l-alanine synthetase)) (db:swissprot) MURC_HAEIN P45066 HAEMOPHILUS INFLUENZAE 727 -11537133 142392 udp-n-acetylmuramate--alanine ligase (cl:udp-n-acetylmuramate--alanine ligase) (ec:6.3.2.8) (db:pir2.dat) E64185 E64185 Haemophilus influenzae 727 -11537133 7500886103 hi1139 udp-n-acetylmuramate--alanine ligase murc (db:genpept-bct1) (de:haemophilus influenzae rd section 109 of 163 of the completegenome.) (nt:similar to gb:d10483 sp:p17952 pid:216505 pid:40859) (le:99) (re:1526) (di:direct) U32794 U32794 g1574695 Haemophilus influenzae Rd 71421 -11537133 5000694370 (de:(hi1139) (pn:udp-n-acetylmuramate--alanine ligase:udp-n-acetylmuranoyl-l- alanine synthetase:udp-n-acetylmuramate-alanine ligase:murc) (gn:murc) (gtcfc:6.7:7.2) (ec:6.3.2.8) (murc_haein) (keggfc:6.6:7.3) (tigrfc:3.2) (db:gtc) HI1139 HI1139 Haemophilus influenzae 727 10026898

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880228	14423	36579	327	108

Description

Hypothetical protein

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880256	14424	36580	972	323

Description

6500733276 naga:hi0140 n-acetylglucosamine-6-phosphate deacetylase (gtcfc:7.1) (ec:3.5.1.25) (keggfc:4.4) (tigrfc:5.1) (db:gtc-haemophilus influenzae) HI0140 HI0140 Haemophilus influenzae 727 -11537134 85158 naga:hi0140 (ec:3.5.1.25) (de:deacetylase)) (db:swissprot) NAGA_HAEIN P44537 HAEMOPHILUS INFLUENZAE 727 -11537134 167018 n-acetylglucosamine-6-phosphate deacetylase (ec:3.5.1.25) (db:pir2.dat) E64050 E64050 Haemophilus influenzae 727 -11537134 7500886258 hi0140 n-acetylglucosamine-6-phosphate deacetylase (db:genpept-bct1) (de:haemophilus influenzae rd section 15 of 163 of the complete genome.) (nt:similar to sp:p15300 gb:x14135 pid:42079 gb:u00096) (le:125) (re:1270) (di:complement) U32700 U32700 g1573096 Haemophilus influenzae Rd 71421 -11537134 5000694371 (de:(hi0140) (pn:n-acetylglucosamine-6-phosphate deacetylase:naga) (gn:naga) (gtcfc:7.1) (ec:3.5.1.25) (naga_haein) (keggfc:4.4) (tigrfc:5.1) (db:gtc-haemophilus influenzae)) HI0140 HI0140 Haemophilus influenzae 727 10027339

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880261	14425	36581	729	242

Description

6500733277 nagb:hi0141 glucosamine-6-phosphate deaminase
protein:glucosamine-6-phosphate isomerase:glucosamine-6-phosphate deaminase
(gtcfc:7.1) (ec:5.3.1.10) (keggfc:4.4) (tigrfc:5.1) (db:gtc-haemophilus
influenzae) HI0141 HI0141 Haemophilus influenzae 727 -11537135 85161
nagb:hi0141 (ec:5.3.1.10) (de:phosphate deaminase) (gnpda)) (db:swissprot)
NAGB_HAEIN P44538 HAEMOPHILUS INFLUENZAE 727 -11537135 142147
glucosamine-6-phosphate isomerase (cl:glucosamine-6-phosphate isomerase)
(ec:5.3.1.10) (db:pir2.dat) F64050 F64050 Haemophilus influenzae 727
-11537135 7500886273 hi0141 glucosamine-6-phosphate isomerase nagb
(db:genpept-bct1) (de:haemophilus influenzae rd section 15 of 163 of the
complete genome.) (nt:similar to gb:m19284 sp:p09375 pid:455176 gb:u00096)
(1e:1543) (re:2355) (di:complement) U32700 U32700 g1573097 Haemophilus
influenzae Rd 71421 -11537135 5000694372 (de:(hi0141)
(pn:glucosamine-6-phosphate isomerase:glucosamine-6-phosphate
deaminase:glucosamine-6-phosphate deaminase protein:nagb) (gn:nagb)
(gtcfc:7.1) (ec:5.3.1.10) (nagb_haein) (keggfc:4.4) (tigrfc:5.1)
(db:gtc-haemophilus) HI0141 HI0141 Haemophilus influenzae 727 10027342

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LENGTH</u>	<u>AA LENGTH</u>
7501880265	14426	36582	579	192

Description

6500733278 murb:hi0268 udp-n-acetylenolpyruvoylglucosamine
reductase:udp-n-acetylmuramate dehydrogenase (gtcfc:7.1:11.4) (ec:1.1.1.158)
(keggfc:4.4) (tigrfc:3.2) (db:gtc-haemophilus influenzae) HI0268 HI0268
Haemophilus influenzae 727 -11537136 84702 murb:hi0268 (ec:1.1.1.158)
(de:acetylmuramate dehydrogenase)) (db:swissprot) MURB_HAEIN P44605
HAEMOPHILUS INFLUENZAE 727 -11537136 157282 udp-n-acetylmuramate
dehydrogenase (cl:udp-n-acetylmuramate dehydrogenase) (ec:1.1.1.158)
(db:pir2.dat) G64058 G64058 Haemophilus influenzae 727 -11537136 7500886098
hi0268 udp-n-acetylenolpyruvoylglucosamine reductase (db:genpept-bct1)
(de:haemophilus influenzae rd section 28 of 163 of the complete genome.)
(nt:similar to sp:p08373 gb:l14557 gb:m10123 pid:145431) (1e:2426) (re:3451)
(di:direct) U32713 U32713 g1573234 Haemophilus influenzae Rd 71421 -11537136
5000694374 (de:(hi0268) (pn:udp-n- acetylmuramate
dehydrogenase:udp-n-acetylenolpyruvoylglucosamine reductase:murb) (gn:murb)
(gtcfc:7.1) (ec:1.1.1.158) (murb_haein) (keggfc:4.4) (tigrfc:3.2)
(db:gtc-haemophilus influenzae)) HI0268 HI0268 Haemophilus influenzae 727
10026893